```
Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENIILVDRTGHIKLVDF 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENIILVDRTGHIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSGVIAYEMIYGR 300
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYRLDCDWWSGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPPF 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPPF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy  481 ILPSVIAKGSARGRCWL 497
            |||||||||||||||||
Db  481 ILPSVIAKGSARGRCWL 497
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RESULT 5
US-10-262-511-4
; Sequence 4, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Bergha, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09

RESULT 4
US-10-311-034-7
; Sequence 7, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAN, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GRETHER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
US-10-311-034-7

; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2004023242A1 3951059CD1
US-10-311-034-7

Query Match   99.5%; Score 2589; DB 15; Length 497;
Best Local Similarity   99.6%; Pred. No. 4.9e-189;
Matches 495; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

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Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy  61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVREKATG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVREKATG 120
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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
;
SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-4

  Query Match             93.8%;   Score 2440;  DB 15;   Length 623;
  Best Local Similarity   99.6%;   Pred. No. 1.5e-177;
  Matches  466;   Conservative    2;   Mismatches    0;   Indels    0;   Gaps    0;

Qy      1  MLKFKYGARNPLDAGAEPIANRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE   60
           ||||||||||||||||||||||: ||||||||||||||||||||||||||||||||||
Db      5  MLKFKYGARNPLDAGAEPIASRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE   64

Qy     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  124

Qy    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  184

Qy    181  DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185  DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  244

Qy    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  304

Qy    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCHPFF  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCHPFF  364

Qy    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGFS  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGFS  424

Qy    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
           ||||||||||||||||||||||||||||||||||||||||||||||||:
Db    425  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM  472


RESULT 6
US-10-028-946-4
; Sequence 4, Application US/10028946
; Publication No. US2002123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
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; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-4

  Query Match             93.8%;   Score 2440;  DB 13;   Length 1958;
  Best Local Similarity   99.6%;   Pred. No. 6.3e-177;
  Matches  466;   Conservative    2;   Mismatches    0;   Indels    0;   Gaps    0;

Qy      1  MLKFKYGARNPLDAGAEPIANRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE   60
           ||||||||||||||||||||||: ||||||||||||||||||||||||||||||||||
Db      1  MLKFKYGARNPLDAGAEPIASRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE   60

Qy     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy    181  DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDF  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDF  240

Qy    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300

Qy    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCHPFF  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCHPFF  360

Qy    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGFS  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGFS  420

Qy    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
           ||||||||||||||||||||||||||||||||||||||||||||||:
Db    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM  468


RESULT 7
US-10-028-946-2
; Sequence 2, Application US/10028946
; Publication No. US2002123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

  Query Match             93.8%;   Score 2440;  DB 13;   Length 2054;
  Best Local Similarity   99.6%;   Pred. No. 6.7e-177;
  Matches  466;   Conservative    2;   Mismatches    0;   Indels    0;   Gaps    0;

Qy      1  MLKFKYGARNPLDAGAEPIANRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE   60
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Left column

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Db    1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
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RESULT 8
US-10-415-011-21
; Sequence 21, Application US/10415011
; Publication No. US2004005339A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION
;  APPLICANT: GURURAJAN, Rajagopal
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: ELLIOTT, Vicki S.
;  APPLICANT: XU, Yuming
;  APPLICANT: ARVIZU, Chandra S.
;  APPLICANT: YAO, Monique G.
;  APPLICANT: RAMKUMAR, Jayalaxmi
;  APPLICANT: DING, Li
;  APPLICANT: TANG, Y. Tom
;  APPLICANT: HAFALIA, April J.A.
;  APPLICANT: NGUYEN, Danniel B.
;  APPLICANT: GANDHI, Ameena R.
;  APPLICANT: LU, Yan
;  APPLICANT: YUE, Henry
;  APPLICANT: BURFORD, Neil
;  APPLICANT: BANDMAN, Olga
;  APPLICANT: TRIBOULEY, Catherine M.
;  APPLICANT: LAL, Preeti G.
;  APPLICANT: THANGAVELU, Kavitha
;  APPLICANT: KHAN, Farrah A.
;  APPLICANT: RECIPON, Shirley A.
;  APPLICANT: LU, Dyung Aina M.
;  APPLICANT: BOROWSKY, Mark L.
;  APPLICANT: THORNTON, Michael B.
;  APPLICANT: SWARNAKER Anita
;  APPLICANT: ISON, Craig H.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0262 USN
;  CURRENT APPLICATION NUMBER: US/10/415,011
;  CURRENT FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: PCT/US01/47728
;  PRIOR FILING DATE: 2001-10-20
;  PRIOR APPLICATION NUMBER: US 60/242,410
;  PRIOR FILING DATE: 2000-10-20
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Right column

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;  PRIOR APPLICATION NUMBER: US 60/244,068
;  PRIOR APPLICATION FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: US 60/245,708
;  PRIOR APPLICATION FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/247,672
;  PRIOR APPLICATION FILING DATE: 2000-11-09
;  PRIOR APPLICATION NUMBER: US 60/249,565
;  PRIOR APPLICATION FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: US 60/252,730
;  PRIOR APPLICATION FILING DATE: 2000-11-22
;  PRIOR APPLICATION NUMBER: US 60/250,807
;  PRIOR APPLICATION FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PERL Program
; SEQ ID NO 21
;   LENGTH: 2054
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US2004005339A1 7484498CD1
US-10-415-011-21

  Query Match             93.8%;   Score 2440;  DB 15;  Length 2054;
  Best Local Similarity   99.6%;   Pred. No. 6.7e-177;
  Matches  466;  Conservative  2;  Mismatches  2;  Indels  0;  Gaps  0;

Qy    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60
        |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db    1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
        |||||||||||||||||||||||||||||||||||||||||||||||:
Db  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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```
RESULT 9
US-10-017-216-2
; Sequence 2, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
;  TITLE OF INVENTION: Kinase and Uses Therefor
;  FILE REFERENCE: 10147-57U1
;  CURRENT APPLICATION NUMBER: US/10/017,216
;  CURRENT FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 60/242,429
;  PRIOR FILING DATE: 2000-10-23
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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-216-2

Query Match     93.4%;  Score 2430;  DB 13;  Length 2053;
Best Local Similarity   99.1%;  Pred. No. 3.9e-176;
Matches  464;  Conservative  3;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 MLKFKYGARNPLDAGAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db    1 MLKFKYGARNPLDAGAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLMEEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
          |||||||||||||||||||||||||||||||||||||||||||||||:
Db  421 YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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RESULT 10
US-10-325-430-12
; Sequence 12, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPI01-294P1RNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-325-430-12

Query Match     93.4%;  Score 2430;  DB 14;  Length 2053;
Best Local Similarity   99.1%;  Pred. No. 3.9e-176;
Matches  464;  Conservative  3;  Mismatches  1;  Indels  0;  Gaps  0;
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RESULT 11
US-10-757-262-52
; Sequence 52, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1641,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
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Qy    1 MLKFKYGARNPLDAGAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db    1 MLKFKYGARNPLDAGAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLMEEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
          |||||||||||||||||||||||||||||||||||||||||||||||:
Db  421 YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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;   PRIOR FILING DATE: 2003-09-26
;   NUMBER OF SEQ ID NOS: 136
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 52
;   LENGTH: 2053
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-757-262-52

Query Match           93.4%;   Score 2430;   DB 16;   Length 2053;
Best Local Similarity 99.1%;   Pred. No. 3.9e-176;
Matches  464; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

Qy    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          |||||||||||||||| : |||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFPEVYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKAT 119

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  120 GDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPG 179

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db  121 GDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPG 180

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVD 239

Qy  301 SPFAEGTSARTFNNIMNFQRFLKPFDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  240 FGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYG 299

Qy  361 SKIDWNNIRNSPPPPVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGFS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 FGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMYG 300

Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
          ||||||||||||||||||||||||||||||||||||||||||||
Db  301 RSPFAEGTSARTFNNIMNFQRFLKPFDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPF 359
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Db  301 RSPFAEGTSARTFNNIMNFQRFLKPFDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPF 360

Db  360 FSKIDWNNIRNSPPPPVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGF 419

Db  361 FSKIDWNNIRNSPPPPVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGGEELPFVGF 420

Db  420 SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

Db  421 SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 469
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RESULT 12
US-10-618-941-67
;   Sequence 67, Application US/10618941
;   Publication No. US2004019792A1
;   GENERAL INFORMATION:
;   APPLICANT: WHYTE, DAVID
;   APPLICANT: MANNING, GERARD
;   APPLICANT: CAENEPEEL, SEAN
;   TITLE OF INVENTION: NOVEL KINASES
;   FILE REFERENCE: 034536-0321
;   CURRENT APPLICATION NUMBER: US/10/618,941
;   CURRENT FILING DATE: 2003-07-15
;   PRIOR APPLICATION NUMBER: 60/395,632
;   PRIOR FILING DATE: 2002-07-15
;   NUMBER OF SEQ ID NOS: 143
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 67
;   LENGTH: 2055
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-618-941-67

Query Match   92.9%;   Score 2418.5;   DB 16;   Length 2055;
Best Local Similarity 98.9%;   Pred. No. 2.9e-175;
Matches 464; Conservative   3; Mismatches   3; Indels   1; Gaps   1;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

RESULT 13
US-09-964-956-11
;   Sequence 11, Application US/09964956
;   Publication No. US20040043926A1
;   GENERAL INFORMATION:
;   APPLICANT: Gerlach, Valerie L
;   APPLICANT: MacDougall, John R
;   APPLICANT: Smithson, Glennda
;   APPLICANT: Millet, Isabelle
;   APPLICANT: Stone, David
;   APPLICANT: Gunther, Erik
;   APPLICANT: Ellerman, Karen
;   APPLICANT: Grosse, William M
;   APPLICANT: Alsobrook II, John P
;   APPLICANT: Lepley, Denise M
;   APPLICANT: Burgess, Catherine E
;   APPLICANT: Padigaru, Muralidhara
;   APPLICANT: Kekuda, Ramesh
;   APPLICANT: Spytek, Kimberly A
;   APPLICANT: Leach, Martin D
;   APPLICANT: Shimkets, Richard A
;   TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
;   FILE REFERENCE: 21402-124
;   CURRENT APPLICATION NUMBER: US/09/964,956
;   CURRENT FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 60/235,631
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/235,633
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/235,808
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,064
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,065
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,066
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,135
;   PRIOR FILING DATE: 2000-09-28
;   PRIOR APPLICATION NUMBER: 60/237,434
;   PRIOR FILING DATE: 2000-10-03

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;  PRIOR APPLICATION NUMBER: 60/238,321
;  PRIOR FILING DATE: 2000-10-05
;  PRIOR APPLICATION NUMBER: 60/238,399
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 60/238,396
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 60/276,667
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/294,823
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/304,868
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 11
;  LENGTH: 2053
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-964-956-11

Query Match        92.7%;  Score 2412.5;  DB 11;  Length 2053;
Best Local Similarity  98.9%;  Pred. No. 8.4e-175;
Matches  463;  Conservative  3;  Mismatches  3;  Indels  1;  Gaps  1;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE  60
          |||||||||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db     1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE  60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    61  ECSQPALMKIKHVSNFVRKCSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy   181  DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GSAAKMNSNK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  299

Qy   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF  359

Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
          ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db   360  SKIDWNNIRNAPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  419

Qy   421  YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
          ||||||||||||||||||||||||||||||||||||||||||||||||:
Db   420  YSKALGILGRSESSVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM  467

RESULT 14
US-10-262-511-2
; Sequence 2, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
;  APPLICANT: Smithson, Glennda
;  APPLICANT: Millet, Isabelle
;  APPLICANT: Peyman, John A.
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT: Ju, Jingfang
;  APPLICANT: Li, Li
;  APPLICANT: Guo, Xiaolia (Sasha)
;  APPLICANT: Paturajan, Meera
;  APPLICANT: Spytek, Kimberly A.
;  APPLICANT: Edinger, Shlomit R.
;  APPLICANT: Ellerman, Karen
```

```
;  APPLICANT: Malyankar, Uriel M.
;  APPLICANT: Ort, Tatiana
;  APPLICANT: Gorman, Linda
;  APPLICANT: Zerhusen, Bryan D.
;  APPLICANT: Anderson, David W.
;  APPLICANT: Zhong, Mei
;  APPLICANT: Catterton, Elina
;  APPLICANT: Ji, Weizhen
;  APPLICANT: Miller, Charles E.
;  APPLICANT: Rastelli, Luca
;  APPLICANT: Stone, David J.
;  APPLICANT: Pena, Carol E. A.
;  APPLICANT: Shenoy, Suresh G.
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT: Rothenberg, Mark E.
;  APPLICANT: Leach, Martin D.
;  APPLICANT: Agee, Michele L.
;  APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
;  PRIOR APPLICATION NUMBER: 60/326,483
;  PRIOR APPLICATION DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: 60/373,815
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 60/327,917
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/381,642
;  PRIOR FILING DATE: 2002-05-17
;  PRIOR APPLICATION NUMBER: 60/328,029
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: 60/381,038
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/328,056
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/373,260
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/373,826
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 60/327,435
;  PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-2

Query Match        92.7%;  Score 2412.5;  DB 15;  Length 2053;
Best Local Similarity  98.9%;  Pred. No. 8.4e-175;
Matches  463;  Conservative  3;  Mismatches  3;  Indels  1;  Gaps  1;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE  60
          |||||||||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db     1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE  60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    61  ECSQPALMKIKHVSNFVRKCSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

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;      ORGANISM: Homo sapiens
US-09-964-956-9

Query Match             92.7%;  Score 2412.5;  DB 11;  Length 2066;
Best Local Similarity   98.9%;  Pred. No. 8.5e-175;
Matches  463;  Conservative  3;  Mismatches  1;  Indels  1;  Gaps  1;

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Db     1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60

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Qy   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
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Db   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300
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Qy   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
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Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
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Qy   421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
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Job time : 148 secs
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Qy   421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
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RESULT 15
US-09-964-956-9
; Sequence 9, Application US/09964956
; Publication No. US2004043926A1
; GENERAL INFORMATION:
;  APPLICANT: Gerlach, Valerie L
;  APPLICANT: MacDougall, John R
;  APPLICANT: Smithson, Glennda
;  APPLICANT: Millet, Isabelle
;  APPLICANT: Stone, David
;  APPLICANT: Gunther, Erik
;  APPLICANT: Ellerman, Karen
;  APPLICANT: Grosse, William M
;  APPLICANT: Alsobrook II, John P
;  APPLICANT: Lepley, Denise M
;  APPLICANT: Burgess, Catherine E
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT: Leach, Martin D
;  APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: No. US2004043926A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 9
;  LENGTH: 2066
;  TYPE: PRT
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                GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    March 18, 2005, 15:31:31 ; Search time 44 Seconds
                                       (without alignments)
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Title:         US-10-724-594-2
Perfect score: 2602
Sequence:      1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497

Scoring table: BLOSUM62
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Searched:      513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:   513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	2602	100.0	497	4	US-09-804-471A-2	Sequence 2, Appli
2	2602	100.0	497	4	US-10-238-709-2	Sequence 2, Appli
3	2440	93.8	1958	4	US-10-028-946-4	Sequence 4, Appli
4	2440	93.8	2054	4	US-10-028-946-2	Sequence 2, Appli
5	2271.5	87.3	494	4	US-09-804-471A-4	Sequence 4, Appli
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7	1284	49.3	257	4	US-09-916-204-2	Sequence 2, Appli
8	1284	49.3	257	4	US-10-282-048-2	Sequence 2, Appli
9	1180	45.3	251	4	US-09-916-204-4	Sequence 4, Appli
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11	1177	45.2	251	4	US-09-916-204-5	Sequence 5, Appli
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16	865	33.2	1388	2	US-08-685-576-4	Sequence 4, Appli
17	865	33.2	1354	2	US-09-976-532-296	Sequence 296, App
18	864.5	33.2	1388	3	US-08-685-871-2	Sequence 2, Appli
19	860.5	33.1	1388	3	US-08-685-576-1	Sequence 1, Appli
20	857.5	33.0	420	3	US-08-685-871-58	Sequence 58, Appl
21	840.5	32.3	420	3	US-08-685-871-59	Sequence 59, Appl
22	828	31.8	582	2	US-08-422-699A-9	Sequence 9, Appli
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24	790.5	30.4	900	2	US-08-630-822A-62	Sequence 62, Appl
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26	790.5	30.4	900	3	US-09-171-156A-21	Sequence 21, Appl
27	790.5	30.4	900	4	US-09-004-730A-21	Sequence 21, Appl
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29	771.5	29.7	638	2	US-08-422-699A-11	Sequence 11, Appl
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35	701	26.9	526	3	US-09-442-100-12	Sequence 12, Appli
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39	683	26.2	404	3	US-08-860-150-3	Sequence 3, Appli
40	683	26.2	404	3	US-09-338-132-3	Sequence 3, Appli
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43	674.5	25.9	465	2	US-08-878-989-18	Sequence 18, Appl
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                             ALIGNMENTS

RESULT 1
US-09-804-471A-2
; Sequence 2, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 497
;  TYPE: PRT
;  ORGANISM: Human
US-09-804-471A-2

Query Match           100.0%;    Score 2602;  DB 4;  Length 497;
Best Local Similarity 100.0%;    Pred. No. 1.5e-242;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPMTQQOMSPLSREGILDALFVLFE  60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
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Db    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
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Qy   181  DLLSLLNRYEDQLDENLIQFYLAELLIAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
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RESULT 2
US-10-238-709-2
; Sequence 2, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-10-238-709-2

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Query Match            100.0%;   Score 2602;   DB 4;   Length 497;
Best Local Similarity  100.0%;   Pred. No. 1.5e-242;
Matches  497;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 MLKFKFYGARNPLDAGAAEPIANRASRINLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
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Db     1 MLKFKFYGARNPLDAGAAEPIANRASRINLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy    61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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Qy   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
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Db   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300
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Db   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF 360
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Db   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF 360

Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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Db   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
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Db   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy   481 ILPSVYAKGSARGRCWL 497
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Db   481 ILPSVYAKGSARGRCWL 497
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RESULT 3

US-10-028-946-4
; Sequence 4, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-4

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Query Match            93.8%;   Score 2440;   DB 4;   Length 1958;
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Qy    61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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Qy   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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Db   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
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Db   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300
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Db   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFPEGLCCHPFF 360

Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
         |||||||||||||||||||||||||||||||||||||||||||||||:
Db   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
```

RESULT 4
US-10-028-946-2
; Sequence 2, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

Query Match    93.8%;  Score 2440; DB 4;  Length 2054;
Best Local Similarity  99.6%;  Pred. No. 5.7e-226;
Matches 466;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPPMTQQMSPLSREGILDALFVLFE 60
        |||||||||||||||||||||  :||||||||||||||||||||||||||||||||||||
Db    1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPPMTQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
        |||||||||||||||||||||||||||||||||||||||||||||:
Db  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468


RESULT 5
US-09-804-471A-4
; Sequence 4, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-804-471A-4

Query Match    87.3%;  Score 2271.5; DB 4;  Length 494;
Best Local Similarity  87.3%;  Pred. No. 1.2e-210;
Matches 432;  Conservative 27;  Mismatches 35;  Indels 1;  Gaps 1;

Qy    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPPMTQQMSPLSREGILDALFVLFE 60
        ||||||| :| :  :||||||||||||||||||| |||||: :|  |||||  ||||:||
Db    1 MLKFKYGVRNPPEASASEPIASRASRLNLFFQGKPPLMTQQQMSALSREGMLDALFALFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
```

```
Db   61 ECSQPALMKMKHVSSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |:||||:|||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        | |||||||||||||::||||||||| ||||||  ||||||||||||| ||||| |||||
Db  181 DFLSLLNRYEDQLDESMIQFYLAELLIAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300
        |||||||||| :||||||||||||||||||||| :| :|||||||||||||||:||| | :
Db  241 GSAAKMNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRGTYGLDCDWWSVGVVAYEMVGK 299

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
        :||:||||||||||||||||||||||||||||: ||| ||||| ||||||||||||||||
Db  300 TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF 359

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
        : :||||||||||||||||||||||||||||||||||   : : :  | :|||||||||
Db  360 ARTDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPABPLAFSGEELPFVGFS 419

Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
        ||||||:|||||||||:|||||| |||||||||||||||||||||||| ||:|||| ||
Db  420 YSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKVSISTAGLRPCSR 479

Qy  481 ILPSVTAKGSARGRC 495
        || |:  :|||  :|
Db  480 ILQSIYAEGSAGGHC 494


RESULT 6
US-10-238-709-4
; Sequence 4, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-238-709-4

Query Match    87.3%;  Score 2271.5; DB 4;  Length 494;
Best Local Similarity  87.3%;  Pred. No. 1.2e-210;
Matches 432;  Conservative 27;  Mismatches 35;  Indels 1;  Gaps 1;

Qy    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPPMTQQMSPLSREGILDALFVLFE 60
        ||||||| :| :  :||||||||||||||||||| |||||: :| |||||  ||||:||
Db    1 MLKFKYGVRNPPEASASEPIASRASRLNLFFQGKPPLMTQQQMSALSREGMDALFALFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||| |||||  || ||||||| |||||| |||||||||||||||||||||||||
Db   61 ECSQPALMKMKHVSSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |:||||:|||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        | |||||||||||||::||||||||| ||||||  ||||||||||||| ||||| |||||
Db  181 DFLSLLNRYEDQLDESMIQFYLAELLIAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Qy  241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGKGTYGLDCDWWSVGVIAYEMIYGR 300
```

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Db  241  GSAAKMNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVGVVAYEMVYGK  299
          |||||||||    :||||||                :|||||||||||||||   |||:||:
Qy  301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSFDLDIQSLLCGQKERLKFEGLCCHPFF  360
          :||:|||||||||||||||||||||||||||:||:|||||||:|||:||||||||||||
Db  300  TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF  359

Qy  361  SKIDWNNIRNSPPPFVPTLKGDDDTSNFDEPEKNSWVSSSPCQLSPSGPSGEELPFVGFS  420
          ::  ||||||||:||||||||||||||||||||||||||      ||||||||||||||
Db  360  ARTDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPAEPLAFSGEELPFVGFS  419

Qy  421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR  480
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||  |||||
Db  420  YSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKVSISTAGLRPCSR  479

Qy  481  ILPSVYAKGSARGRC  495
          || :|:|:||| |||
Db  480  ILQSIYAEGSAGGHC  494
```

RESULT 7
US-09-916-204-2
; Sequence 2, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL00l164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-09-916-204-2

Query Match   49.3%;   Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%;   Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy    1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
          |||||||||||                |||||||||||||||||||||||||||||||||
Db    1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60

Qy   61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy  121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy  181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy  241  GSAAKMNSNKMV  252
          ||||||||||||
Db  241  GSAAKMNSNKMV  252
```

RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL00l164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2

Query Match   49.3%;   Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%;   Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy    1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
          |||||||||||                |||||||||||||||||||||||||||||||||
Db    1  MLKFKYGARNPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE          60

Qy   61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy  121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy  181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy  241  GSAAKMNSNKMV  252
          ||||||||||||
Db  241  GSAAKMNSNKMV  252
```

RESULT 9
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL00l164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-916-204-4

Query Match   45.3%;   Score 1180; DB 4; Length 251;
Best Local Similarity 90.4%;   Pred. No. 1.2e-105;
Matches 227; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

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Qy    1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
          |||||||||:||                |||||:||||:||||||||||:|||||||:||
Db    1  MLKFKYGVRNPSEASAPEPIASRASRLNLFFQGKPPLMTQQQMSALSREGVLDALFVLLE   60

Qy   61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          |||||||||||||||:|||||||||||||:||||:||:||||||||||||||||||||||
Db   61  ECSQPALMKIKHVSSFVRKYSDTIAELRELQPSVRDFEVRSLVGCGHFAEVQVVREKATG  120

Qy  121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          |:|||||:|||||:|||||||||||||:|||||||||||||||:||||||||||||||||
Db  121  DVYAMKIMKKAALRAQEQVSFFEEERNILSQSTSPWIPQLQYAFQDKNNLYLVMEYQPGG  180
```

```
Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        |||||||||||||:||::|||||||||||||||| ||||||||||||||:|||||||||||
Db 181 DLLSLLNRYEDQLDENMIQFYLAELLLAVHSVHQMGYVHRDIKPENILIDRTGHIKLVDF 240

Qy 241 GSAAKMNSNKM 251
        ||||||||:||
Db 241 GSAAKMNSNKV 251
```

RESULT 10
US-10-282-048-4
; Sequence 4, Application US/10282048
; Patent No. 692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-282-048-4

```
Query Match   45.3%;   Score 1180;  DB 4;  Length 251;
Best Local Similarity   90.4%;   Pred. No. 1.2e-105;
Matches 227;  Conservative 13;  Mismatches 11;  Indels 0;  Gaps 0;

Qy   1 MLKFKYGARNPLDAGAEPIANRASRINLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60
        ||||||| ||| :| |:||||:|||||||||||| :|:||||||||||| |||||| |:
Db   1 MLKFKYGVRNPSEASAPEPIASRASRINLFFQGKPPLMTQQQMSALSREGVLDALFVLLE 60

Qy  61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||||||||| ||||||||||||:||||||:|||||||||||||||||||||||||
Db  61 ECSQPALMKIKHVSSFVRKYSDTIAELRELQPSVRDFEVRSLVGCGHFAEVQVVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |:|||:|||| || ||||||||||||||||::|||||||||||||||:|:||||||||||
Db 121 DVYAMKIMKKAALRAQEQVSFFEEERNILSQSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        |||||||||||||:||::|||||||||||||||| ||||||||||||||:||||||||||
Db 181 DLLSLLNRYEDQLDENMIQFYLAELLLAVHSVHQMGYVHRDIKPENILIDRTGHIKLVDF 240

Qy 241 GSAAKMNSNKM 251
        ||||||||:||
Db 241 GSAAKMNSNKV 251
```

RESULT 11
US-09-916-204-5
; Sequence 5, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-916-204-5

```
Query Match   45.2%;   Score 1177;  DB 4;  Length 251;
Best Local Similarity   90.0%;   Pred. No. 2.4e-105;
Matches 226;  Conservative 16;  Mismatches 9;  Indels 0;  Gaps 0;

Qy   1 MLKFKYGARNPLDAGAEPIANRASRINLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60
        ||||||| ||| :| |:||||:|||||||||||| :|:||||||||||:|||||| |||
Db   1 MLKFKYGVRNPPEASASEPIASRASRINLFFQGKPPLMTQQQMSALSREGMLDALFALFE 60

Qy  61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||| :||| ||:||||||||||:||||||:|||||||||||||||||||||||||
Db  61 ECSQPALMKMGHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |:|||:|||||||||||||||||||||||||||||||||||||||||:|:||||||||||
Db 121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        ||||||||||||||::||:|||||||||||||| |||||||||||||||:||||:||||||
Db 181 DFLSLLNRYEDQLDESMIQFYLAELLLAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Qy 241 GSAAKMNSNKM 251
        ||||||||:||
Db 241 GSAAKMNSNKV 251
```

RESULT 12
US-09-916-204-6
; Sequence 6, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-916-204-6

```
Query Match   45.2%;   Score 1177;  DB 4;  Length 251;
Best Local Similarity   90.0%;   Pred. No. 2.4e-105;
Matches 226;  Conservative 16;  Mismatches 9;  Indels 0;  Gaps 0;

Qy   1 MLKFKYGARNPLDAGAEPIANRASRINLFFQGKPPMTQQQMSPLSREGILDALFVLFE 60
        ||||||| ||| :| |:||||:|||||||||||| :|:||||||||||:|||||| |||
Db   1 MLKFKYGVRNPPEASASEPIASRASRINLFFQGKPPLMTQQQMSALSREGMLDALFALFE 60

Qy  61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        |||||||| :||| ||:||||||||||:||||||:|||||||||||||||||||||||||
Db  61 ECSQPALMKMGHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        |:|||:|||||||||||||||||||||||||||||||||||||||||:|:||||||||||
Db 121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        ||||||||||||||::||:|||||||||||||| |||||||||||||||:||||:||||||
Db 181 DFLSLLNRYEDQLDESMIQFYLAELLLAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Qy 241 GSAAKMNSNKM 251
        ||||||||:||
Db 241 GSAAKMNSNKV 251
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RESULT 13
US-10-282-048-5

; Sequence 5, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-5

Query Match   45.2%;   Score 1177;   DB 4;   Length 251;
Best Local Similarity 90.0%;   Pred. No. 2.4e-105;
Matches 226;   Conservative 16;   Mismatches 16;   Indels 9;   Gaps 0;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
            |||||| ||| :||:|||||:|||||| ||||||:||||||||:|||||:|||| |||
Db   1 MLKFKYGVRNPPEASASEPIASRASRLNLFQGKPPLMTQQQMSALSREGMLDALFALFE   60

Qy   61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG   120
            ||||||||:|||||::||||||||||:|||||||:|||||||||||||||||||||||
Db   61 ECSQPALMKMKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG   120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG   180
            |:||||:|||||||||||||||||||||||||||||||||||||||:||||||||||||
Db 121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG   180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF   240
            | |||||||||||||:::|||||||||||||| ||||||||||||||||:|||:|||||
Db 181 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF   240

Qy 241 GSAAKMNSNKM   251
            ||||||||:
Db 241 GSAAKMNSNKV   251

RESULT 14
US-10-282-048-6
; Sequence 6, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-6

Query Match   45.2%;   Score 1177;   DB 4;   Length 251;
Best Local Similarity 90.0%;   Pred. No. 2.4e-105;
Matches 226;   Conservative 16;   Mismatches 16;   Indels 9;   Gaps 0;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
            |||||| ||| :||:|||||:|||||| ||||||:||||||||:|||||:|||| |||
Db   1 MLKFKYGVRNPPEASASEPIASRASRLNLFQGKPPLMTQQQMSALSREGMLDALFALFE   60

Qy   61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG   120
            ||||||||:|||||::||||||||||:|||||||:|||||||||||||||||||||||

Db   61 ECSQPALMKMKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG   120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG   180
            |:||||:|||||||||||||||||||||||||||||||||||||||:||||||||||||
Db 121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG   180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF   240
            | |||||||||||||:::|||||||||||||| ||||||||||||||||:|||:|||||
Db 181 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF   240

Qy 241 GSAAKMNSNKM   251
            ||||||||:
Db 241 GSAAKMNSNKV   251

RESULT 15
US-09-949-016-8511
; Sequence 8511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8511
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8511

Query Match   34.4%;   Score 894.5;   DB 4;   Length 509;
Best Local Similarity 38.8%;   Pred. No. 1.4e-77;
Matches 187;   Conservative 93;   Mismatches 145;   Indels 57;   Gaps 9;

Qy   31 FQGKP----------------------PFMTQQQMSPLSREGILDALFVLFEECSQPAL   67
            ||||| : :: |||: :||| || ::| ::|:|
Db   1 FKGKPAEIEANMSGBVRLRQLEQFILDGPAQTNGQC--FSVETLLDLILCLYDECNNSPL   58

Qy   68 MKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKV   127
            | : |||||: :: ||||| ||||||||| :|||||||::|||
Db   59 RREKNILEYLEWAKPFTSKVKQMRLHREDFEILKVIGRGAFGEVAVVKLKNADKVFAMKI   118

Qy 128 MKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLN   187
            :| :|:|: :||||||| || | | ||:|| ||::|||::||||| ::|:|:
Db 119 LNKWEMLKRASTACFREERDVLVNGDNKWITTLHYAFQDDNNLYLVMDYYVGGDLLTLLS   178

Qy 188 RYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMN   247
            |:|||| :||:|| :|:| || :| |||||||||||||| :| ||::||||| ::|
Db 179 KFEDRLPEDMARFYLAEMVIAIDSVHQLHYVHRDIKPDNILMDMNGHIRLADFGSCLKLM   238

Qy 248 SNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWSVGVIAYEMIYGRSPPFAEGT   307
            :   :: : | | | : : | | :| | | ||::| ::: | | |
Db 239 EDGTVQSSVAVGTPDYISPEILQAME-DGKGRYGPSCDWWSLGVCMYEMLYGETPFYAES   297

Qy 308 SARTFNNIMNFQRFLKPDD-PKVSSDFLDLIQSLLCGQKERLKFFGL---CCHPFFSKI   363
            . |:: ::| | :: |:   :| : :|:: | ::|||:|
Db 298 LVETYGKIMNHKERFQFPAQVTDVSENAKDLIRRLICSREHRLGQNGIEDFKKHPFFSGI   357

Qy 364 DWNIRNSPPFVPTLKSDDDTSNFDEPE---KNSWVSSSPCQLSPSGFSGEELPFVGFS   420
            ||::|: ::: ||| | ||: | :: :::|: | :: || |
Db 358 DWDNIRNCEAPYIPEVSSPTDTSNFDVDDCLKNSETMPPP---THTAFSGHHLPFVGFT   414

Qy 421 YSKALGILGRS----------------------ESVVSGLDSPAKTSSMEKKL-------LIKSKELQ   459

```
Db   415 YTSSCVLSDRSCLRVTAGPTSLDLDVNVQRTLDNNLATEAYERRIKRLEQEKLELSRKLQ 474
         |::: :: ||      :|   ||: |:  |:::        |  | |::||
Qy   460 DS 461
         :|
Db   475 ES 476
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Search completed: March 18, 2005, 15:41:38
Job time : 45 secs

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                GenCore version 5.1.6
        .Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    March 18, 2005, 15:22:34 ; Search time 174 Seconds
                                       (without alignments)
                           1462.663 Million cell updates/sec

Title:       US-10-724-594-2
Perfect score: 2602
Sequence:    1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:      1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt 03:*
             1: uniprot_sprot:*
             2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	2440	93.8	2027	2	Q86UQ9	Q86uq9 homo sapien
2	2425	93.2	482	2	Q6XUH8	Q6xuh8 homo sapien
3	2271.5	87.3	494	2	O88937	O88937 mus musculu
4	2172.5	83.5	2055	2	O88938	O88938 mus musculu
5	2157.5	82.9	448	2	O88527	O88527 rattus norv
6	929	35.7	717	2	Q8AVM0	Q8avm0 xenopus lae
7	929	35.7	1551	2	Q6DT37	Q6dt37 homo sapien
8	922	35.4	1854	2	Q9VTY8	Q9vty8 drosophila
9	897.5	34.5	1592	2	O01583	O01583 caenorhabdi
10	896.5	34.5	492	2	Q86XZ8	Q86xz8 homo sapien
11	896.5	34.5	933	2	Q86TJ1	Q86tj1 homo sapien
12	896.5	34.5	1711	2	Q9YSS2	Q9yss2 homo sapien
13	896.5	34.5	1760	2	Q9ULU5	Q9ulu5 homo sapien
14	891	34.2	496	2	Q99646	Q99646 homo sapien
15	891	34.2	1573	2	Q7PV87	Q7pv87 anopheles g
16	891	34.2	1638	2	Q86XX2	Q86xx2 homo sapien
17	891	34.2	1719	2	Q86XX3	Q86xx3 homo sapien
18	891	34.2	1732	2	O54874	O54874 rattus norv
19	890	34.2	1638	2	Q8IWQ7	Q8iwq7 homo sapien
20	883	33.9	1702	2	O54875	O54875 rattus norv
21	883	33.9	1713	2	Q7TT49	Q7tt49 rattus norv
22	880	33.8	1713	2	Q7TT50	Q7tt50 mus musculu
23	876.5	33.7	1173	2	P92199	P92199 caenorhabdi
24	874	33.6	1375	2	O73732	O73732 xenopus lae
25	867	33.3	1375	2	Q90Y37	Q90y37 brachydanio
26	866.5	33.3	1354	1	ROC1_MOUSE	P70335 mus musculu
27	865	33.2	1388	1	ROC2_HUMAN	O75116 homo sapien
28	864.5	33.2	1354	1	ROC1_HUMAN	Q13464 homo sapien
29	862.5	33.1	1369	1	ROC1_RAT	Q63644 rattus norv
30	862.5	33.1	1354	1	ROC1_RABIT	O77819 o rho-assoc
31	860.5	33.1	1388	1	ROC2_BOVIN	Q28021 bos taurus
32	857.5	33.0	629	2	Q6P5Z6	Q6p5z6 homo sapien
33	857.5	33.0	1613	2	O44368	O44368 drosophila
34	857.5	32.8	1637	2	Q9W1B0	Q9w1b0 drosophila
35	853.5	32.8	1388	1	ROC2_MOUSE	P70336 mus musculu
36	847	32.6	631	1	DMK_MOUSE	P54265 mus musculu
37	837.5	31.6	1379	1	ROC2_RAT	Q62868 rattus norv
38	822.5	31.6	639	1	DMK_HUMAN	Q09013 homo sapien
39	809	31.1	1390	2	Q961D4	Q961d4 drosophila
40	809	31.1	1390	2	Q9U779	Q9u779 drosophila
41	809	31.1	1390	2	Q9VXE3	Q9vxe3 drosophila
42	778.5	29.9	865	2	Q98SN6	Q98sn6 gallus gall
43	763.5	29.3	289	2	O00565	O00565 homo sapien
44	763	29.3	605	2	Q6DI71	Q6di71 mus musculu
45	732.5	28.2	556	2	Q6L535	Q6l535 oryza sativ

ALIGNMENTS

```
RESULT 1
Q86UQ9
ID   Q86UQ9          PRELIMINARY;       PRT;    2027 AA.
AC   Q86UQ9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rho/rac-interacting citron kinase.
GN   Name=CIT;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AY257469; AAP13528.1; -.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR005479; Cphp_synth_L_D2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR000861; REM_repeat.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00130; C1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00867; CPASE_2; UNKNOWN_1; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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Left column

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DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   2027 AA;  231429 MW;  6B1D8C3F661F357B CRC64;

Query Match             93.8%;  Score 2440;  DB 2;  Length 2027;
Best Local Similarity   99.6%;  Pred. No. 5.7e-153;
Matches  466;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
          ||||||||||||||||||||||||||||||||||||||||||||||| :
Db    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 2
Q6XUH8
ID   Q6XUH8          PRELIMINARY;       PRT;   482 AA.
AC   Q6XUH8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Citron Rho-interacting kinase short form.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mao Y., Xie Y., Wu Q.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY209000; AAP43922.1; -.
DR   HSSP; P05132; 1ATP.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
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Right column

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DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   482 AA;  54353 MW;  4F02AF6A32C73BAE CRC64;

Query Match             93.2%;  Score 2425;  DB 2;  Length 482;
Best Local Similarity   98.9%;  Pred. No. 9.2e-153;
Matches  463;  Conservative   3;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          ||||||||||||| |||||||:||||||||||||||||||||||||||||||||||:|||||
Db      1 MLKFKYGARNPSDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALLVLFE 60

Qy     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYLHRDIKPENILVDRTGHIKLVDF 240

Qy    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
          |||||||||||||||||||||||||||||||||||||||||||||||:
Db    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 3
O88937
ID   O88937          PRELIMINARY;       PRT;   494 AA.
AC   O88937;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rho/rac-interacting citron kinase short isoform.
GN   Name=Cit; Synonyms=Crik-sk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;
RA   Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,
RA   Dotto G.P.;
RT   "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase
RT   encompassing the Rho-Rac-binding protein Citron.";
RL   J. Biol. Chem. 273:29706-29711(1998).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AF086823; AAC72822.1; -.
DR   HSSP; P31751; 1MRV.
DR   MGD; MGI:105313; Cit.
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DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase_C; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   494 AA; 55742 MW; 2C60D2294B28A185 CRC64;

Query Match   87.3%; Score 2271.5; DB 2; Length 494;
Best Local Similarity   87.3%; Pred. No. 1.5e-142;
Matches 432; Conservative   27; Mismatches   35; Indels   1; Gaps   1;

Qy   1 MLKFKFYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
              |||||||||| :||||| :|:||||||||||||||||||||||| ||||| |||||||| ||
Db   1 MLKFKFYGVRNPPEASASEPIASRASRLNLFFQGKPPLMTQQQMSALSREGMLDALFALFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
              ||||||||||:|||| ||:|||||||||:|||||| |||||||||||||||||||||||||
Db   61 ECSQPALMKMKGHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
              |:|||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
              | ||||||||||||:|:||||||||||||||||||:|||||:||||||||||:|:|||||
Db   181 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
              ||||||||: |:|||||||||||||||||||||:| |:|||||||||||||| ||||:|:
Db   241 GSAAKMNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVGVVAYEMVYGK 299

Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
              :|||||||||||||||||||||||||||||:|||||||:|||:|| ||||||||||||||
Db   300 TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF 359

Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
              ::||||||||||||||||||||||||||||||||| |||||| : |||||||||||||||
Db   360 ARTDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPAPLAFSGEELPFVGFS 419

Qy   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
              |||||| ||||||||||||| ||:|||||||||||||||||||||||||||||||| ||:
Db   420 YSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKVSISTAGLLRPCSR 479

Qy   481 ILPSVYAKGSARGRC 495
              |||:||:||||:|:|
Db   480 ILQSIYAEGSAGGHC 494

RESULT 4
O88938
ID   O88938   PRELIMINARY;   PRT; 2055 AA.
AC   O88938;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rho/rac-interacting citron kinase.
GN   Name=Cit; Synonyms=Crik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;
RA   Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,
RA   Dotto G.P.;
RT   "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase
RT   encompassing the Rho-Rac-binding protein Citron.";
RL   J. Biol. Chem. 273:29706-29711(1998).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AF086824; AAC72823.1; -.
DR   HSSP; P31751; 1MRV.
DR   MGD; MGI:105313; Cit.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR005479; Cphp_synth_L_D2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR000861; REM_repeat.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR000533; Tropomyosin.
DR   Pfam; PF00130; C1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   PRINTS; PR00194; TROPOMYOSIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   2055 AA; 235480 MW; 2120CB5E454DA940 CRC64;

Query Match   83.5%; Score 2172.5; DB 2; Length 2055;
Best Local Similarity   88.0%; Pred. No. 3.3e-135;
Matches 412; Conservative   26; Mismatches   29; Indels   1; Gaps   1;

Qy   1 MLKFKFYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
              |||||||||| :||||| :|:||||||||||||||||||||||| ||||| ||||||||||
Db   1 MLKFKFYGVRNPPEASASEPIASRASRLNLFFQGKPPLMTQQQMSALSREGMLDALFALFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
              ||||||||||:|||| ||:|||||||||:|||||| |||||||||||||||||||||||||
Db   61 ECSQPALMKMKGHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120

Qy   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
              |:|||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   121 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG 180

Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
              | ||||||||||||:|:||||||||||||||||||:|||||:||||||||||:|:|||||
Db   181 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF 240

Db 181 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGVYHRDIKPENILIDRTGEIKLVDF 240

Qy 241 GSAAKMVNSKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
Db 241 GSAAKMNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVGVVAYEMVYGK 299

Qy 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 300 TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF 359

Qy 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSMEKKLLIKSKELQDSQDKCHKV 468
Db 360 ARTDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPAEPLAFSGEELPFVGFS 419

Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 420 YSKALGYLGRSESVVSGLDSPAKVSSMEKKLLIKSKELQDSQDKCHKM 467

RESULT 5
O88527
ID   O88527   PRELIMINARY;   PRT;   448 AA.
AC   O88527;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Citron-K kinase (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Madaule P., Eda M., Watanabe N., Fujisawa K., Matsuoka T., Bito H.,
RA   Ishizaki T., Narumiya S.;
RT   "Role of Citron kinase as a target of the small GTPase Rho in
RT   cytokinesis.";
RL   Nature 0:0-0(1998).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AF070065; AAC27932.1; -.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER   448   448
SQ   SEQUENCE   448 AA; 50650 MW; 548CA5AEAE4A6394 CRC64;

Query Match   82.9%; Score 2157.5; DB 2; Length 448;
Best Local Similarity   90.9%; Pred. No. 4.8e-135;
Matches 408; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
Db   1 MLKFKYGVRNPSEASAPEPIASRASRLNLFFQGKPLMTQQQMSALSREGVLDALFVLLE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVVRSLVGCGHFAEVQVVREKATG 120
Db   61 ECSQPALMKIKHVSSFVRKYSDTIAELRELQPSVRDFEVVRSLVGCCHFAEVQVVREKATG 120

Qy 121 DIYAMKVMKKRALLAEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
Db 121 DVYAMKIMKKAALRALAQEQVSFFEEERNILSQSTSPWIPQLQYAFQDKKNLYLVMEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGVYHRDIKPENILVDRTGHIKLVDF 240
Db 181 DLLSLLNRYEDQLDEMIQFYLAELILAVHSVHQMGVYHRDIKPENILIDRTGHIKLVDF 240

Qy 241 GSAAKMVNSKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
Db 241 GSAAKMNSNK-VDAKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVGVVAYEMLYGK 299

Qy 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 300 TPFTEGTSARTFNNIMNFQRFLKFPDDPKVSSELLDLIQSLLCVQKERLKFEGLCCHPFF 359

Qy 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
Db 360 ARTDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 419

Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEK 449
Db 420 YSKALGYLGRSESVVSGLDSPAKVSSMEK 448

RESULT 6
Q8AVM0
ID   Q8AVM0   PRELIMINARY;   PRT;   717 AA.
AC   Q8AVM0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cdc42bpb protein (Fragment).
GN   Name=Cdc42bpb;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).

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RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC041741; AAH41741.1; -.
DR   HSSP; P49137; 1NXK.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER   717   717
SQ   SEQUENCE   717 AA;   83371 MW;   2D295D4A8A5B733A CRC64;

Query Match           35.7%;  Score 929;  DB 2;  Length 717;
Best Local Similarity 41.7%;  Pred. No. 3.1e-53;
Matches  196;  Conservative  84;  Mismatches  148;  Indels  42;  Gaps  10;

Qy     23  RASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFV--RK   79
                                                                 :
Db      6  RLKRLEQLLLDGP----QRNEAAVSVETLLDVLLCLYTECTSSTLRRDKYVSEFLEWAKP  61

Qy     80  YSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVVREKATGDIYAMKVMKKALLAQEQV  139

Db     62  FTDL--LKGMQLHRDDFEIIKVIGRGAFGEVAVVRLKSTERIYAMKILNKWEMLKRAET  118

Qy    140  SFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQ  199

Db    119  ACFRRERNVLVNGDCQWITTLHYAFQDENYLYLVMDYYVVGGDLLTLLSKFEDRLPEDMSR 178

Qy    200  FYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMSNKMVNAKLPIG  259

Db    179  FYLAEMVLAIHSIHQLHYVHRDIKPDNILLDMNGHIRLADFGSCLKMNKDGTVQSSVAVG  238

Qy    260  TPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQ  319

Db    239  TPDYISPEILQAME-DGMGKYGPECDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHE  297

Qy    320  RFLKFPDD-PKVSSDFLDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPF  375

Db    298  ERFQFPSHIGDVSESAKDLIQRLICSRERRLGQNGIDDFKAHPFFBGIDWDNIRNLEAPY  357

Qy    376  VPTLKSDDDTSNFDEPB---KNSWVSSSPCQLSPSGFSGEELPFVGFSYSK-------  423

Db    358  IPDVSSPSDTSNFDVDDDILRNPEVIPSS---THSGFSGFHLPFVGFTYTTDSCFSDRGS  414

Qy    424  -----ALGILGRSESVVSGLDSPAKTSSMEKKL-------LIKSKELQDS  461

Db    415  LKDTIHANAVTKDEDVQRGLQNSLQVDAYBRRIRRLEQBKELENRKLQES  464

RESULT 7
Q6DT37
ID   Q6DT37           PRELIMINARY;   PRT;   1551 AA.
AC   Q6DT37;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
```

```
DE   Myotonic dystrophy kinase-related CDC42-binding kinase gamma.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ng Y., Tan I., Lim L., Leung T.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AY648038; AAT67172.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulatory/interacting protein. ..; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000095; PAKbox/Rhobndng.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011036; PH_related.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00130; C1_1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00786; PBD; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50108; CRIB; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   1551 AA;   172517 MW;   6B2DCED7BFE57B1E CRC64;

Query Match           35.7%;  Score 929;  DB 2;  Length 1551;
Best Local Similarity 43.8%;  Pred. No. 8.2e-53;
Matches  184;  Conservative  83;  Mismatches  125;  Indels  28;  Gaps  7;

Qy     49  EGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGGCHF  108

Db     23  DGLLDLLLALHHELSSGPLRRERSVAQFLSWASPFVSKVKELRLQRDDFEILKVIGRGAF   82

Qy    109  AEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKN  168

Db     83  GEVTVVRQRDTGQIFAMKMLHKWEMLKRAETACFRRERDVLVKGDSRWVTTLHYAFQDEE  142

Qy    169  HLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENIL  228

Db    143  YLYLVMDYYAGGDLLTLLSRFEDRLPPELAQFYLAEMVLAIHSLHQLGYVHRDVKPDNVL  202

Qy    229  VDRTGHIKLVDFGSAAKMSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWS  288

Db    203  LDVNGHIRLADFGSCLRLNTNGMVDSSVAVGTPDYISPEILQAME-EGKGHYGPQCDWWS  261

Qy    289  VGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLLCGQKE  347
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Db    262  LGVCAYELLFGETPFYAESLVETYGKIMNHEDHLQFPPDVPDVPASAQDLIRQLLCRQEE  321
           :|||||||:::|    ||||  |   |::||      :|:||||    || :|
Qy    348  RLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPPCQL  404
           :   ||||    ||::|  |||  :||||  ::|
Db    322  RLGRGGLDDFRNHPFFEGVDWERLASSTAPYIPELRGPMDTSNFDVDDD---TLNHPGTL  378
           CG10522-PA.
Qy    405  SP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTS----SMEKKLJIKSKE  457
           :       |||||||:|:|    ||||||  :||||
Db    379  PPPSHGAFSGHHLPFVGFTYT---------------SGSHSPBSSEAWAALERKLQCLEQE  425
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RESULT 8
Q9VTY8
ID   Q9VTY8   PRELIMINARY;   PRT;   1854 AA.
AC   Q9VTY8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG10522-PA.
GN   ORFNames=CG10522;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Butler H., Butler J., Center A., Chandra I.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H.,
RA   Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
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Right column:

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RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AE003541; AAF49907.2; -.
DR   HSSP; P31751; 1MRY.
DR   IntAct; Q9VTY8; -.
DR   FlyBase; FBgn0036295; CG10522.
DR   GO; GO:0000910; P:cytokinesis; IMP.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE 1854 AA;  211323 MW;  93E5B69FE63DEE1D CRC64;

Query Match             35.4%;  Score 922;  DB 2;  Length 1854;
Best Local Similarity   40.1%;  Pred. No. 3e-52;
Matches 194;  Conservative 99;  Mismatches 129;  Indels 62;  Gaps  9;

Qy     18  EPIANRASRLNLFFQGKP----------------PFMTQQQMSPLS----------REG  50
           |||:||| |::|:|||||                 ::|:: | ||||          |||
Db      6  EPISVRTARLNNLILGKGAGVCAKPAGSASGSGIPASTRRSIVPVSTTSAAVABAICREG  65

Qy     51  ILDALFVLFPECSQPALMK-IKHVSNFVRKYSDTIABLQBLQPSAKDFEVRSLVGCGHFA  109
           |||| || | | :|| || | :|  ||  || |  |:    :    |   | | |:  ||
Db     66  LLDAFCLLYNECDKDTLKKRDRNIAEFVNKFRPIIEETRKIRVNADDFLIKTLIGQGYFG  125
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Qy  110 EVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYAFQDKNH 169
            :.|:.| |||||||| ::|||:|: .   |: |:||: |:| :: | :|||||||| ::
Db  126 NVHLVVERQTNDIYAMKKKIKKSVVTTSQ----VKEERDIMSIRNSEWLINLQYAFQDNDN 181

Qy  170 LYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILV 229
            ||||||| |||||||| ::   | |:|||:||||| :||:|::|:|||||||||||||:
Db  182 LYLVMEYMPGGDLLSLLMSRH-GPFDEDLARFYLAELTVALHTLHEMGYVHRDIKPENILI 240

Qy  230 DRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGD--GKGTYGLDCDWW 287
            || |||||| ||:|| ::: :|   | |:||||:|||:|  :|: :   |  : | .||
Db  241 DRFGHIKLADFGNAAALDRDGHVLSLSPVGTPDYIAPELLQTISTYKLSKSMHDVSCDYW 300

Qy  288 SVGVIAYEMIYGRSPPAEGTSARTFNNIM------NFQRFLKFPDDPKVSSDFLDLIQSL 341
            |:|:| ||:   :.|  | :: | :.    :    | :| | |||:|:| ||:||:|||
Db  301 SMGIIGYBLICETTPFHEDNVHETYSKILSHCEESHLKELISFPADLKVSVNYRNLIESL 360

Qy  342 LCGQKERLKFEGLCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDE-------PEKN 394
            : . |:|   : ||:||||| ||  ||:| |:  |:   |:|||||| :        |:
Db  361 VTNPSKRLSYERIKNHPFFSEIPWGSIRSQVPPIIPTVRSDDDTSNFEDGIRHKTRREQG 420

Qy  395 SWVSSSPCQLSPSGFPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIK 454
            :  .     : |:|  | ::| |:| | .           ::: : :      :::|: |
Db  421 VAKKSLTTNMKSNDFSGKDLPFIGYSFVH-----------------MEKSAISATTDEKLQEK 466

Qy  455 SKEL 458
            .|||
Db  467 LKEL 470
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RESULT 9
001583
ID   001583          PRELIMINARY;      PRT;   1592 AA.
AC   001583;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Temporarily assigned gene name protein 59.
GN   Name=tag-59; ORFNames=K08B12.5;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Becker M., Wohldmann P.;
RT   "The sequence of C. elegans cosmid K08B12.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RG   WormBase Consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; U97001; AAB52260.3; -.
DR   PIR; T25808; T25808.
DR   HSSP; P49137; 1NXK.
DR   WormBase; WBGene00006437; K08B12.5.
DR   WormPep; K08B12.5; CE30818.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulator/interacting protein. .; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000095; PAKbox/Rhobndng.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00130; C1_1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF04433; Pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00285; PBD; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS50108; CRIB; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   1592 AA;  180743 MW;  F909FA8F5C9C876C CRC64;

Query Match             34.5%;  Score 897.5;  DB 2;  Length 1592;
Best Local Similarity   40.5%;  Pred. No. 1e-50;
Matches  178;  Conservative  91;  Mismatches  150;  Indels  21;  Gaps  8;

Qy   28 NLFFQGKPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAEL 87
            |::     :|||:|.| |::|| :| |:  |  ::|
Db   19 NIYMDG------PSKKPEALSFETLIDSLICLYDECNSTLRKEKCIAEFVESVKTVISKA 73

Qy   88 QELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERN 147
            :.: ||   :. ||:|:.|||::|||||||||||||||::|
Db   74 KKLRLSRDDFEVLKVIGKGAFGEVAVVRMRGVGEIYAMKILNKWEMVKRAETACFREERD 133

Qy  148 ILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIL 207
            |.| ||| |||:| :::|| :|:|||||:|||||||||||||||:||.|||:|:||||||
Db  134 VLVYGDRRWITNLHAYAFQDEKNLYFVMDYYIGGDMLTLLSKFVDHIPESMAKFYIAEMVL 193

Qy  208 AVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPE 267
            | ||:||:|||||||||||| :||:| |:|||| .|    :|  :  |||||||||:: |
Db  194 AIDSLHRLGYVHRDVKPDNVLLDMQGHIRLADFGSCLRILADGSVASNVAVGTPDVISPE 253

Qy  268 VLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPPAEGTSARTFNNIMNFQRFLKFPDD 327
            :|  :.|.| ||:|| :  |||||||||:|||| ||.| | |  :.|:  || |||:|||
Db  254 ILRAME-DGRGRYGKECDWWSLGICMYEMLYGTTPFYSERLVDTYGKIMSHQDMLDFPDD 312

Qy  328 P--KVSSDFLDLIQSLLCGQKERLKFEGLC---CHPFFSKIDWNNIRNSPPPFVPPLKS 381
            :    ::.|   :: :  |:|::|||: ||    |||||||||||||:.| || |:
Db  313 EIDWVVSEEAKDLIRQLICSSDVRFGRNGLSDFQLHPFFEGIDWNTIRDSNPPYVPBVSS 372

Qy  382 DDDTSNFDEPBKNSWVSSSPC--QLSP----SGFSGEELPFVGFSYSKALGILGRSESVV 435
            |:||||||:  ||.||:|:|     |:     ||.||.||||||:|:|:||:|| :..|
Db  373 PEDTSNFDVDVCED--DFTPCLQETQPRVLAAFTGNHLPFVGFSYTHG-GLLSDARSLT 429
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Qy   436  SGLDSPAKTSSMEKKLLIKS 455
               :|:  :|:|  ||
Db   430  DEIRAIAQRCGQDAELMEKS 449
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RESULT 10
Q86XZ8

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ID   Q86XZ8;      PRELIMINARY;      PRT;   492 AA.
AC   Q86XZ8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CDC42BP protein (Fragment).
GN   Name=CDC42BPB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC048261; AAH48261.1; -.
DR   HSSP; P31751; 1MRY.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER      492    492
SQ   SEQUENCE   492 AA;  56805 MW;  5F9FBD9CC1D2AEFC CRC64;

  Query Match             34.5%;  Score 896.5;  DB 2;  Length 492;
  Best Local Similarity   42.1%;
  Matches  185;  Conservative   85;  Mismatches  140;  Indels   29;  Gaps    9;
```

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Qy    44  SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
Db    23  SALSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKEMQLHREDFBIIKVI  82

Qy   104  GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILsRSTSPWIPQLQYA 163
Db    83  GRGAFGEVAVVKMNTERIYAMKILNKWEMLKRAETACFRERDVLVNGDCQWITALHYA 142

Qy   164  FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
Db   143  FQDENHLYLVMDYYVVGGDLLITLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202

Qy   224  PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
Db   203  PDNVLLDVNGHIRLADFGSCLKMNDDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 261

Qy   284  CDWWSVGVIAYEMIYGRSPFABGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
Db   262  CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHBERFQPPSHVTDVSEEAKDIIQRLI 321

Qy   343  CGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPE---KNSW 396
Db   322  CSRERRLGQNGIEDPKKHAFPEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381

Qy   397  VSSSPCQLSP---SGFSGEELPFVGPSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
Db   382  I------LPPGSHTGPSGLHLPFIGFTFT------TESCFS--DRGSLKSIMQSNTLT 425

Qy   454  KSKELQDSQDKCHKVPISA 472
Db   426  KDEDVQ--RDLEHSLQMEA 442
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RESULT 11
Q86TUJ

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ID   Q86TUJ;      PRELIMINARY;      PRT;   933 AA.
AC   Q86TUJ;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CDC42BP protein (Fragment).
GN   Name=CDC42BPB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC047871; AAH47871.1; -.
DR   HSSP; P31751; 1MRY.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS01107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER      933    933
SQ   SEQUENCE   933 AA;  108543 MW;  38E7179C3253F521 CRC64;

Query Match             34.5%;  Score 896.5;  DB 2;  Length 933;
Best Local Similarity   42.1%;  Pred. No. 6.2e-51;
Matches  185;  Conservative   85;  Mismatches  140;  Indels   29;  Gaps    9;

Qy   44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
          |||:||||||||| ||||:|||  ||:|: :|:|:|| .|:::| |
Db   23 SALSVETLLDVLVCLYTECSHSALRRDKYVABFLEWAKPTQLVKEMQLHREDFEIIKVI   82

Qy  104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
          | |||:|||||:|| |||| ||||| |||
Db   83 GRGAFGEVAVVKMKNTERIYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYA 142

Qy  164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
          ||||:|||||| | :|| :| |:| ||||||||||||
Db  143 FQDENHLYLVMDYYVVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202

Qy  224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLD 283
          ||:|:|| ||:||||||||  ::  | |: ::|:|| |||||| |  ||:
Db  203 PDNVLLDVNGHIRLADFGSCLKMNDDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 261

Qy  284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
          |||| |||| ||:|||||||
Db  262 CDWWSLGVCMYEMLYGETPYAESLVETYGKIMNHEERFQFPSHVTDVSEEAKDLIQRLI  321

Qy  343 CGQXERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDTSNFDEPE---KNSW 396
          |:|| :|| :  |  |||  |:|  |: || :|
Db  322 CSRERRLGQNGIEDFKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381

Qy  397 VSSSPCQLSP--SGPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
          :||   |||    |||
Db  382 I-----LPPGSHTGFSGLHLPFIGFTFT------TESCFS--DRGSLKSIMQSNTLT    425

Qy  454 KSKELQDSQDKCHKVFISA 472
          :| | :| |  ::|
Db  426 KDEDVQ--RDLEHSLQMEA 442
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RESULT 12

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ID   Q9Y5S2       PRELIMINARY;      PRT;   1711 AA.
AC   Q9Y5S2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CDC42-binding protein kinase beta.
GN   Name=CDC42BPB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99216425; PubMed=10198171; DOI=10.1006/geno.1999.5769;
RA   Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;
RT   "Cloning and chromosomal localization of human Cdc42-binding protein
RT   kinase beta.";
RL   Genomics 57:297-300(1999).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AF128625; AAD37506.1; -.
DR   HSSP; P31751; 1MRY.
DR   GO; GO:0005856; C:cytoskeleton; TAS.
DR   GO; GO:0004672; F:protein kinase activity; TAS.
DR   GO; GO:0007163; P:establishment and/or maintenance of cell po...; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000095; PAKbox/Rhobndng.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00130; C1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00786; PBD; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00285; PBD; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS50108; CRIB; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   1711 AA;  194356 MW;  3A3731D40A363497 CRC64;

Query Match             34.5%;  Score 896.5;  DB 2;  Length 1711;
Best Local Similarity   42.1%;  Pred. No. 1.3e-50;
Matches  185;  Conservative   85;  Mismatches  140;  Indels   29;  Gaps    9;

Qy   44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
          |||:||||||||| ||||:|||  ||:|: :|:|:|| .|:::| |
Db   23 SALSVETLLDVLVCLYTECSHSALRRDKYVABFLEWAKPTQLVKEMQLHREDFEIIKVI   82

Qy  104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
          | |||:|||||:|| |||| ||||| |||
Db   83 GRGAFGEVAVVKMKNTERIYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYA 142

Qy  164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
          ||||:|||||| | :|| :| |:| ||||||||||||
Db  143 FQDENHLYLVMDYYVVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202

Qy  224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLD 283
          ||:|:|| ||:||||||||  ::  | |: ::|:|| |||||| |  ||:
Db  203 PDNVLLDVNGHIRLADFGSCLKMNDDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 261

Qy  284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
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DR   PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS05011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER   1
SQ   SEQUENCE   1760 AA; 199208 MW; 3A1CA9A7A4BF5FA3 CRC64;

Query Match   34.5%; Score 896.5; DB 2; Length 1760;
Best Local Similarity   42.1%; Pred. No. 1.4e-50;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

Qy   44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
            :.||::. .::|::. |:||: .:| :|:.::|:   ::||::: ||: .::. ::
Db   72 SALSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKEMQLHREDFEIIKVI 131

Qy   104 GCGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
            ||| |||||.|| |:||||||||| || | ||||.||:|||| |:| :| :|| ||
Db   132 GRGAFGEVAVVKMKNTERIYAMKILNKWEMLKRAETACFRERERDVLVNGDCQWITALHYA 191

Qy   164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
            |||:|||||||||| |||: ||.:.|:||| ||::||::|:|:||:|:||||||||||
Db   192 FQDENHLYLVMDYYVVGGDLLTLLSKFPEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 251

Qy   224 PENILVDRTGHIKLVDFGSAAKWNSNKMVNAKLPIGTGPDYMAPEVLTVMNGDGKGTYGLD 283
            |||:|:|.|||:|||||||: | ||| ||| |:| ||| ||| ::||:|| |.| ||| |
Db   252 PDNVLLDVNGHIRLADFGSCLKMNDDGTVQSSVAVGTPDYISPEILQAME-DGMGKYGPE 310

Qy   284 CDWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
            |||| |||||::|||:||| | ||| ||||.|:||:|: :|| |:.|::|::||:||
Db   311 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQPPSHVTDVSEEAKDLIQRLI 370

Qy   343 CGQKRLKFEGL---CCHPFFSKIDWNNIRNSPPPVFVPTLKSDDDTSNFDEPE---KNSW 396
            |||||||||| ::|||| .:::|::.| .. :|:| ::.:|:|:| ||:|
Db   371 CSRERRLGQNGIEDFKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNTE 430

Qy   397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
            ||:::| ||| | ||| | :|:|:||| :|: | :: |||| : :::.::|::::.
Db   431 I------LPPGSHTGFSGLHPFIGFTFT-------TESCFS--DRGSLKSIMQSNTLT 474

Qy   454 KSKELQDSQDKCHKVFISA 472
            |:|:||| |:|||||:|:|
Db   475 KDEDVQ--RDLEHSLQMEA 491

RESULT 14
Q99646
ID   Q99646;   PRELIMINARY;   PRT;   496 AA.
AC   Q99646;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ser-thr protein kinase PK428.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhao Y., Kidd V., Kraft A.S.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; U59305; AAB37126.1; -.
DR   HSSP; P31751; 1MRY.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.

Db   262 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQPPSHVTDVSEEAKDLIQRLI 321
            ||||:|:| .:||::| ||: |.:::|::..| :.:|:| :|| .::||:||::|:
Qy   343 CGQKRLKFEGL---CCHPFFSKIDWNNIRNSPPPVFVPTLKSDDDTSNFDEPE---KNSW 396
            |:| :| ::| | :|||| .::::|::.| .. :|:| ::.:|:| ||:|
Db   322 CSRERRLGQNGIEDFKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381

Qy   397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
            ||:::| ||| | ||| | :|:|:||| :|: | :: |||| : :::.::|::::.
Db   382 I------LPPGSHTGFSGLHPFIGFTFT-------TESCFS--DRGSLKSIMQSNTLT 442

Qy   454 KSKELQDSQDKCHKVFISA 472
            |:|:||| |:|||||:|:|
Db   426 KDEDVQ--RDLEHSLQMEA 442

RESULT 13
Q9ULU5
ID   Q9ULU5;   PRELIMINARY;   PRT;   1760 AA.
AC   Q9ULU5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   KIAA1124 protein (Fragment).
GN   Name=KIAA1124;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 PH domain.
EMBL; AB032950; BAA86438.2; -.
HSSP; P31751; 1MRY.
DR   Genew; HGNC:1738; CDC42BPB.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000095; PAKbox/Rhobndng.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00130; C1_1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00786; PBD; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00036; CNH; 1.
DR   SMART; SM00285; PBD; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS50108; CRIB; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

```
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   496 AA;   56991 MW;  069186D74AE9C936 CRC64;

Query Match           34.2%;   Score 891;  DB 2;  Length 496;
Best Local Similarity 40.3%;  Pred. No. 6.5e-51;   Indels  34;  Gaps   8;
Matches 183;   Conservative  92;  Mismatches 145;

Qy     36  PFMTCQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAK   95
               :  :    ||| : ::  :: ::      : :::::::::::::::::::::
Db     18  PAQTNGQY--FSVETLLDILICLYDECNNSPLRREKNILEYLEWAKPFTSKVKQMRLHRE   75

Qy     96  DFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSP  155
           ||| :::| |||:|||| ||: :  | :||||::| ::||:|||: |||||::|: ::
Db     76  DFEILKVIGRGAFGEVAVVKLKNADKVFAMKILNKWEMLKRAETACFREERDVLVNGDNK  135

Qy    156  WIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIIAVHSVHLM  215
           ||  |:||||| :|||||::| ||||||:|||::|:|| |::|:|||||::||:|:||::
Db    136  WITTLHYAFQDDNNLYLVMDYVVGGDLLTLLSKFEDRLPEDMARFYILAEMVIAIDSVHQL  195

Qy    216  GYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGD  275
            |||||||:|||:||: ||:||:||||||| |  : :||  :  ||||:|:|:|  || |
Db    196  HYVHRDIKPDNILMDMNGHIRLADFGSCLKLMEDGTVQSSVAVGTPDYISPEILQAME-D  254

Qy    276  GKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDF  334
           |||:||:||||||:||:||||:||::||:|:| : |::|||:::: : |    ::|:::
Db    255  GKGRYGPECDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHKERFQFPAQVTDVSENA  314

Qy    335  LDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEP  391
            ||::||:| :::||: : |   ||||||| |||:|||| | |::|:: ||||||||| :
Db    315  KDLIRRLICSREHRLGQNGIEDFKKGHPFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVD  374

Qy    392  E---KNSWVSSSPCQLSPSGFSGSGEELPFVGFSYSKALGILGRS---------ESV  434
           :   ||||  :    ::|  ||| | ||||||| |:::  :| |          :::
Db    375  DDCLKNSEIMPPP---THTAFSGHHLPFVGFTYTSSCVLSDRSCLRVTAGPTSLDLDVNV  431

Qy    435  VSGLDSPAKTSSMEKKL------LIKSKELQDS  461
            : |   ::  |::::|      ::|:||:|:|
Db    432  QRTLDNNLATEAYERRIKRLEQEKLELSRKLQES  465
```

RESULT 15

```
Q7PV87
ID   Q7PV87           PRELIMINARY;       PRT;   1573 AA.
AC   Q7PV87;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000009214 (Fragment).
GN   Name=ENSANGG00000006898;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008986; EAA00280.2; -.
DR   HSSP; P31751; 1MRV.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001180; Citron.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000095; PAKbox/Rhobndng.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00130; C1_1; 1.
DR   Pfam; PF00780; CNH; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50108; CRIB; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER          1      1
FT   NON_TER       1573   1573
SQ   SEQUENCE   1573 AA;  179568 MW;  36C3826EADFDA04E CRC64;

Query Match           34.2%;   Score 891;  DB 2;  Length 1573;
Best Local Similarity 41.0%;  Pred. No. 2.8e-50;   Indels  20;  Gaps   6;
Matches 178;   Conservative  90;  Mismatches 146;

Qy     46  LSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGC  105
           || | :|| |||||:||:| : |: ||::: :    ::  : : :   ::    : :
Db      4  LSVETMLDCLVVLYDECNNSLRREKTVSDFIELMKSVVQSVKQLRLSRDDFEVLKVVIGR   63

Qy    106  GHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQ  165
           |:|.EV.VVR   : :IYAMK::.| :|:|:||: |:|||:::|:     |:  |:|||| :
Db     64  GAFGEVCVVRMHHTSQIYAMKILNKWEMLKRAETACFREERDVLVFGDRRWITNLHYAFQ  123

Qy    166  DKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIIAVHSVHLMGYVHRDIKPE  225
           | ::||::| |  ||||| |||::|:||| :: |:|:||::|:|| :|: :|||||||:
Db    124  DDINLYIIMDYYCGGDLLTLLSKFEDRLPEDMARFYIAEMVLAIHSIHELKYVHRDIKPD  183

Qy    226  NILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCD   285
           |::||: ||::|.||||| |: :  : || ::.||||| ::|:|   :||:|:||:||
Db    184  NIVLDASGHVRLADFGSCLRLGPQGTVQSNVAVGTPDYISPEILRAME-DGQGKYGPECD  242

Qy    286  WWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPK---VSSDFLDLIQSLL  342
           |||:||:||||:.|::||:|:| : ||::||:::: : |    ::   :: :  |:::::
Db    243  WWSLGVCMYEMLFGETPFYAESLVETYGKIMNHKNSFDFPNDDDEFGVSEQAKDLIRRLI  302

Qy    343  CGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSS  399
           | :: ||  :|    | ||:|  |.|:|||| | |::|   |||||||:       :  |
Db    303  CAPEYRLGQNGIDDFKAHPWFEGISWDTIRNGQAPYIPEVSSPTDTSNFNFDVDDTDIKLSD  362

Qy    400  SPCQLSPSGFSGSGEELPFVGFSYSK-ALGILGRSESVVSGLDSPA--------KTSSME  448
                :   |::  |::||||||   ::    :: |  :::: |:            |:: :
Db    363  AVPPTTNPAFSGHHLPFVGFTFTKDSSLSDVGRLSRAITSNSASQPLPPLKLEKGHGSEE  422

Qy    449  KKLLI--KSKELQD  460
           | || |  |::|:||
Db    423  KQRLSPDSTRKLQD  436
```

Search completed: March 18, 2005, 15:40:01
Job time : 179 secs

OM protein - protein search, using sw model

```
            Copyright   GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:     March 18, 2005, 15:30:56 ; Search time 42 Seconds
                                 (without alignments)
                                 1138.565 Million cell updates/sec

Title:      US-10-724-594-2
Perfect score: 2602
Sequence:   1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497
Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5
```

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
            Maximum Match 100%
            Listing first 45 summaries

```
Database :  PIR 79:*
            1:  pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	908.5	34.9	1548	2	T25808	hypothetical prote
2	891	34.2	1732	2	T14039	protein kinase (EC
3	883	33.9	1702	2	T14050	protein kinase (EC
4	876.5	33.7	1173	2	T25539	hypothetical prote
5	866.5	33.3	1354	2	S74244	serine/threonine-s
6	864.5	33.2	1354	2	S69211	serine/threonine-s
7	863	33.2	624	2	B49364	protein kinase (EC
8	860.5	33.1	1388	2	S70633	serine/threonine-s
9	853.5	32.8	1388	2	S74245	serine/threonine-s
10	847	32.6	557	2	S71829	serine/threonine-s
11	721	27.7	522	2	G86431	protein kinase T5I
12	711	27.3	479	2	S42864	protein kinase (EC
13	704	27.1	756	2	S60966	probable protein k
14	701	26.9	526	2	S49077	protein kinase PKT
15	700	26.9	469	2	T41723	serine/threonine-s
16	697	26.8	596	2	P84589	probable protein k
17	693	26.6	569	2	A86170	hypothetical prote
18	687.5	26.4	474	2	I78396	myotonic dystrophy
19	685	26.3	441	2	I78393	myotonic dystrophy
20	685	26.3	516	2	I78394	myotonic dystrophy
21	682.5	26.2	1356	2	T16718	hypothetical prote
22	676.5	26.0	443	2	D71405	probable protein k
23	676.5	26.0	475	2	H85156	protein kinase (lim
24	674.5	25.9	465	2	I38133	protein kinase (EC
25	665.5	25.6	500	2	S42867	protein kinase (EC
26	660.5	25.4	483	2	T05188	protein kinase F4I
27	639	24.6	545	2	T01288	protein kinase F27
28	636.5	24.5	598	2	T47254	serine/threonine k
29	636.5	24.5	665	2	S70706	probable protein k
30	636	24.4	480	2	T47255	serine/threonine k
31	636	24.4	620	2	S22711	probable protein k
32	608	23.4	908	2	T25035	hypothetical prote
33	606.5	23.3	412	2	I78395	myotonic dystrophy
34	604	23.2	1099	2	A56155	tumor suppressor p
35	548	21.1	607	2	S62556	probable serine/th
36	536	20.6	624	2	T41341	probable serine-th
37	532.5	20.5	564	2	S59776	protein kinase DBF
38	522	20.1	572	2	S64387	protein kinase DBF
39	520.5	20.0	726	2	S22258	probable protein k
40	520	20.0	1092	2	H96509	protein F27F5.23 [
41	516	19.8	893	2	S63378	hypothetical prote
42	515	19.8	425	2	S41099	protein kinase (EC
43	510.5	19.6	646	2	T38171	probable serine/th
44	510	19.6	462	1	T17287	protein kinase (EC
45	509	19.6	569	2	T50414	probable prolifera

ALIGNMENTS

```
RESULT 1
T25808
hypothetical protein K08B12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T25808
R;Becker, M.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid K08B12.
A;Reference number: Z20091
A;Accession: T25808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1548  <BEC>
A;Cross-references: UNIPROT:O01583; EMBL:U97001; PIDN:AAB52260.1; GSPDB:GN00023; CESP:K0...
A;Experimental source: strain Bristol N2; clone K08B12
C;Genetics:
A;Gene: CESP:K08B12.5
C;Superfamily: protein kinase homology
F;956-1005/Domain: protein kinase C zinc-binding repeat homology <KZN>
A;Map position: 5
A;Introns: 39/1; 66/1; 156/3; 278/2; 391/3; 628/1; 1022/2; 1273/3; 1326/1; 1423/2; 1489/...

Query Match             34.9%;   Score 908.5;  DB 2;  Length 1548;
Best Local Similarity   40.6%;   Pred. No. 2.3e-33;
Matches  178;  Conservative  91;  Mismatches 150;  Indels  19;  Gaps  7;

Qy   28  NLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAEL  87
             ||:       :::   :||||| |:||| |::| :||           ::||
Db   19  NIYMDG------PSKKPEALSFETLIDSLICLYDECNSTLRKEKCIAEFVESVKTVISKA  73

Qy   88  QELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMCKKALLAQEQVSFFEEERN  147
             |||| |::   |:||:|| |:|| :|||||| ||||||: ||:|||||:::|:
Db   74  KKLRLSRDDFEVLKVIGKGAFGEVAVVRMRGVGEIYAMKILNKWEMVKRAETACFRERD  133

Qy  148  ILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIL  207
          |:  :||:|:|:|: :||||:|:||||||||||||| ||||:||||||:||||:||:|
Db  134  VLVYGDRRWITNLHYAFQDEKNLYFVMDYYIGGDMLTLLSKFVDHIPESMAKFYIAEMVL  193

Qy  208  AVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPE  267
          |:|: ||:|||||:||:|||| :  :| |:|||| |:|  :  |   |::|||||||||
Db  194  AIDSLHRLGYVHRDVKPDNVLLDMQGHIRLADFGSCLRILADGSVASNVAVGTPDYISPE  253

Qy  268  VLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFABGTSARTFNNIMNFQRFLKFPDD  327
          |||: |  :   :| | : || |:|:|||||||| :::|  :||||::| |:|:| ||
Db  254  ILRAME-DGRGRYGKSCDWWSLGICMEMLYGTTPFYSERLVDTYGKIMSHQDMLDFPDD  312

Qy  328  P--KVSSDFLDLIQSLLCGQKERLKPEGLC---CHPFFSKIDWNNIRNSPPPFVPTLKS  381
               |  : :||: |:|||  | ||||:   | ||||||||||:|:::|||||:
Db  313  EIDWVVSEEAKDLIRQLICSSDVRFGRNGLSDFQLHPFFEGIDWNTIRDSNPPYVPEVSS  372

Qy  382  DDDTSNFDEPEKNSWVSSSPCQLSP----SGFSGEELPFVGFSYSKALGILGRSESVVSG  437
```

Left column

```
Db  373 PEDTSNFDVDVCED--DFTPCETQPPRVLAAFTGNHLPFVGFSYTHG-SLLSDARSLTDE 429
            :||:        ||||||||:       :|:|  ||||||||
Qy  438 LDSPAKTSSMEKKLLIKS 455
            :|: :|: ||
Db  430 IRAIAQRCQGDAELMEKS 447
```

RESULT 2
T14039
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
C;Accession: T14039
R;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector
A;Reference number: Z17862; MUID:98078670; PMID:9418861
A;Accession: T14039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1732 <LEU>
A;Cross-references: UNIPROT:O54874; EMBL:AF021935; NID:g2736150; PID:g2736151; PIDN:AAC0
C;Genetics:
A;Gene: MRCK
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase
F;75-343/Domain: protein kinase homology <KIN>
F;1013-1062/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match   34.2%;   Score 891;   DB 2;   Length 1732;
Best Local Similarity 40.3%; Pred. No. 1.5e-32;
Matches 183; Conservative 91; Mismatches 146; Indels 34; Gaps 8;

Qy   36 PFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAK 95
            ||:|:||: ||||||| |:|:| |||:|:|::|:|:||::||:
Db   18 PAQTNGQC--FSVETLLDIILCLYDECNNSPLRREKNILEYLEWAKPFTSKVKQMRLHRE 75

Qy   96 DFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSP 155
            ||||:|:|||||:| :|| |||||||||:|: ||||||||||||||||||||||
Db   76 DFEILKVIGRGAFGEVAVVKLKNADKVFAMKILNKKWEMLKRAETACFREERDVLVNGDSK 135

Qy 156 WIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLM 215
            |||||:|::| |||||||||||:|:||:||||:|:||:||: ||||||||:|||||
Db 136 WITTLHYAFQDDNNLYLVMDYYVGGDLLTLLSKFEDRLPEMARFYIAIDSVHQL 195

Qy 216 GYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGD 275
            |:||||||||||||||||||||||||||:|||:|:||||||||||||||||:|:|:||
Db 196 HYVHRDIKPDNILMDMNGHIRLADFGSCLKLMEDGTVQSSVAVGTPDYISPEILQAME-D 254

Qy 276 GKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDF 334
            ||||:|||:|||||||| |||::|| ||||||||:|||||:||||||||| ||||::
Db 255 GKGRYGPECDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHERFQPFTVDVSENA 314

Qy 335 LDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEP 391
            ||||:|:|: |: :|||||| |||||||||||||||||||||||||||||||||||
Db 315 KDLIRRLICSREHRLGQNGIEDFKKGHPFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVD 374

Qy 392 E---KNSWVSSSPCQLSPSGFSGEELPFVGFSYSKALGILGRS------------ESV 434
            | :|:: ||
Db 375 DDCLKNSETMPPP---THTAFSGHHLPFVGFTYTSSCVLSDRSCLRVTAGPTSLDLDVNV 431

Qy 435 VSGLDSPAKTSSMEKKL------LIKSKELQDS 461
            ||: :|: |||:| || :::|||
Db 432 QRTLDNNLATEAYERRIKRLEQEKLELTRKLQES 465
```

RESULT 3
T14050
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
C;Accession: T14050

Right column

R;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector
A;Reference number: Z17862; MUID:98078670; PMID:9418861
A;Accession: T14050
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1702 <LEU>
A;Cross-references: UNIPROT:O54875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AAC0
A;Experimental source: brain
C;Genetics:
A;Gene: MRCK-beta
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase
F;74-342/Domain: protein kinase homology <KIN>
F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match   33.9%;   Score 883;   DB 2;   Length 1702;
Best Local Similarity 40.5%; Pred. No. 3.4e-32;
Matches 182; Conservative 90; Mismatches 139; Indels 38; Gaps 9;

Qy   44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
            ||: :|||||||| |:|:| |||:|:|::|:|:||::||:
Db   23 SSLSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKDMQLHREDFEIIKVI 82

Qy 104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
            |||:| :|| |||||||||:|: ||||||||||||||||||||:||||:|||||
Db   83 GRGAFGEVAVVKMNTERIYAMKILNKKWEMLKRAETACFREERDVLVNGDCQWITALHYA 142

Qy 164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
            ||| |||||||||||:|:||:||||:|:||:||: |||||||||:|||||:|||||||||
Db 143 FQDENYIYLVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202

Qy 224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
            |:|:|||||||||||||||||:|||:|:||||||||||||||:|:|:|||:|:|:|:
Db 203 PDNVLLDVNGHIRLADFGSCLKMNDDGTVQSSVAVGTPDYISPEIIQAME-DGMGKYGPE 261

Qy 284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
            |||||:|||| |||::|| ||||||||:|||||:||||||||| ||||::|:||:|:||
Db 262 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHERFQPFSHVTDVSERAKDLLIQRLI 321

Qy 343 CGQKERLKFEGL---CCHPFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPE---KNSW 396
            ||: :|||||| |||||||||||||||||||||||||||||:||: || :|:
Db 322 CSRERRLGQNGIEDFKKGHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNIE 381

Qy 397 VSSSPCQLSP---SGFSGEELPFVGFSYS----------KAL--GILGRSESVVSGLD 439
            |::|:| :|| |::| || |:||
Db 382 I------LPDGSHTGFSGLHLPFIGFTFTTESCFSDRGSLKSMIQSNTLTKDEDVQRDLE 435

Qy 440 SPAKTSSMEKKL-------LIKSKELQDS 461
            ||:|||:| || :::|||
Db 436 NSLQIRAYERRIRRLEQEKELSRKLQES 464
```

RESULT 4
T25539
hypothetical protein C10H11.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25539
R;Dante, M.; Wamsley, P.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C10H11.
A;Reference number: Z20047
A;Accession: T25539
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1173 <DAN>
A;Cross-references: UNIPROT:P92199; EMBL:U88311; PIDN:AAB42348.1; GSPDB:GN000019; CESP:C1C
A;Experimental source: strain Bristol N2; clone C10H11
C;Genetics:
A;Gene: CESP:C10H11.9
A;Map position: 1

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A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology

Query Match        33.7%;   Score 876.5; DB 2;  Length 1173;
Best Local Similarity  40.9%;  Pred. No. 4.7e-32;
Matches  168;  Conservative  88;  Mismatches 142;  Indels  13;  Gaps  6;

Qy  44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
        |||:|:|::|||||::||| ||:|||||:||:| :::: ||: ||||
Db  15 SPINIESLLDTITALVNDCKIPVLMRKSVDNFISRYERVVESLAALRMKAADFRQLKVI 74

Qy 104 GCGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
        |:|||||:||||||| :| ||| ||||||:||:|:|
Db  75 GRGAFGEVHLVRHTRTNTVYAMKMLNKDDMIKRADSAFFWERDIMAHANSEWIVRLQYA 134

Qy 164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
        |||||||:|||||||||:|||::: :||| ||:::|| |||:| |||||||||||
Db 135 FQDPRHLYMVMEYMPGGDLVNLMTSYE--VSEKWTRFYTAEIVEALAALHSMGYIHRDVK 192

Qy 224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
        |:|||||||||||||||||||:|::::| |||  || :|||||:|||||:
Db 193 PDNMLISISGHIKLADFGTCVKMNANGVVRCSTAVGTPDYISPEVLRNQGQDAE--FGKE 250

Qy 284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLC 343
        ||||||||||:: :|   |:: ::|||::|
Db 251 VDWWSVGVFIYEMLVGETPFVAEALVSTYTNIMNHKTSLKFPDEPLISTQAKDIIKKFLS 310

Qy 344 GQKERL---KFEGLCCHPFFSKIDWN--NIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVS 398
        ||||:|   |:     ||  :|   ||: :||:::
Db 311 AAPDRLGRNSVDDIRNHKFFVNDEWTFATLREASPVIPSLKSDDDTTHFEEIETRDRDN 370

Qy 399 SSPCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEK 449
        |:| |:    :  ||  |: :  | :| ||  || :  |
Db 371 AGDFQL-PKTFNGNQLPFIGFTYSNEYSPV--KNLLKGHGAGSKQNGIEQ 417


RESULT 5
S74244
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C;Accession: S74244
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74244
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <NAK>
A;Cross-references: UNIPROT:P70335; EMBL:U58512; NID:g1514695; PIDN:AAC53132.1; PID:g151
C;Superfamily: protein kinase homology
C;Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase <KIN>
F;74-338/Domain: protein kinase homology <KIN>
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match        33.3%;   Score 866.5; DB 2; Length 1354;
Best Local Similarity  40.0%;  Pred. No. 1.5e-31;
Matches  186;  Conservative  93;  Mismatches 157;  Indels  29;  Gaps  10;

Qy  44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
        ||: ::||  :||:|:  ||  ||:| ||:||::||| :|| |||:
Db  23 SEVNSDCLLDGLDALVYDLDFPALRKNKNIDNFLSRYKDTINKIRDLRMKAEDYEVVKVI 82

Qy 104 GCGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
        | |||||||:||| :| :|||| | :::||| |||::| |||:: :| |||:::|::||
Db  83 GRGAFGEVQLVRHKSTRKVYAMKLLSKFEMIKRSDSAFFWERDIMAFANSPWVVQLFYA 142

Qy 164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
        |||:::||:|||| ||||| :|: ::  ||  | ::||:||:: |:|: |||: |||||
Db 143 FQDDRYLYMVMEYMPGGDLVNLMSNYD--VPEKWARFYTAEVVLALDAIHSMGFIHRDVK 200

Qy 224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
Db 201 PDNMLLDKSGHIKLADFGTCMKMNKEGMVRCDTAVGTPDYISPEVLKSQGGD--GYYGRE 258

Qy 284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLC 343
Db 259 CDWWSVGVFLYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318

Qy 344 GQKERLKFEG---LCCHPFFSKID--WNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVS 398
Db 319 DREVRLGRNGVEIKRHLFFKNDQWAWETLRDTVAPVVPDLSSDIDTSNFDDLEEDKGDE 378

Qy 399 SS-PCQLSPSGFSGEELPFVGFSY------SKALGILGRSESVV--SGLDSPAKTSSME 448
Db 379 ETFPI--PKAFVGNQLPFVGFTYSSNRRYLPSANASENRSSSNVDKSLQESLQKTIYKL 435

Qy 449 KKLLIKSKELQDS-QDKCHKVFISAAGLLPCSRILPSVYAKGSAR 492
Db 436 BEQLHNEMQLKDEMEQKCR------TSNLKLDKIMKELDEEGNQR 474


RESULT 6
S69211
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
C;Accession: S69211; S71910
R;Ishizaki, T.; Maekawa, M.; Fujisawa, K.; Okawa, K.; Iwamatsu, A.; Fujita, A.; Watanabe
EMBO J. 15, 1885-1893, 1996
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot
A;Reference number: S69211; MUID:96203110; PMID:8617235
A;Accession: S69211
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <ISH1>
A;Cross-references: UNIPROT:Q13464; EMBL:U43195; NID:g1276900; PIDN:AAB02814.1; PID:g127
A;Accession: S71910
A;Molecule type: protein
A;Residues: 187-195;281-288;465-473;573-587;818-828;885-893;934-945 <ISH2>
C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology
C;Date: 06-Dec-1996 #sequence_revision; serine/threonine-specific protein kinase
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase <KIN>
F;74-338/Domain: protein kinase homology <KIN>
F;82-90/Region: protein kinase ATP-binding motif
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match        33.2%;   Score 864.5; DB 2;  Length 1354;
Best Local Similarity  41.1%;  Pred. No. 1.8e-31;
Matches  180;  Conservative  89;  Mismatches 146;  Indels  23;  Gaps  9;

Qy  44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIABLQELQPSAKDFEVRSIV 103
        ||: ::||  :||:|:  ||  ||:| ||:||::||| :|| |||:
Db  23 SEVNSDCLLDGLDALVYDLDFPALRKNKNIDNFLSRYKDTINKIRDLRMKABDYEVVKVI 82

Qy 104 GCGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEERNILSRSTSPWIPQLQYA 163
        | |||||||:||| :| :|||| | :::||| |||::| |||:: :| |||:::|::||
Db  83 GRGAFGEVQLVRHKSTRKVYAMKLLSKFEMIKRSDSAFFWERDIMAFANSPWVVQLFYA 142

Qy 164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
        |||:::||:|||| ||||| :|: ::  ||  | ::||:||:: |:|: |||: |||||
Db 143 FQDDRYLYMVMEYMPGGDLVNLMSNYD--VPEKWARFYTAEVVLALDAIHSMGFIHRDVK 200

Qy 224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
Db 201 PDNMLLDKSGHIKLADFGTCMKMNKEGMVRCDTAVGTPDYISPEVLKSQGGD--GYYGRE 258

Qy 284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLC 343
Db 259 CDWWSVGVFLYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318

Qy 344 GQKERLKFEG---LCCHPFFSKID--WNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVS 398
Db 319 DREVRLGRNGVEIKRHLFFKNDQWAWETLRDTVAPVVPDLSSDIDTSNFDDLEEDKGBE 378

Qy 399 SS-PCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSME--KKLLIKS 455
```

```
Db    379 ETFPI---PKAFVGNQLPFVGFTYYSNRRYLSSANPNDNRTSSNADKSLQESLQKTIYKL 435
              :   :         :||||||||:||
Qy    456 KE-------LQDS-QDKC 465
              :|   |   :|:||
Db    436 EEQLHNEMQLKDEMEQKC 453
```

```
RESULT 7
B49364
protein kinase (EC 2.7.1.37), myotonin protein kinase
N;Alternate names: myotonin protein kinase
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: B49364; S48681; A42101
R;Shaw, D.J.; McCurrach, M.; Rundle, S.A.; Harley, H.G.; Crow, S.R.; Sohn, R.; Thirion,
Genomics 18, 673-679, 1993
A;Title: Genomic organization and transcriptional units at the myotonic dystrophy locus.
A;Reference number: A49364; MUID:94140369; PMID:7905855
A;Accession: B49364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-624 <SHA>
A;Cross-references: UNIPROT:Q09013; GB:L19268; NID:g307176; PIDN:AAA36206.1; PID:g307177
R;Sasagawa, N.; Sorimachi, H.; Maruyama, K.; Arahata, K.; Ishiura, S.; Suzuki, K.
FEBS Lett. 351, 22-26, 1994
A;Title: Expression of a novel human myotonin protein kinase (McPK) cDNA clone which enc
A;Reference number: S48681; MUID:95357271; PMID:8076686
A;Accession: S48681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'PPGQVRGRLLAVGGA', 57-550,'WLWASARWWGQA', 564-624 <BRO>
A;Cross-references: GB:M94203; GB:M91465; NID:g186755; PIDN:AAA64884.1; PID:g186756
A;Note: sequence extracted from NCBI backbone (NCBIN:82640, NCBIP:82641)
C;Genetics:
C;Gene: GDB:DM
A;Cross-references: GDB:119097; OMIM:160900
A;Map position: 19q13.2-19q13.3
C;Superfamily: protein kinase homology
C;Keyword: ATP; phosphotransferase
F;69-339/Domain: protein kinase homology <KIN>
F;77-85/Region: protein kinase ATP-binding motif

Query Match             33.2%;  Score 863;  DB 2;  Length 624;
Best Local Similarity   40.8%;  Pred. No. 1e-31;
Matches  179;  Conservative  88;  Mismatches  154;  Indels  18;  Gaps  7;

Qy     46 LSREGILDALFVLFECSQPALMKIKHSVNFVRKYSDTIAELQELQPSAKDFEVRSLVGC 105
             |||||:|||||||||||:|| :     ||:|| ||:|:| : |||::|||:
Db     20 LGLEPLDLLLGVHQELGASELAQDKYVADFLQWAEPIVRLKEVRLQRDDFEILKVIGR 79

Qy    106 GHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQLQYAFQ 165
             ||:||||||||||||||||||| |      ||:|||||||:|||||||||||||:| ||
Db     80 GAFSEVAVVKMKQTGQVYAMKIMNKWDMLKRGEVSCFREERDVLVNGDRRWITQLHFAFQ 139

Qy    166 DKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPE 225
             ||:||:|||||||||||||||||||||||||:||||||||:|| ||::|||||||||||
Db    140 DENYLYLVMEYVPGGDLLTLLSKFGERIPAEMARFYLAEIVMAIDSVHRLGYVHRDIKPD 199

Qy    226 NILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVL-TVMNGDGKGTYGLDC 284
             ||| ||:|||||:|||||||| : ||||:|||:|:||::||:|: |||:|||||||||||
Db    200 NILLDRCGHIRLRADFGSCLKLRADGTVRSLVAVGTPDYLSPEILQAVGGGPGTGSYGPEC 259

Qy    285 DWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP-DDPKVSSDFLDLIQSLLC 343
             ||||||||||||||||||||||||:|||||||||||||||| |||||||||||||||:||
```

A;Residues: 1-522 <STO>
A;Cross-references: UNIPROT:Q9SA79; GB:AE005172; NID:g4587520; PIDN:AAD25751.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis thaliana protein kinase T5I8.9; protein kinase homology

```
Query Match      27.7%;  Score 721;  DB 2;  Length 522;
Best Local Similarity  35.9%;  Pred. No. 1.8e-25;
Matches 158;  Conservative 82;  Mismatches 132;  Indels 68;  Gaps 9;

Qy    69 KIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVM 128
            :|||:||::|:.: |||::| |:|| ||| ||.:.|||:::|||:|.:||||||||:
Db   196 NLIQFYLAELILAVSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMN-------- 247

Qy    93 KMDILKNFEKKEMEYM-RLQRQKMGVDDFELLSIIGRGAPGEVRICKEKSTGSVYAMKKL 151
            |:| |:::::::|: |:::|:: |:|||:||:.::|:|:|||:| |:|||
Db   138 DEARFVVAETILAIESIHKNYIHRDIKPDNLLLDKFGHLRLSDFGLCKPLDCSTLEEKD 197

Qy   129 KKKALLAQEQVSFFEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNR 188
                                     --SNKMVNAKLPIGTPDYMAPEVLTVMNGDG 276
Db   248 --------------------------
            :| ||||||||||||||||:|| |

Qy   152 KKSEMLRRGQVEHVKAERNVLAEVDSPFIVKLCYSFQDDEHLYLIMEYLPGGDMMTLLMR 211
            |:|| ||||||||||||||||||||||||||:|||||||||:||||||||||||||||
Db   198 FEVNNGNGGSPSNEGSTKPRRTQQEQLQHWQKNRRMLAYSTVGTPDYIAPEVLL------ 251

Qy   189 YEDQLDENLJQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNS 248
            :|||||||::|::::||||||:::.||||||||||||:: | |
Db   277 KGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLD 336

Qy   212 -KDTLREDETRFYVAQTILAIESIHKNYVHRDIKPDNLLITRNGHIKLSDFGLSKSLES 270
             |||| |||: | :|:|:::||||: |||||||||:||
Db   252 KKGYGMECDWWSLGAIMYEMLVGYPFYSDDPMSTCRKIVNWRTHLKFPEEAKLSPEAKD 311

Qy   249 ---------------------------NKMVNAKLPIGTPDYM 264
                                       :||||||
Db   337 LIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEK 393

Qy   265 APEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKF 324
            |||||:::|||| |:: |:::|||::|: |::::|||::
Db   312 LISKLLCNVTQRLGSNGAHEIKLHPWFNGIDWERIYQMEAAFIPEVNDELDTQNFEKFEE 371

Qy   331 APEVLL------KKGYGMECDWWSLGAIMFEMLVGFPPFYSEEPLATCRKIVNWKTCLKF 384
            |||||       :||:::|
Db   394 NSWVSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESSVVSGLDSPAKTSSMEKKL 451

Qy   325 PDDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKS 381
            | :|:  |:::| |: |:|  |:  : : |:|||:|
Db   372 ADNSSQSTSKAGPWRKMLSSKDLNFVGYTY-KNFEIV--NDYQVPGIAELKKKDTKPKRP 428

Qy   385 PDEAKLSIEVKDLIRRLLCNVEQRLGTKGVHEIKAHPWFRGVEWERLYESNAPYIPQVKH 444
            |||:::| :|:||:| |||  |:::| : :
Db   429 SIKSLFEDESSD 440

Qy   382 DDDTSNFDEPEKNSWVSSSPCQLSPSG------FSGEELPFVGFSYSKALGILGRSESVV 435
            |||:||||||:|:|| ||:|| |||:       ::|||||:|||||||:|| ||||:|.
Db   452 LIKSKELQDSOD 463

Qy   445 ELDTQNFEKFDE----VPSTCQTSKSSPWRKMISSKDANFLGYTF-KNLEIV--DEHHI 497

Qy   436 SGLDSPAKTSSMEKKLLIKS 455
            : :|  |::|:|::|:
Db   498 PGMAELKRKSKSKTANKPSLKT 517

RESULT 12
S42864
protein kinase (EC 2.7.1.-) - common ice plant (fragment)
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 06-Jan-1995 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: S42864
R;Baur, B.; Winter, K.; Fischer, K.; Dietz, K.
submitted to the EMBL Data Library, March 1994
A;Description: Molecular cloning and characterization of several protein kinases from pl
A;Reference number: S42864
A;Accession: S42864
A;Molecule type: mRNA
A;Residues: 1-479 <BAU>
A;Cross-references: UNIPROT:Q9LW99; EMBL:Z30329; NID:g457688; PIDN:CAA82990.1; PID:g4576
C;Superfamily: Arabidopsis thaliana protein kinase T5I8.9; protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
F;38-338/Domain: protein kinase homology <KIN>
F;46-54/Region: protein kinase ATP-binding motif

```
Query Match      27.3%;  Score 711;  DB 2;  Length 479;
Best Local Similarity  36.8%;  Pred. No. 4.5e-25;
Matches 159;  Conservative 74;  Mismatches 145;  Indels 54;  Gaps 7;

Qy    76 FVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLA 135
            |:||||||||||||||||| ::: ||::|:||||||||:||||||:|||||:::::|
Db    19 FLEKKETEYMRLQRHKMGADDFELLTMIGKGAFGEVRVCREKTTGHVYAMKCLKKSEMLR 78

Qy   136 QEQVSFFEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDE 195
            ||||| |||||||||||||||||||||||||||||||||||||||||||||:|:|:||
Db    79 RGQVEHVKAERNLLAEVDSNCIVKLYCSFQDEEYLYLIMEYLPGGDMMTLLMR-KDTLTE 137
```

RESULT 13
S60966
probable protein kinase YNL161w (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N1727
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S60966; S63113; S63813
R;Nasr, F.; Becam, A.M.; Herbert, C.J.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 con
tonic dystrophy kinase.
A;Reference number: S60958
A;Accession: S60966
A;Molecule type: DNA
A;Residues: 1-756 <NAS>
A;Cross-references: UNIPROT:P53894; EMBL:X92517; NID:g1050783; PIDN:CAA63278.1; PID:g105(
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62967
A;Accession: S63113
A;Molecule type: DNA
A;Residues: 1-756 <NAW>
A;Cross-references: EMBL:Z71437; NID:g1302127; PIDN:CAA96048.1; PID:e239962; PID:g130212(
A;Experimental source: strain S288C
R;Nasr, F.; Becam, A.M.; Herbert, C.J.
Yeast 12, 169-175, 1996
A;Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete
dystrophy kinase.
A;Reference number: S63805; MUID:96287653; PMID:8686380
A;Accession: S63813
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 307-756 <NAF>
A;Cross-references: EMBL:X92517
C;Genetics:
A;Gene: SGD:CBK1
A;Cross-references: SGD:S0005105
A;Map position: 14L
A;Note: YNL161w
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase
F;350-672/Domain: protein kinase homology <KIN>
F;358-366/Region: protein kinase ATP-binding motif

```
Query Match      27.1%;  Score 704;  DB 2;  Length 756;
Best Local Similarity  32.7%;  Pred. No. 1.4e-24;
Matches 163;  Conservative 82;  Mismatches 159;  Indels 94;  Gaps 10;
```

Qy   426 GILGRSESVVSGLDSPA--KTSSMEKKLLIKSKELQDSQDKCH 466
              :|| : ||| |::|
Db   420 LLLS-------DSPSCKENDSIQSR--KNEESQEIQKKLY 450

RESULT 9
S74245
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform II, Rho-associated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C;Accession: S74245
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74245
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1388 <NAK>
A;Cross-references: UNIPROT:P70336; EMBL:U58513; NID:g1514697; PIDN:AAC53133.1; PID:g151
C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase
F;90-354/Domain: protein kinase homology <KIN>
F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match   32.8%; Score 853.5; DB 2; Length 1388;
Best Local Similarity   40.0%; Pred. No. 5.7e-31;
Matches 177; Conservative 95; Mismatches 144; Indels 27; Gaps 9;

Qy   32 QGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQ 91
             ||: ||: |::||:||::|||:|:||||| :|||:||| :|||:||::|:| : ::||
Db   27 QRKLEALIRDPRSPINVESLLDGLNSLVLDLDFPALRKNKNIDNFLNRYEKIVKKIRGLQ 86

Qy   92 PSAKDFEVRSLVGCCHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFEEERNILSR 151
           : :: :||||: ||| | ||::| ::|| :||||| |||| ::||:| |||:|::
Db   92 GEVDVKVIGRGAFGEVQLVRHKASQKYYAMKLLSKFEMIKRSDSAFWEERDIMAF 146

Qy   152 STSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHS 211
            || ||:|||||| :::|||:|||||:||||||||||||: ::||||||||||||||||:
Db   147 ANSPWVVQLFCAFQDDRYLIWMVEVMPGGDLVNLMSNYD--VPEKWAKFYTAEVVLALDA 204

Qy   212 VHLMGYVHRDIKPENLIVDRTGHIKLVDFGSAAKMNSKMVNAKLPIGTPDYMAPEVLTV 271
             | :|||||||||||::| | |:|::|||:|: ||| |: : : : :|||||||||:|
Db   205 IHSMGLIHRDVKPDNMLLDKHGHLKLADFGTCMKRMDETGMVHCDTAVGTPDYISPEVLKS 264

Qy   272 MNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVS 331
           ||||||||||| |:||| |||||||||||||||| :|||| ||||||:|| :|||||:
Db   272 PAEIRLGRGGAGDFQKHPFFFGLDWEGLRDSVPPFTPDFEGATDTCNFDVVEDRLTAMVS 331

Qy   332 SDFLDLIQSLLCGQKERLKPFG----LCCHPFFSKIDWN--NIRNSPPPFVPTLKSDDDTS 386
           |||||:|||||||:|||:|||| |||||||:|||: ::||||||||:|||:|| :|
Db   323 KHAKNLICAFLTDREVRLGRNGVEEIKQHPFFKNDQWNWDNIRETAAPVVPELSSDIDSS 382

Qy   387 NFDEPEKNSW-VSSSPCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSP--AK 443
           ||| ||:|| |:||||:||: || ||||:|| |
Db   383 NFDDIEDDKGDVETFPI---PKAFVGNQLPFIGFTYFRENLLS----------DSPPCRE 430

Qy   444 TSSMEKKLLIKSKELQDSQDKCH 466
           ||||||||||||||:|||||||
Db   431 NDAIQTR--KSEESQEIQKKLY 450

RESULT 10
S71829
serine/threonine-specific protein kinase (EC 2.7.1.-) - mouse
N;Alternate names: myotonic dystrophy-associated protein kinase; myotonin protein kinase
C;Species: Mus musculus (house mouse)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
C;Accession: S71829; S38815
R;Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Worm
submitted to the EMBL Data Library, January 1993
A;Description: Structure and genomic sequence of the myotonic dystrophy kinase (DM kinas

A;Reference number: S71829
A;Accession: S71829
A;Molecule type: DNA
A;Residues: 1-557 <MAH>
A;Cross-references: UNIPROT:P54265; EMBL:Z21505
R;Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Worm
Hum. Mol. Genet. 2, 299-304, 1993
A;Title: Structure and genomic sequence of the myotonic dystrophy (DM kinase) gene.
A;Reference number: S38815; MUID:93271990; PMID:8499920
A;Accession: S38815
A;Molecule type: DNA
A;Residues: 1-53 <MAW>
A;Cross-references: EMBL:Z21503
C;Genetics:
A;Introns: 54/1; 84/3; 112/3; 144/2; 194/2; 225/3; 294/3; 382/3; 411/2; 448/3; 503/2
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
F;69-339/Domain: protein kinase homology <KIN>
F;77-85/Region: protein kinase ATP-binding motif

Query Match   32.6%; Score 847; DB 2; Length 557;
Best Local Similarity   44.3%; Pred. No. 4.7e-31;
Matches 171; Conservative 75; Mismatches 130; Indels 10; Gaps 5;

Qy   46 LSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGC 105
             |:| |::: | || :::| |||::::| : ::|:|
Db   20 LGLEPLLDLLLGVHQELGASHLAQDKYVADFLQWVEPIAARLKEVRLQRDDFEILKVIGR 79

Qy   106 GHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFEEERNILSRSTSPWIPQLQYAFQ 165
           ||| |||:|::|||| :||||| |||| :||:|: |||::||||:|||:|||||||
Db   80 GAFSEVAVVKMKQTGQVYAMKIMNKWDMLKRGEVSCFREERDVLVKGDRRWITQLHFAFQ 139

Qy   166 DKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPE 225
           |||:|:|||||:||||||:|||||: :||||||||:|||:|:|||: |:||||||||
Db   140 DENYLYLVMEYVVGGDLLTLLSKFGERIPAEMARFVLAEIVMAIDSVHRLGYVHRDIKPD 199

Qy   226 NILVDRTGHIKLVDFGSAAKMNSKMVNAKLPIGTPDYMAPEVL-TVMNGDGKGTYGLDC 284
           ||| ||:|||:|:|||:|:|| |: ::| : :|||||:|: | :::| |::|| |
Db   200 NILLDRCGHIRLADFGSCLKLQPDGMVRSLVAVGTPDYLSPEILQAVGGGPGAGSYGPEC 259

Qy   285 DWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP-DDPKVSSDFLDLIQSLLC 343
           |||: ||:|||||||||||:| :|:||:|:|::||||| :|:|||||||||||||
Db   260 DWWALGVFAYEMFYGQTPFYADSTAETYAKIVHYREHLSLPLADTVVPEEAQDLIRGLLC 319

Qy   344 GQKERLKFEG----LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFD--EPEKNSWVS 398
           ||||||||| |||||||||:||||||||:||||||||:||||:|| | ||||:||
Db   320 PAEIRLGRGGAGDFQKHPFFFGLDWEGLRDSVPPFTPDFEGATDTCNFDVVEDRLTAMVS 379

Qy   399 SSPCQLSPSGFS---GEELPFVGFSY 421
           ||||||||||| :|||||||||
Db   380 GGGETLSDMQEDMPLGVRLPFVGYSY 405

RESULT 11
G86431
protein kinase T5I8.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86431
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, 1
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86431
A;Status: preliminary
A;Molecule type: DNA

```
Qy    4 FKYGARNP--LDAGAAEPIANRASRINLFPQGKPPMTQQMSPLSREGILDALFVLFEE      61
           :  ::|: |:  .::::||: |:|||:||  .|
Db  265 YMYFERRRPDILLTKGTQDKAAAVKLKIENFYQSSVKYAIERNERRVELETELTSHNWSEER  324

Qy   62 CSQPALMKIGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATGD   121
        |:  ||||||||:||:|:|||:|
Db  325 KSRQLSSLGKKESQFLR------LRRTRISLEDFHTVKVIGKGAFGEVRLVQKKDTGK     376

Qy  122 IYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGD   181
        |||:||  :::.:.|||||||||| |||||||||||||||||||||||||||
Db  377 IYAMKTLLKSEMYKKDQLAHVKAERDVLAGSDSPWVVSLYYSFQDAQYLYLIMEFLPGGD   436

Qy  182 LLSLLNRYEDQLDENLIQFYLAELLAVHSVHLMGYVHRDIKPENLLVDRTGHIIKLVDFG   241
        ||||||||||||||||||||:||||||:||||||||||||||||||||||||||||||
Db  437 LMTMLIRWQ-LFTEDVTRFYMAECILAIETIHKLGFIHRDIKPDNILIDIRGHIKLSDFG   495

Qy  242 --------SAAKWNSN-------                                       249
               :|:
Db  496 LSTGFHKTHDSNYYKKLLQQDEATNGISKPGTYNANTTDTANKRQTMVVDSISLTMSNRQ   555

Qy  250 -------KMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRS    301
                :|||||||||||||||||||||||||||||||||||||||
Db  556 QIQTWRKSRRLMAVSTVGTPDYIAPEIFLYQG------YGQECDWWSLGAIMYECLIGWP   609

Qy  302 PFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEG----LCCH   357
        :|  |  |: :|| :|:| :| |  ||||||||||||||||||
Db  610 PFCSETPQETYRKIMNFEQTLQFPDDIHISYEAEDIIRRLLTHADORLGRHGGADEIKSH   669

Qy  358 PFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPC--------QLSPSG   408
        |||:.|| |:|| :  |
Db  670 PFFRGVDWNTIRQVEAPYIPKLSSITDTRFPTDELEN-VPDSPAMAQAAKQREQMTKQG   728

Qy  409 FSG---EELPPVGFSYSK                                           423
         |.|:|:|:::|:
Db  729 GSAPVKEDLPFIGYTYSR                                           746
```

RESULT 14
S49077
protein kinase PKTL7 (EC 2.7.1.-) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49077
R;Huang, Y.; Wan, J.; Ko, K.; Dennis, D.T.
submitted to the EMBL Data Library, December 1992
A;Description: A cAMP-dependent protein kinase homolog in tobacco leaf.
A;Reference number: S49077
A;Accession: S49077
A;Molecule type: mRNA
A;Residues: 1-526 <HUA>
A;Cross-references: UNIPROT:Q40547; EMBL:X71057; NID:g506533; PIDN:CAA50374.1; PID:g5065
C;Superfamily: Arabidopsis thaliana protein kinase TSI8.9; protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
P;109-420/Domain: protein kinase homology <KIN>
F;117-125/Region: protein kinase ATP-binding motif

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Query Match         26.9%;   Score 701;  DB 2;  Length 526;
Best Local Similarity   35.9%;   Pred. No. 1.4e-24;
Matches  160;  Conservative   74;  Mismatches 144;  Indels  68;   Gaps    8;

Qy   76 FVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEV---------QVVREKATGDIYA    124
Db   90 FLEKKETEYMRLQRHRHMGADDFELLTMIGKGAFGEPICMIGFSVITGQNCREKTGQVYA   149

Qy  125 MKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLS   184
Db  150 MKKLKKSEMLRRGQVEHVKAERNLLAEVDSDCIVKLYYSFQDDYLYLVMEYLPGGDMMT    209

Qy  185 LLNRYEDQLDENLIQFYLAELLAVHSVHLMGYVHRDIKPENILVDRTGHIIKLVDFG     244
Db  210 LLMR-KDILTEDEARFYVAETVLAIESIHKHNYIHRDIKPDNLLLDRYGHLKLSDFGLCK   268
```

```
Qy  245 KMN-----------------------------SNKMVNAKLPIGTPDYMA           265
        ::|
Db  269 PLDCSTLEEKDFSVGDNANGGSRSDSPPAPKRTQQELEHWQKNRRMLAYSTVGTPDYIA   328

Qy  266 PEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP   325
Db  329 PEVLL-------KKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVWKNHLKFP   382

Qy  326 DDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSD   382
Db  383 EEAKLSPEAKDIISRLLCNVTERLGSNGADEIKVHSWFKGIDWDRIYQMEAAFIPEVNDE   442

Qy  383 DDTSNFDEPEKNSWVSSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESVVSGLDS   440
Db  443 LDTQNFEKFEESESHSQSGRSGPWRKMLSSKDINFVGYTYKNFKVV---NDYQVPGMVE   499

Qy  441 PAKTSMEKKLLIKS---KELQDSQD                                    463
Db  500 LKKTNTKPKKPTIKSLFGDESEASED                                   525
```

RESULT 15
T41723
serine/threonine-specific protein kinase (EC 2.7.1.-) orb6 - fission yeast (Schizosacchar
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T41723; T43526
R;Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z22012
A;Accession: T41723
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-469 <RIE>
A;Cross-references: UNIPROT:O13310; EMBL:AL121770; PIDN:CAB57446.1; GSPDB:GN00066; SPDB:S
A;Experimental source: strain 972h-; cosmid c821
R;Verde, F.; Wiley, D.J.; Nurse, P.;
Proc. Natl. Acad. Sci. U.S.A. 95, 7526-7531, 1998
A;Title: Fission yeast orb6, a ser/thr protein kinase related to mammalian rho kinase and
th the cell cycle.
A;Reference number: Z22544; MUID:98301608; PMID:9636183
A;Accession: T43526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-469 <VER>
A;Cross-references: EMBL:AF009512; NID:g2443510; PIDN:AAC32420.1; PID:g2443511
C;Genetics:
A;Gene: orb6; SPAC821.12
A;Map position: 1
A;Introns: 48/2; 106/3
C;Function:
A;Description: coordinates maintenance of cell polarity during interphase with the onset
A;Note: interacts genetically with orb2, which encodes the Pak1/Shk1 protein kinase
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase

```
Query Match         26.9%;   Score 700;  DB 2;  Length 469;
Best Local Similarity   39.2%;   Pred. No. 1.4e-24;
Matches  148;  Conservative   63;  Mismatches 113;  Indels  54;   Gaps    8;

Qy   93 SAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRS   152
Db   89 SLEDFSTIKVIGKGAFGEVRLVQKLDTGKIYAMKSLLKTEMFKRDQLAHVKAERDLLVES   148

Qy  153 TSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELLILAVHSV  212
Db  149 DSPWVVSLYYAFQDSLYLYLIMEFLPGGDLMTLINY-DTFSEDVTRFYMAECVLAIADV    207

Qy  213 HLMGYVHRDIKPENILVDRTGHIKLVDFG-------SAAKM--------            246
Db  208 HRMGYIHRDIKPDNLILDRDGHIKLSDFGLSTGFYKQDQSASYMKPRTGNTVKRGQMVDA   267

Qy  247 -----------------NSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVI  292
```

```
Db   268 IWLTMSSKDKMATWKKNRRVMAYSTVGTPDYIAPEIF-LQQG-----YGQDCDWWSLGAI 321
             :|:|   |     :||||||:|||::       |     ||  ||||||:|

Qy   293 AYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDDPKVSSDFLDLIQSLLCGQKERLKFE 352
             :|:||   ||   ||:   ||:|   |||:|    :|:|  :    |||:|:|

Db   322 MFECLIGWPPFCSENSHETYRKIINWRETLTFPNDIHLSIEARDLMDRLMTDSEHRLGRG 381

Qy   353 G--LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNF--DEPEK--NSWVSSSPCQLS 405
              |  |:||||: |||::||:|||:||   ||: |      | :| ——      |

Db   382 GAIEIMQHPFFTGIDWDHIRETAAPFIPNLKSITDTHYFPVDELEQVPEQPVTQQPASVD 441

Qy   406 PSGFSGEELPVGFSYSK 423
         |  |:|::||

Db   442 PQTLEQTNLAFLGYTYKK 459
```

Search completed: March 18, 2005, 15:40:47
Job time : 45 secs

```
            GenCore version 5.1.6
      Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:  . March 18, 2005, 15:21:39 ; Search time 174 Seconds
                                       (without alignments)
                                       1104.712 Million cell updates/sec

Title:          US-10-724-594-2
Perfect score:  2602
Sequence:       1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2105692 seqs, 38676038l residues

Total number of hits satisfying chosen parameters:      2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_16Dec04:*
          1:    geneseqp1980s:*
          2:    geneseqp1990s:*
          3:    geneseqp2000s:*
          4:    geneseqp2001s:*
          5:    geneseqp2002s:*
          6:    geneseqp2003a8:*
          7:    geneseqp2003bs:*
          8:    geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2602	100.0	497	6	ABU10126	Abu10126 Novel hum
2	2602	100.0	497	8	AAE39504	Aae39504 Human kin
3	2602	100.0	497	8	ADO40592	Ado40592 Human uro
4	2597	99.8	497	6	ABP97687	Abp97687 Amino aci
5	2589	99.5	497	6	AAE16261	Aae16261 Human kin
6	2589	99.5	497	6	ABU10127	Abu10127 Variant n
7	2582	99.2	495	6	ABP97681	Abp97681 Amino aci
8	2440	93.8	620	8	ADN62809	Adn62809 Human NOV
9	2440	93.8	623	6	ADA05644	Ada05644 Human NOV
10	2440	93.8	1958	8	ABB81928	Abb81928 Human kin
11	2440	93.8	2054	5	ABB81927	Abb81927 Human kin
12	2440	93.8	2054	5	AAE24150	Aae24150 Human kin
13	2440	93.8	2054	6	AAO26959	Aao26959 Human CRI
14	2430	93.4	2053	7	AAE24079	Aae24079 Human MDP
15	2430	93.4	2053	8	ADF60994	Adf60994 Pain asso
16	2430	93.4	2053	8	ADQ89100	Adq89100 Human uro
17	2418.5	92.9	2053	4	AAU03501	Aau03501 Human pro
18	2418.5	92.9	2055	5	ADJ96610	Adj96610 Human cit
19	2412.5	92.7	2053	5	ABG78363	Abg78363 RHO/RAC-i
20	2412.5	92.7	2053	8	ADA05642	Ada05642 Human NOV
21	2412.5	92.7	2053	8	ADN63228	Adn63228 Human NOV
22	2412.5	92.7	2053	8	ADN62807	Adn62807 Human NOV
23	2412.5	92.7	2066	6	ABG78362	Abg78362 Human pro
24	2412.5	92.7	2066	5	ADA05654	Ada05654 Human NOV
25	2400.5	92.3	2066	8	ADN62819	Adn62819 Human NOV
26	2271.5	87.3	6	494	ABP97682	Abp97682 Polypepti
27	2271.5	87.3	8	494	ADO40594	Ado40594 Mouse cit
28	2172.5	83.5	6	2055	ABP97683	Abp97683 Polypepti
29	2172.5	83.5	6	2055	AAO26960	Aao26960 Human CRI
30	1652	63.5	7	319	ADN62730	Adn62730 Human cit
31	1627	62.5	5	349	ABG15566	Abg15566 Novel hum
32	1284	49.3	4	257	ADJ79947	Adj79947 Human kin
33	1180	45.3	7	251	ADJ79949	Adj79949 Rat kinas
34	1177	45.2	7	251	ADJ79950	Adj79950 Mouse kin
35	932.5	35.8	8	1565	ADP47967	Adp47967 Human MRC
36	929	35.7	6	475	AAE24131	Aae24131 Human kin
37	929	35.7	6	1197	ABJ37881	Abj37881 NOVX prot
38	929	35.7	6	1247	ABJ37882	Abj37882 NOVX prot
39	929	35.7	8	1551	ADI40850	Adi40850 Human kin
40	929	35.7	8	1553	ADC99064	Adc99064 Human KPP
41	929	35.7	8	1569	ADF95102	Adf95102 Human ser
42	929	35.7	5	1572	AAE19162	Aae19162 Human kin
43	929	35.7	8	1572	ADJ96611	Adj96611 Human dys
44	929	35.7	8	1572	ADQ15094	Adq15094 Human can
45	926	35.6	8	1648	ADF95100	Adf95100 Human ser

ALIGNMENTS

```
RESULT 1
ABU10126
ID   ABU10126 standard; protein; 497 AA.
XX
AC   ABU10126;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Novel human kinase.
XX
KW   Human; enzyme; gene therapy; kinase; antisense.
XX
OS   Homo sapiens.
XX
PN   US2003022340-A1.
XX
PD   30-JAN-2003.
XX
PF   11-SEP-2002; 2002US-00238709.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-438978/41.
DR   N-PSDB; ACA61394.
XX
PT   New human kinase peptides useful as models or targets for the development
PT   of therapeutic agents that modulate kinase activity, for eliciting immune
PT   response, and in identifying compounds that modulate kinase activity or
PT   expression.
XX
PS   Claim 1; Fig 2; 207pp; English.
XX
CC   The invention relates to a novel isolated human kinase. The kinase
CC   peptides and nucleic acids are useful as models for the development of
CC   human therapeutic targets, in the identification of therapeutic proteins,
CC   and serve as targets for the development of human therapeutic agents that
CC   modulate kinase activity in cells and tissues that express the kinase.
CC   The proteins can be used to raise or to elicit another immune response,
CC   as a reagent in assays designed to determine the levels of the protein in
CC   biological fluids, as markers for tissue in which the corresponding
CC   protein is preferentially expressed, in the identification of modulators
CC   of the peptides and in pharmacogenomic analysis. The nucleic acids are
CC   useful as hybridisation probes, in constructing vectors, host cells or
CC   transgenic animals expressing all or a part of the nucleic acid, for
```

```
CC    monitoring the effectiveness of modulating compounds on the expression or
CC    activity of the transporter gene in clinical trials or in treatment
CC    regimen, in gene therapy and as antisense constructs to control
CC    transporter gene expression in cells, tissue and organisms. The present
CC    sequence represents the amino acid sequence of a novel human kinase
XX
SQ    Sequence 497 AA;

Query Match      100.0%;     Score 2602;  DB 6;  Length 497;
Best Local Similarity   100.0%;  Pred. No. 2.1e-254;
Matches  497;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy    61 ECSQPALMKIKIHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ECSQPALMKIKIHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy   121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLYAFQDKNHLYLVMEYQPGG 180

Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENLLVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENLLVDRTGHIKLVDF 240

Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy   481 ILPSVYAKGSARGRCWL 497
          |||||||||||||||||
Db   481 ILPSVYAKGSARGRCWL 497


RESULT 2
AAE39504
ID   AAE39504 standard; protein; 497 AA.
XX
AC   AAE39504;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human kinase protein.
XX
KW   Human; kinase protein; diagnostic; therapeutic; immune response; enzyme;
KW   pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic.
XX
OS   Homo sapiens.
XX
FH   Key    Location/Qualifiers
FT   Modified-site    50..55
FT           /note= "N-myristoylation site"
FT   Modified-site    78..81
FT           /note= "cAMP and cGMP dependent protein kinase
FT           phosphorylation site"
FT   Modified-site    83..86
FT           /note= "Caesin kinase II phosphorylation site"
FT   Modified-site    93..96
FT           /note= "Caesin kinase II phosphorylation site"
FT                   93..95
FT   Region
FT           /note= "Protein kinase C phosphorylation site"
FT                   103..126
FT   Modified-site
FT           /note= "Protein kinase ATP-binding region signature"
FT                   140..143
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   197..217
FT   Region
FT           /note= "Helix I"
FT                   217..229
FT   Active-site
FT           /note= "Serine/Threonine protein kinase active-site
FT           signature"
FT                   248..250
FT   Modified-site
FT           /note= "Protein kinase C phosphorylation site"
FT                   308..310
FT   Modified-site
FT           /note= "Protein kinase C phosphorylation site"
FT                   361..364
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   365
FT   Misc-difference
FT           /note= "This residue changes to Cys during single
FT           nucleotide polymorphism (SNP)"
FT                   378..380
FT   Modified-site
FT           /note= "Protein kinase C phosphorylation site"
FT                   381..384
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   386..389
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   410..413
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   436..439
FT   Modified-site
FT           /note= "Caesin kinase II phosphorylation site"
FT                   445..448
FT   Region
FT           /note= "Helix II"
FT                   467..487
FT   Modified-site
FT           /note= "N-myristoylation site"
FT                   474..479
FT   Modified-site
FT           /note= "N-myristoylation site"
FT                   489..494
FT   Modified-site
FT           /note= "Protein kinase C phosphorylation site"
FT                   490..492
XX
PN   US200213322-A1.
XX
PD   19-SEP-2002.
XX
PF   13-MAR-2001; 2001US-00804471.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (WEBS/) WEBSTER M.
PA   (YANC/) YAN C.
PA   (DFRA/) DI FRANCESCO V.
PA   (BEAS/) BEASLEY E M.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-687480/65.
DR   N-PSDB; AAD59937, AAD59938.
XX
PT   New isolated human kinase proteins, useful as models for developing human
PT   therapeutic targets, or for treating a disorder associated with an
PT   absence of, inappropriate or unwanted expression of the protein, e.g.
PT   cancer.
XX
PS   Claim 1; Fig 2; 0pp; English.
XX
CC   The present invention relates to human kinase proteins and nucleic acids
CC   encoding them all of which are useful in the development of human
CC   therapeutics and diagnostic composition and methods. The invention is
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents. The invention is also useful in
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CC   drug screening assays, in assays to determine the biological activity of
CC   the protein, to raise antibodies and to elicit another immune response.
CC   The antibodies are useful in pharmacogenomic analysis, for inhibiting
CC   protein function and for tissue typing. The transgenic animals are useful
CC   for studying the function of kinase protein, identifying and evaluating
CC   modulators of kinase protein activity. The invention is also used in gene
CC   therapy. The present sequence is the human kinase protein. The human
CC   kinase gene is located on chromosome 12
XX
SQ   Sequence 497 AA;

Query Match             100.0%;  Score 2602;  DB 7;  Length 497;
Best Local Similarity   100.0%;  Pred. No. 2.1e-254;
Matches  497;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy   121  DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy   301  SPFAEGTSARTFNNIMNFQRPLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SPFAEGTSARTFNNIMNFQRPLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy   421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy   481  ILPSVYAKGSARGRCWL 497
          |||||||||||||||||
Db   481  ILPSVYAKGSARGRCWL 497
```

RESULT 3
ADO40592
```
ID   ADO40592 standard; protein; 497 AA.
XX
AC   ADO40592;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Human kinase protein.
XX
KW   Kinase; rho/rac-interacting citron kinase; drug screening;
KW   kinase related disorder; human; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Modified-site  50 .55
FT                  /note= "N-myristoylation site"
FT   Modified-site  78 .81
FT                  /note= "cAMP and cGMP dependent protein kinase
FT                  phosphorylation site"
```

```
FT   Modified-site  83 .86
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  93 .96
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  93 .95
FT                  /note= "Protein kinase C phosphorylation site"
FT   Binding-site   103 .126
FT                  /note= "Protein kinase ATP-binding region signature"
FT   Modified-site  140 .143
FT                  /note= "Casein kinase II phosphorylation site"
FT   Region         197 .217
FT                  /note= "Helix 1"
FT   Active-site    217 .229
FT                  /note= "Serine/Threonine protein kinase active-site
FT                  signature"
FT   Modified-site  248 .250
FT                  /note= "Protein kinase C phosphorylation site"
FT   Modified-site  308 .310
FT                  /note= "Protein kinase C phosphorylation site"
FT   Modified-site  361 .364
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  378 .380
FT                  /note= "Protein kinase C phosphorylation site"
FT   Modified-site  381 .384
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  386 .389
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  410 .413
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  436 .439
FT                  /note= "Casein kinase II phosphorylation site"
FT   Modified-site  445 .448
FT                  /note= "Casein kinase II phosphorylation site"
FT   Region         467 .487
FT                  /note= "Helix 2"
FT   Modified-site  474 .479
FT                  /note= "N-myristoylation site"
FT   Modified-site  489 .494
FT                  /note= "N-myristoylation site"
FT   Modified-site  490 .492
FT                  /note= "Protein kinase C phosphorylation site"
XX
PN   US2004091993-A1
XX
PD   13-MAY-2004.
XX
PF   02-DEC-2003; 2003US-00724594.
XX
PR   13-MAR-2001; 2001US-00804471.
PR   11-SEP-2002; 2002US-00238709.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2004-374957/35.
DR   N-PSDB; ADO40591, ADO40591, ADO40593.
XX
PT   New isolated human kinase proteins and nucleic acids, useful for
PT   developing human therapeutic targets, identifying therapeutic proteins or
PT   serve as targets for the development of human therapeutic agents that
PT   modulate kinase activity.
XX
PS   Claim 1; SEQ ID NO 2; 207pp; English.
XX
CC   The present invention provides a kinase polypeptide and its encoding
CC   polynucleotide. The polypeptide and polynucleotide of the invention are
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents that modulate kinase activity in
CC   cells and tissues that express the kinase. The invention is also useful
CC   for biological assays related to kinases, in drug screening assays, for
CC   treating disorders characterized by an absence of inappropriate and
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CC   unwanted expression of the protein. The present sequence is the human
CC   kinase protein.
XX
SQ   Sequence 497 AA;

Query Match             100.0%;    Score 2602;   DB 8;   Length 497;
Best Local Similarity   100.0%;    Pred. No. 2.1e-254;
Matches 497;    Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60

Qy     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy    181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR  300

Qy    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360

Qy    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420

Qy    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR  480

Qy    481  ILPSVYAKGSARGRCWL  497
           |||||||||||||||||
Db    481  ILPSVYAKGSARGRCWL  497


RESULT 4
ABP97687
ID   ABP97687 standard; protein; 497 AA.
XX
AC   ABP97687;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Amino acid sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression.
XX
OS   Homo sapiens.
XX
PN   WO200304629-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
PR   25-APR-2002; 2002US-0375015P.
```

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XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   N-PSDB; AB268726.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 19; 145pp; English.
XX
CC   The present sequence represents a human citron rho/rac-interacting kinase
CC   -short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
CC   associated with the polypeptide dysfunction. The expression vector or the
CC   reagent is useful in the preparation of a medicament for modulating the
CC   activity of a human citron rho/rac-interacting kinase-short kinase in a
CC   disease, such as obesity or chronic obstructive pulmonary disease. These
CC   may also be used for treating obesity/ overweight-associated
CC   comorbidities, such as hypertension, diabetes, coronary artery disease,
CC   hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC   apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced
CC   fertility, and depression
XX
SQ   Sequence 497 AA;

Query Match             99.8%;    Score 2597;   DB 6;   Length 497;
Best Local Similarity   99.8%;    Pred. No. 6.9e-254;
Matches 496;    Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
           |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db      1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60

Qy     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy    181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR  300

Qy    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360

Qy    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420

Qy    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR  480

Qy    481  ILPSVYAKGSARGRCWL  497
           |||||||||||||||||
Db    481  ILPSVYAKGSARGRCWL  497


RESULT 5
AAE16261
```

ID   AAB16261 standard; protein; 497 AA.
XX
AC   AAB16261;
XX
PS   Claim 1; Page 146-147; 197pp; English.
XX
DT   26-MAR-2002 (first entry)
XX
DE   Human kinase PKIN-7 protein.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections;
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-7 protein.
XX
SQ   Sequence 497 AA;

     Query Match   99.5%; Score 2589; DB 5; Length 497;
     Best Local Similarity   99.6%; Pred. No. 4.5e-253;
     Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDKGTYRLDCDWWSVGVIAYEMIYGR 300

Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy   481 ILPSVYAKGSARGRCWL 497
                |||||||||||||||||
Db   481 ILPSVYAKGSARGRCWL 497

RESULT 6
ABU10127

ID
XX
AC
XX
XX
DT
XX
DE
XX
KW   Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;
KW   Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Domain   86..124
FT   /label= Protein_kinase_domain
FT   Domain   96..153
FT   /label= Protein_kinase_domain
FT   Domain   97..360
FT   /note= "Eukaryotic protein kinase domain"
FT   Domain   98..241
FT   /label= Protein_kinase_domain
FT   Domain   99..349
FT   /label= Protein_kinase_domain
FT   Domain   101..241
FT   /label= Protein_kinase_domain
FT   Domain   102..241
FT   /label= Protein_kinase_domain
FT   Domain   249..349
FT   /label= Protein_kinase_domain
FT   Domain   258..445
FT   /label= Protein_kinase_domain
FT   Domain   258..349
FT   /label= Protein_kinase_domain
FT   Domain   361..390
FT   /note= "Protein kinase C terminal domain"
XX
PN   WO200196547-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX
PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y,
PI   Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
PI   Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
PI   Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI   Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI   Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX
DR   WPI; 2002-090207/12.
DR   N-PSDB; AAD26454.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.

```
ID   ABU10127 standard; protein; 497 AA.
XX
AC   ABU10127;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Variant novel human kinase.
XX
KW   Human; enzyme; gene therapy; kinase; antisense.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 365
FT                  /note= "Wild-type Trp substituted by Cys as a result of a
FT                  single nucleotide polymorphism"
XX
PN   US2003022340-A1.
XX
PD   30-JAN-2003.
XX
PF   11-SEP-2002; 2002US-00238709.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-438978/41.
XX
PT   New human kinase peptides useful as models or targets for the development
PT   of therapeutic agents that modulate kinase activity, for eliciting immune
PT   response, and in identifying compounds that modulate kinase activity or
PT   expression.
XX
PS   Disclosure; Page; 207pp; English.
XX
CC   The invention relates to a novel isolated human kinase. The kinase
CC   peptides and nucleic acids are useful as models for the development of
CC   human therapeutic targets, in the identification of therapeutic proteins,
CC   and serve as targets for the development of human therapeutic agents that
CC   modulate kinase activity in cells and tissues that express the kinase.
CC   The proteins can be used to raise or to elicit another immune response,
CC   as a reagent in assays designed to determine the levels of the protein in
CC   biological fluids, as markers for tissue in which the corresponding
CC   protein is preferentially expressed, in the identification of modulators
CC   of the peptides and in pharmacogenomic analysis. The nucleic acids are
CC   useful as hybridisation probes, in constructing vectors, host cells or
CC   transgenic animals expressing all or a part of the nucleic acid, for
CC   monitoring the effectiveness of modulating compounds on the expression or
CC   activity of the transporter gene in clinical trials or in treatment
CC   regimen, in gene therapy and as antisense constructs to control
CC   transporter gene expression in cells, tissue and organisms. The present
CC   sequence represents the amino acid sequence of a variant novel human
CC   kinase. Note: The present sequence is not shown in the specification but
CC   was created by the indexer using the information given in figure 3
XX
SQ   Sequence 497 AA;

Query Match             99.5%;  Score 2589;  DB 6;  Length 497;
Best Local Similarity   99.8%;  Pred. No. 4.5e-253;
Matches  496;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy     61 ECSQPALMKIKGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ECSQPALMKIKGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy    181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENLLVDRTGHIKLVDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENLLVDRTGHIKLVDF 240

Qy    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SKIDCNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSSPCQLSPSGSGFSGEELPFVGFS 420

Qy    421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy    481 ILPSVYAKGSARGRCWL 497
          |||||||||||||||||
Db    481 ILPSVYAKGSARGRCWL 497


RESULT 7
ABP97681
ID   ABP97681 standard; protein; 495 AA.
XX
AC   ABP97681;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Amino acid sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression.
XX
OS   Homo sapiens.
XX
PN   WO200300462P9-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
PR   25-APR-2002; 2002US-0375015P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   N-PSDB; ABZ68725.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 2; 145pp; English.
XX
CC   The present sequence represents a human citron rho/rac-interacting kinase
CC   -short kinase polypeptide and polypeptide of the
CC   -short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
```

```
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT   preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT   cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 1; Page 100-101; 586pp; English.
XX
CC   The present invention describes NOVX proteins, where X can be 1 to 55
CC   (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC   described above and a carrier; (2) a kit comprising, in one or more
CC   containers, the composition described above; (3) an isolated nucleic acid
CC   molecule which encodes a NOVX protein of the invention; (4) a vector
CC   comprising the nucleic acid molecule described above; (5) a cell
CC   comprising the above vector; (6) an antibody that immunospecifically
CC   binds to the polypeptide described above; (7) methods for determining the
CC   presence or amount of the above polypeptide or nucleic acid molecule in a
CC   sample; (8) methods for determining the presence or of predisposition to
CC   a disease associated with altered levels of expression of the above
CC   polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC   method of identifying an agent that binds to the polypeptide described
CC   above; (10) a method for identifying a potential therapeutic agent for
CC   use in treating a pathology that is related to an aberrant expression or
CC   aberrant physiological interactions of the polypeptide; (11) a method of
CC   screening for a modulator of activity or of latency or predisposition to
CC   a pathology associated with the polypeptide described above; (12) a method of modulating
CC   the activity of the polypeptide described above; (13) methods of treating
CC   or preventing a pathology associated with the above polypeptide in a
CC   mammal; and (14) a method for producing the above polypeptide. NOVX
CC   sequences have antidiabetic, anorectic, antibacterial, virucide,
CC   immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC   and antilipaemic activities, and can be used in gene therapy. The
CC   polypeptide is useful in manufacturing a medicament for treating a
CC   syndrome associated with a human disease. The polypeptide or the nucleic
CC   acid molecule may be used to diagnose, treat or prevent metabolic
CC   disorders such as diabetes or obesity, infections, cachexia, cancer,
CC   neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC   disease, immune disorders, haematopoietic disorders and various
CC   dyslipidaemias. The nucleic acids can also be used as hybridisation
CC   probes, in chromosome mapping, tissue typing, preventive medicine and
CC   pharmacogenomics. The present sequence represents a human NOVX from the
CC   present invention.
XX
SQ   Sequence 623 AA;

Query Match             93.8%;  Score 2440;  DB 6;  Length 623;
Best Local Similarity   99.6%;  Pred. No. 8.6e-238;
Matches  466;  Conservative    2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
          |||||||||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db     5  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   64

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    65  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  124

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  184

Qy   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  244

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWSVGVIAYEMIYGR  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWSVGVIAYEMIYGR  304

Qy   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  364

Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  424

Qy   421  YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV              468
          |||||||||||||||||||||||||||||||||||||||||||||:
Db   425  YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKM              472


RESULT 10
ABB81928
ID   ABB81928 standard; protein; 1958 AA.
XX
AC   ABB81928;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human kinase #2.
XX
KW   Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
KW   Citron rho-interacting kinase; gene therapy; mental disorder; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200259325-A2.
XX
PD   01-AUG-2002.
XX
PF   20-DEC-2001; 2001WO-US050497.
XX
PR   27-DEC-2000; 2000US-0258335P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Yu X, Miranda M, Friddle CJ;
XX
DR   WPI; 2002-599796/64.
DR   N-PSDB; ABQ78871.
XX
PT   Novel polynucleotide encoding human proteins that are structurally
PT   similar to animal kinases, including serine-threonine kinases,
PT   particularly Citron rho-interacting kinases, useful for drug screening, diagnosis, in gene
PT   therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT   applications.
XX
PS   Claim 4; Page 46-50; 50pp; English.
XX
CC   The invention relates to a novel human protein that shares structural
CC   similarity with animal kinases, including serine-threonine kinases,
CC   particularly Citron rho-interacting kinases. The proteins of the
CC   invention have nootropic and cytostatic activity. The polynucleotides may
CC   have a use in gene therapy. The encoded novel polypeptides are useful for
CC   generating antibodies, as reagents in diagnostic assays, for identifying
CC   other cellular gene products related to NHP and as reagents in assays for
CC   screening for compounds that are useful in the treatment of mental,
CC   biological or medical disorders and diseases including cancer. The
CC   sequence represents a novel human kinase of the invention
XX
SQ   Sequence 1958 AA;

Query Match             93.8%;  Score 2440;  DB 5;  Length 1958;
Best Local Similarity   99.6%;  Pred. No. 5.7e-237;
Matches  466;  Conservative    2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60
          |||||||||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db     1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE   60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
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Query Match   93.8%;   Score 2440; DB 5;   Length 2054;
Best Local Similarity   99.6%;   Pred. No. 6.1e-237;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQMSPLSREGILDALFVLFE   60
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db     1  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQMSPLSREGILDALFVLFE   60

Qy    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG  120

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180

Qy   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR  300

Qy   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360

Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSSGEELPFVGFS  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSSGEELPFVGFS  420

Qy   421  YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV  468
          ||||||||||||||||||||||||||||||||||||||||||||:
Db   421  YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKM  468
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RESULT 12
AAE24150
ID   AAE24150 standard; protein; 2054 AA.
XX
AC   AAE24150;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Human kinase (PKIN)-21 protein.
XX
KW   Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
KW   acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW   asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW   development; hepatitis; cardiovascular; hypertension; drug screening;
KW   myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW   fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW   hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-HIV;
KW   neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;
KW   hyperlipidaemia; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Domain   97. .360
FT   /note= "Eukaryotic protein kinase domain"
FT   Domain   98..241
FT   /note= "Protein kinase domain"
FT   Domain   99..349
FT   /note= "Protein kinase domain"
FT   Domain   101..241
FT   /note= "Protein kinase domain"
FT   Domain   102..241
FT   /note= "Protein kinase domain"
FT   Domain   249. .349
FT   /note= "Protein kinase domain"
FT   Domain   258. .445

Db   121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
Qy   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
Db   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
Qy   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
Db   241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
Qy   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Db   301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
Qy   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSSGEELPFVGFS 420
Db   361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSSGEELPFVGFS 420
Qy   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468
Db   421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 11
ABB81927
ID   ABB81927 standard; protein; 2054 AA.
XX
AC   ABB81927;
XX
DT   10-OCT-2002 (first entry)
XX
DE   Human kinase #1.
XX
KW   Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
KW   Citron rho-interacting kinase; gene therapy; mental disorder; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200259325-A2.
XX
PD   01-AUG-2002.
XX
PF   20-DEC-2001; 2001WO-US050497.
PR   27-DEC-2000; 2000US-0258335P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Yu X, Miranda M, Friddle CJ;
XX
DR   WPI; 2002-599796/64.
DR   N-PSDB; ABQ78870.
XX
PT   Novel polynucleotide encoding human proteins that are structurally
PT   similar to animal kinases, useful for drug screening, diagnosis, in gene
PT   therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT   applications.
XX
PS   Claim 2; Page 39-43; 50pp; English.
XX
CC   The invention relates to a novel human protein that shares structural
CC   similarity with animal kinases, including serine-threonine kinases,
CC   particularly Citron rho-interacting kinases. The proteins of the
CC   invention have nootropic and cytostatic activity. The polynucleotides may
CC   have a use in gene therapy. The encoded novel polypeptides are useful for
CC   generating antibodies, as reagents in diagnostic assays, for identifying
CC   other cellular gene products related to NHP and as reagents in assays for
CC   screening for compounds that are useful in the treatment of mental,
CC   biological or medical disorders and diseases including cancer. The
CC   sequence represents a novel human kinase of the invention
XX
SQ   Sequence 2054 AA;

CC	associated with the polypeptide dysfunction. The expression vector or the
CC	reagent is useful in the preparation of a medicament for modulating the
CC	activity of a human citron rho/rac-interacting kinase-short kinase in a
CC	disease, such as obesity or chronic obstructive pulmonary disease. These
CC	may also be used for treating obesity/ overweight-associated
CC	comorbidities, such as hypertension, diabetes, coronary artery disease,
CC	hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC	apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced
CC	fertility, and depression
XX	
SQ	Sequence 495 AA;

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Query Match             99.2%;  Score 2582;  DB 6;  Length 495;
Best Local Similarity   99.8%;  Pred. No. 2.3e-252;
Matches 494;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy    121 DIYAMKVMKKCALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DIYAMKVMKKCALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy    181 DLLSLLNRYEDQLDENLIQFYLAELLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DLLSLLNRYEDQLDENLIQFYLAELLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSSDFLDLIQSLLCGQXERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSSDFLDLIQSLLCGQXERLKFEGLCCHPFF 360

Qy    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy    481 ILPSVYAKGSARGRC 495
          |||||||||||||||
Db    481 ILPSVYAKGSARGRC 495
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RESULT 8		
ADN62809		
ID	ADN62809 standard; protein; 620 AA.	
XX		
AC	ADN62809;	
XX		
DT	01-JUL-2004 (first entry)	
XX		
DE	Human NOV1b.	
XX		
KW	human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;	
KW	anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;	
KW	Alzheimer's disease; Parkinson's disease; immune disorder;	
KW	haematopoietic disorder; dyslipidaemia; metabolic syndrome X;	
KW	wasting disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	US2004038223-A1.	
XX		

PD	26-FEB-2004.	
XX		
PF	01-OCT-2002; 2002US-00262511.	
XX		
PR	02-OCT-2001; 2001US-0326483P.	
PR	05-OCT-2001; 2001US-0327435P.	
PR	05-OCT-2001; 2001US-0327449P.	
PR	09-OCT-2001; 2001US-0327917P.	
PR	09-OCT-2001; 2001US-0328029P.	
PR	09-OCT-2001; 2001US-0328044P.	
PR	09-OCT-2001; 2001US-0328056P.	
PR	12-OCT-2001; 2001US-0328849P.	
PR	15-OCT-2001; 2001US-0329414P.	
PR	17-OCT-2001; 2001US-0330142P.	
PR	18-OCT-2001; 2001US-0330309P.	
PR	22-OCT-2001; 2001US-0341058P.	
PR	24-OCT-2001; 2001US-0339266P.	
PR	24-OCT-2001; 2001US-0343629P.	
PR	29-OCT-2001; 2001US-0349575P.	
PR	01-NOV-2001; 2001US-0346357P.	
PR	17-APR-2002; 2002US-0373260P.	
PR	19-APR-2002; 2002US-0373815P.	
PR	19-APR-2002; 2002US-0373817P.	
PR	19-APR-2002; 2002US-0373826P.	
PR	19-APR-2002; 2002US-0373884P.	
PR	22-APR-2002; 2002US-0374977P.	
PR	16-MAY-2002; 2002US-0381037P.	
PR	16-MAY-2002; 2002US-0381038P.	
PR	16-MAY-2002; 2002US-0381042P.	
PR	17-MAY-2002; 2002US-0381642P.	
PR	28-MAY-2002; 2002US-0383656P.	
PR	29-MAY-2002; 2002US-0383831P.	
PR	25-JUN-2002; 2002US-0391335P.	
XX		
PA	(SMIT/)	SMITHSON G.
PA	(MILL/)	MILLET I.
PA	(PEYM/)	PEYMAN J A.
PA	(KEKU/)	KEKUDA R.
PA	(JUJJ/)	JU J.
PA	(LILL/)	LI L.
PA	(GUOX/)	GUO X.
PA	(PATT/)	PATTURAJAN M.
PA	(SPYT/)	SPYTEK K A.
PA	(EDIN/)	EDINGER S R.
PA	(ELLE/)	ELLERMAN K.
PA	(MALY/)	MALYANKAR U M.
PA	(ORTT/)	ORT T.
PA	(GORM/)	GORMAN L.
PA	(ZERH/)	ZERHUSEN B D.
PA	(ANDE/)	ANDERSON D W.
PA	(ZHON/)	ZHONG M.
PA	(CATT/)	CATTERTON E.
PA	(JIWW/)	JI W.
PA	(MILL/)	MILLER C E.
PA	(RAST/)	RASTELLI L.
PA	(STON/)	STONE D J.
PA	(PENA/)	PENA C E A.
PA	(SHEN/)	SHENOY S G.
PA	(SHIM/)	SHIMKETS R A.
PA	(ROTH/)	ROTHENBERG M E.
PA	(LEAC/)	LEACH M D.
PA	(AGEE/)	AGEE M L.
PA	(BERG/)	BERGHS C.
PA	(DIPI/)	DIPIPPO V A.
PA	(EISE/)	EISEN A.
PA	(GANG/)	GANGOLLI E A.
PA	(RIEG/)	RIEGER D K.
PA	(SPAD/)	SPADERNA S K.
XX		
PI	Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;	
PI	Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;	
PI	Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;	
PI	Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;	

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PI   Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR   WPI; 2004-213931/20.
DR   N-PSDB; ADN62808.
XX
PT   Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT   diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS   Claim 1; SEQ ID NO 4; 395pp; English.
XX
CC   The invention relates to isolated NOVX polypeptides and polynucleotides.
CC   NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC   treat a medical condition in human related to the aberrant expression and
CC   activity of NOVX polypeptides. For example, NOVX polypeptides and
CC   polynucleotides may be used to treat disorders associated with decreased
CC   expression or activity of NOVX by supplementing the patient our
CC   production or to rectify mutations. Conversely, antisense NA molecules
CC   may be administered to down regulate expression of NOVX polypeptides by
CC   binding with the cells own genes and preventing their expression. NOVX
CC   polynucleotides and complementary sequences may also be used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar sequences in samples, and so which patients may be in need of
CC   restorative therapy. NOVX polypeptides may also be used as antigens in
CC   the production of antibodies and in assays to identify modulators
CC   (agonists and antagonists) of the expression and activity of NOVX. The
CC   anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC   used to modulate NOVX polynucleotide expression and activity of NOVX
CC   polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC   diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC   polypeptides and polynucleotides may be used in this way to prevent,
CC   diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC   disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC   disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC   haematopoietic disorders, and the various dyslipidaemias, metabolic
CC   disturbances associated with obesity, the metabolic syndrome X and
CC   wasting disorders associated with chronic diseases and various cancers.
CC   They may also be used as antibacterial agents. The present sequence
CC   represents the amino acid sequence of a human NOVX protein.
XX
SQ   Sequence 620 AA;

Query Match             93.8%;  Score 2440;  DB 8;  Length 620;
Best Local Similarity   99.6%;  Pred. No. 8.5e-238;
Matches  466;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFB   60
          ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db     5  MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFB   64

Qy    61  ECSQPALMKIKGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVREKATG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    65  ECSQPALMKIKGHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVREKATG  124

Qy   121  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125  DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG  184

Qy   181  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185  DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF  244

Qy   241  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCWMWSVGVIAYEMIYGR  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245  GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCWMWSVGVIAYEMIYGR  304

Qy   301  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305  SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF  364

Qy   361  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365  SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS  424
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(continued above)

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Qy   421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV  468
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   425  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM  472
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```
RESULT 9
ADA05644
ID   ADA05644 standard; protein; 623 AA.
XX
AC   ADA05644;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human NOV1b protein SEQ ID NO:4.
XX
KW   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW   immunomodulator; cytostatic; nootropic; neuroprotective;
KW   antiparkinonian; antilipaemic; gene therapy; human disease;
KW   metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS   Homo sapiens.
XX
PN   WO200302924-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031373.
XX
PR   02-OCT-2001; 2001US-0326483P.
PR   05-OCT-2001; 2001US-0327435P.
PR   05-OCT-2001; 2001US-0327449P.
PR   09-OCT-2001; 2001US-0327917P.
PR   09-OCT-2001; 2001US-0328029P.
PR   09-OCT-2001; 2001US-0328044P.
PR   09-OCT-2001; 2001US-0328056P.
PR   12-OCT-2001; 2001US-0328849P.
PR   15-OCT-2001; 2001US-0329414P.
PR   17-OCT-2001; 2001US-0330142P.
PR   18-OCT-2001; 2001US-0330309P.
PR   22-OCT-2001; 2001US-0341058P.
PR   24-OCT-2001; 2001US-0339266P.
PR   24-OCT-2001; 2001US-0343629P.
PR   29-OCT-2001; 2001US-0349575P.
PR   01-NOV-2001; 2001US-0346357P.
PR   17-APR-2002; 2002US-0373260P.
PR   19-APR-2002; 2002US-0373815P.
PR   19-APR-2002; 2002US-0373817P.
PR   19-APR-2002; 2002US-0373826P.
PR   19-APR-2002; 2002US-0373884P.
PR   22-APR-2002; 2002US-0374977P.
PR   16-MAY-2002; 2002US-0381037P.
PR   16-MAY-2002; 2002US-0381038P.
PR   16-MAY-2002; 2002US-0381042P.
PR   17-MAY-2002; 2002US-0381642P.
PR   28-MAY-2002; 2002US-0383656P.
PR   29-MAY-2002; 2002US-0383831P.
PR   25-JUN-2002; 2002US-0391335P.
PR   01-OCT-2002; 2002US-00262511.
XX
PA   (CURA-) CURAGEN CORP.
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PI   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI   Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI   Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI   Ji W, Miller CB, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI   Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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DR   WPI; 2003-381626/36.
DR   N-PSDB; ADA05643.
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RESULT 2
US-10-238-709-2
; Sequence 2, Application US/10238709
; Publication No. US20030022340A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Human
US-10-238-709-2

Query Match   100.0%;   Score 2602; DB 14; Length 497;
Best Local Similarity 100.0%;   Pred. No. 4.9e-190;
Matches 497; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
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Qy  481 ILPSVYAKGSARGRCWL 497
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; Sequence 2, Application US/10724594
; Publication No. US20040091993A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV II
; CURRENT APPLICATION NUMBER: US/10/724,594
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-594-2

Query Match   100.0%;   Score 2602; DB 15; Length 497;
Best Local Similarity 100.0%;   Pred. No. 4.9e-190;
Matches 497; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
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Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

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Db  421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy  481 ILPSVYAKGSARGRCWL 497
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Db  481 ILPSVYAKGSARGRCWL 497
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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    March 18, 2005, 15:40:07 ; Search time 146 Seconds
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Title:          US-10-724-594-2
Perfect score:  2602
Sequence:       1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497

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Searched:       1401741 seqs, 330541175 residues

Total number of hits satisfying.chosen parameters:       1401741

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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  1    2602   100.0    497   9  US-09-804-471A-2         Sequence 2, Appli
  2    2602   100.0    497  14  US-10-238-709-2          Sequence 2, Appli
  3    2602   100.0    497  15  US-10-724-594-2          Sequence 2, Appli
  4    2589    99.5    497  15  US-10-311-034-7          Sequence 7, Appli
  5    2440    93.8    623  15  US-10-262-511-4          Sequence 4, Appli
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  8    2440    93.8   2054  15  US-10-415-011-21         Sequence 21, Appl
  9    2430    93.4   2053  13  US-10-017-216-2          Sequence 2, Appli
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 23    1180    45.3    251  14  US-10-282-048-4          Sequence 4, Appli
 24    1177    45.2    251  14  US-10-282-048-5          Sequence 5, Appli
 25    1177    45.2    251  14  US-10-282-048-6          Sequence 6, Appli
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 28    929     35.7   1572  16  US-10-333-314-20         Sequence 20, Appl
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 31    896.5   34.5   1000  15  US-10-369-493-6347       Sequence 6347, Ap
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ALIGNMENTS

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; Sequence 2, Application US/09804471A
; Patent No. US2002013222A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 497
;  TYPE: PRT
;  ORGANISM: Human
US-09-804-471A-2

Query Match             100.0%;  Score 2602;  DB 9;  Length 497;
Best Local Similarity   100.0%;  Pred. No. 4.9e-190;
Matches  497;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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PF   20-OCT-2001; 2001WO-US047728.
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PR   20-OCT-2000; 2000US-0242410P.
PR   20-OCT-2000; 2000US-0244068P.
PR   27-OCT-2000; 2000US-0245708P.
PR   03-NOV-2000; 2000US-0247672P.
PR   09-NOV-2000; 2000US-0249565P.
PR   16-NOV-2000; 2000US-0252730P.
PR   22-NOV-2000; 2000US-0252730P.
PR   01-DEC-2000; 2000US-0250807P.
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PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;
PI   Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
PI   Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
PI   Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
PI   Thangavelu K, Khan FA, Ison CH;
XX
DR   WPI; 2002-454603/48.
DR   N-PSDB; AAD38864.
XX
PT   New human kinase polypeptide, for diagnosing, preventing and treating
PT   cancer, immune system disorders, growth and development disorders,
PT   cardiovascular disorders and lipid disorders.
XX
PS   Claim 1; Page 177-182; 210pp; English.
XX
CC   The invention relates human Kinases (PKIN) and their corresponding
CC   nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC   treating and preventing cancer, an immune system disorder (e.g., acquired
CC   immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
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CC   atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC   growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC   cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC   Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC   Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC   hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC   compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC   condition or a disease associated with the expression of PKIN in a
CC   biological sample. A composition comprising PKIN or an agonist or
CC   antagonist of PKIN is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional PKIN.
CC   PKIN is useful in a number of drug screening techniques and to analyse
CC   the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC   knockin humanised animals or transgenic animals to model human diseases,
CC   and in somatic or germline gene therapy. The present sequence is human
CC   PKIN protein
XX
SQ   Sequence 2054 AA;

Query Match             93.8%;    Score 2440;  DB 5;  Length 2054;
Best Local Similarity   99.6%;    Pred. No. 6.1e-237;
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Db      1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGVVHRDIKPENLLVDRTGHIKLVDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGVVHRDIKPENLLVDRTGHIKLVDF 240

Qy    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGSGEELPFVGFS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGSGEELPFVGFS 420

Qy    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSELQDSQDKCHKV 468
          ||||||||||||||||||||||||||||||||||:||||||||||||:
Db    421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSELQDSQDKCHKM 468

RESULT 13
AAO26959
ID   AAO26959 standard; protein; 2054 AA.
XX
AC   AAO26959;
XX
DT   01-MAY-2003 (first entry)
XX
DE   Human CRIK protein sequence, SEQ ID No 2.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
```

```
Qy  241 GSAAKMNSNKMVNAKLPIGTDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GSAAKMNSNKMVNAKLPIGTDYMAPEVLTVMNGDKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
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Db  301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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Db  361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy  421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468
        ||||||||||||||||||||||||||||||||||||||||:
Db  421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKM 468
```

RESULT 14
AAE24079
ID   AAE24079 standard; protein; 2053 AA.
XX
AC   AAE24079;
XX
DT   04-OCT-2002 (first entry)
XX
DE   Human MDPK protein.
XX
KW   Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;
KW   tumourigenesis; tumour growth; tumour metastasis; viral infection;
KW   skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;
KW   immune disorder; neoplastic disorder; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Domain   53..303
FT   /note="pkinase domain"
FT   Domain   97..360
FT   /note="pkinase domain"
FT   Region   195..210
FT   /note="Antigenic epitope"
FT   Region   217..229
FT   /note="Antigenic epitope"
FT   /note="Serine/Threonine protein kinase active site
FT   signature"
FT   Region   455..475
FT   /note="Antigenic epitope"
FT   Domain   1568..1865
FT   /note="CNH domain"
XX
PN   WO20234896-A2.
XX
PD   02-MAY-2002.
XX
PF   23-OCT-2001; 2001WO-US050636.
XX
PR   23-OCT-2000; 2000US-0242429P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R;
XX
DR   WPI; 2002-479720/51.
DR   N-PSDB; AAD39191.
XX
PT   Human myotonic dystrophy type protein kinase polypeptide and
PT   polynucleotide useful for prognosticating, diagnosing, preventing or
PT   inhibiting tumorigenesis, tumor growth, tumor metastasis and viral
PT   infection.
XX
PS   Claim 8; Fig 3; 148pp; English.
XX
CC   The invention relates to human myotonic dystrophy type protein kinase

KW   diabetes; pain.
XX
OS   Homo sapiens.
XX
PN   WO200300452 3-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0338651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
DR   N-PSDB; AAL55214.
XX
PT   New human citron rho/rac-interacting kinase (CRIK)
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Claim 1; Fig 2; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human
CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho/rac-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This sequence represents the human CRIK protein of the
CC   invention
XX
SQ   Sequence 2054 AA;

Query Match   93.8%; Score 2440; DB 6; Length 2054;
Best Local Similarity   99.6%; Pred. No. 6.1e-237;
Matches   466; Conservative   2; Mismatches   0; Indels   0; Gaps   0;
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Qy    1 MLKFKFYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
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Db    1 MLKFKFYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

Qy  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
```

CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules
CC encoding such polypeptides. 13245 molecules are used to develop
CC diagnostic and therapeutic agents for prognosticating, diagnosing,
CC preventing, inhibiting, alleviating or curing MDPK-related disorders.
CC Polypeptides of the invention are used to develop diagnostic and
CC therapeutic agents for 13245-mediated or related disorders such as
CC tumourigenesis, tumour growth, tumour metastasis, viral infection of a
CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),
CC immune disorders and neoplastic disorders. The invention is also used in
CC gene therapy. The present sequence is human MDPK protein
XX
SQ Sequence 2053 AA;

Query Match   93.4%;   Score 2430; DB 5;   Length 2053;
Best Local Similarity 99.1%; Pred. No. 6.3e-236;
Matches 464; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||: ||||||
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLMEEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy 241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
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Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
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Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 15
ADF60994
ID   ADF60994 standard; protein; 2053 AA.
XX
AC   ADF60994;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Pain associated human 2207 polypeptide.
XX
KW   Pain modulation; pain disorder; painful disorder; potassium channel;
KW   kinase expression; inflammatory pain; chronic pain; neuropathic pain;
KW   causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;
KW   analgesic; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   US2003153525-A1.
XX
PD   14-AUG-2003.
XX
PF   19-DEC-2002; 2002US-00325430.
XX

PR   19-DEC-2001; 2001US-0341953P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Silos-Santiago I, Rosenfeld JB;
XX
DR   WPI; 2003-897732/82.
DR   N-PSDB; ADF60992, ADF60993.
XX
PT   Identifying a compound capable of treating a pain disorder comprises
PT   assaying the ability of the compound to modulate specific, e.g., kinases
PT   or potassium channel, nucleic acid expression or polypeptide activities.
XX
PS   Disclosure; SEQ ID NO 12; 80pp; English.
XX
CC   The present invention relates to a method for identifying a compound
CC   capable of modulating pain or painful disorders. The method comprises
CC   assaying the ability of the compound to modulate specific nucleic acid
CC   expression or polypeptide activity e.g. potassium channel, or kinase
CC   expression/activity. The method and compounds are useful for treating
CC   pain or painful disorders e.g. inflammatory pain, chronic pain,
CC   neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache
CC   pain and tissue pain. The present sequence represents a human protein
CC   associated with pain.
XX
SQ   Sequence 2053 AA;

Query Match   93.4%;   Score 2430; DB 7;   Length 2053;
Best Local Similarity 99.1%; Pred. No. 6.3e-236;
Matches 464; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||: ||||||
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLMEEYQPGG 180

Qy 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 DLLSLLNRYEDQLDENLIQFYLAELLLAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240

Qy 241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300

Qy 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360

Qy 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420

Qy 421 YSKALGILGRSESVVSGLDSQDKCHKV 468
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Job time : 179 secs

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OM nucleic - nucleic search, using sw model

Run on:      March 19, 2005, 08:21:42 ; Search time 347.017 Seconds
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Searched:    5665259 seqs, 502332750 residues

Total number of hits satisfying chosen parameters:      11130518

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	945.4	63.8	957	1	PCT-US03-11189-1	Sequence 1, Appli
2	925	62.5	1048	7	US-10-450-763-15557	Sequence 15557, A
3	225.6	15.2	1830	7	US-10-450-763-29273	Sequence 29273, A
4	225.6	15.2	6303	7	US-10-450-763-21232	Sequence 21232, A
5	213.2	14.4	5754	1	US-10-450-763-13871	Sequence 13871, A
6	202.4	13.7	204	1	PCT-US03-11189-11	Sequence 11, Appl
7	196	13.2	5333	1	PCT-US04-42360-13	Sequence 13, Appl
8	176	11.9	176	1	PCT-US03-11189-7	Sequence 7, Appli
9	175.6	11.9	4055	7	US-10-450-763-17152	Sequence 17152, A
10	171.8	11.6	489	8	US-11-060-756-1334	Sequence 1334, Ap
11	171.8	11.6	489	8	US-11-060-756-1335	Sequence 1335, Ap
12	171.8	11.6	489	8	US-11-060-756-5606	Sequence 5606, Ap
13	171.8	11.6	489	1	US-11-060-756-5607	Sequence 5607, Ap
14	143	9.7	143	1	PCT-US03-11189-9	Sequence 9, Appli
15	142	9.6	142	1	PCT-US03-11189-6	Sequence 6, Appli
16	121	8.2	3593	6	PCT-US04-42360-673	Sequence 673, App
17	106.8	7.2	2304	6	US-10-932-182A-2150	Sequence 2150, Ap
18	102	6.9	102	1	PCT-US03-11189-8	Sequence 8, Appli
19	98.4	6.6	1695	6	US-10-932-182A-2703	Sequence 2703, Ap
20	97.4	6.6	1695	6	US-10-932-182A-79012	Sequence 79012, A
21	96.2	6.5	1572	6	US-10-932-182A-81056	Sequence 81056, A
22	94	6.3	94	1	PCT-US03-11189-10	Sequence 10, Appl
23	92.2	6.2	1951	1	PCT-US03-35712-114	Sequence 114, App
24	92.2	6.2	2945	1	PCT-US03-35712-115	Sequence 115, App
25	92.2	6.2	2945	6	US-10-287-436A-132	Sequence 132, App
26	92.2	6.2	2945	6	US-10-287-436A-748	Sequence 748, App
27	92	6.2	2694	6	US-10-932-182A-2262	Sequence 2262, Ap
28	91.4	6.2	1722	6	US-10-932-182A-987	Sequence 987, App
29	90.6	6.1	2137	1	PCT-US04-42360-1088	Sequence 1088, Ap
30	90.6	6.1	2137	1	PCT-US04-42360-2103	Sequence 2103, Ap
31	90.6	6.1	2137	8	US-11-059-535-2455	Sequence 2455, Ap
32	90.6	5.9	4535	1	PCT-US03-35712-111	Sequence 111, App
33	88	5.9	1570	8	US-11-063-691-1	Sequence 1, Appli
34	85.6	5.8	607	7	US-10-450-763-17151	Sequence 17151, A
35	84.4	5.7	96	1	PCT-US03-11189-5	Sequence 5, Appli
36	84	5.7	1400	8	US-11-060-756-3844	Sequence 3844, Ap
37	84	5.7	1400	8	US-11-060-756-8116	Sequence 8116, Ap
38	83.6	5.6	2577	9	US-60-655-875-19008	Sequence 19008, A
39	83.6	5.6	2577	9	US-60-655-875-83745	Sequence 83745, A
40	82.4	5.6	3010	1	PCT-US04-23309-57	Sequence 57, Appl
41 (c)	80	5.4	80	1	PCT-US03-11189-58	Sequence 58, Appl
42 (c)	80	5.4	80	1	PCT-US03-11189-59	Sequence 59, Appl
43	79	5.3	654	9	US-60-655-875-93506	Sequence 93506, A
44	79	5.3	1194	6	US-10-932-182A-1331	Sequence 1331, Ap
45	78	5.3	936	1	PCT-US03-35712-108	Sequence 108, App

ALIGNMENTS

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RESULT 1
PCT-US03-11189-1
; Sequence 1, Application PC/TUS0311189
; GENERAL INFORMATION:
;    APPLICANT: Bristol-Myers Squibb Company
;    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
;    TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
;    FILE REFERENCE: D0193 PCT
;    CURRENT APPLICATION NUMBER: PCT/US03/11189
;    CURRENT FILING DATE: 2003-04-11
;    PRIOR APPLICATION NUMBER: U.S. 60/372,745
;    PRIOR FILING DATE: 2002-04-12
;    NUMBER OF SEQ ID NOS: 77
;    SOFTWARE: PatentIn version 3.2
;    SEQ ID NO 1
;    LENGTH: 957
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(957)
PCT-US03-11189-1

Query Match           63.8%;     Score 945.4;   DB 1;   Length 957;
Best Local Similarity 99.9%;     Pred. No. 1.5e-240;
Matches 946;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy    1  TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGGGAAGCCATTGCCAACCGGG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11  TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGGGAAGCCATTGCCAACCGGG  70

Qy   61  CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71  CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy  121  CTCCTCTTTCCGAGAAGGGATATTAGATGCGCCTCTTTGTCTCTTTGAACAAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  131  CTCCTCTTTCCGAGAAGGGATATTAGATGCGCCTCTTTGTCTCTTTGAACAAATGCAGTC  190

Qy  181  AGCCTGCTCTGATGAAGATTAAGCACGTGACACTTGTCCGGAGTATTCCGACACCA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  191  AGCCTGCTCTGATGAAGATTAAGCACGTGACACTTGTCCGGAGTATTCCGACACCA  250

Qy  241  TAGCTGAGTTACAGGAGCTCGAAGTCAGGACTTCGAAAGGACTTCAGAAGTCTTGTAG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  251  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCAGAAGTCTTGTAG  310
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Query Match        62.5%;    Score 925;  DB 7;  Length 1048;
Best Local Similarity 99.5%;  Pred. No. 3.7e-235;
Matches  928;  Conservative  0;  Mismatches  0;  Indels  5;  Gaps  0;

Qy   15 CGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGCCTCCAGGCTGAAT   74
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  116 CGGAATCCTTTGCATGCTGCTGCTGCTGAACCCATTGCCAGCGGCCGACCTCCAGGCTGAAT  175

Qy   75 CTGTTCTTCCAGGGGAAACCACACCCTTATGACTCAACAGCAGAGTCTCCTCTTCCCGA  134
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  176 CTGTTCTTCCAGGGGAAACCACACCCTTTATGACTCAACAGCAGAGTCTCCTCTTCCCGA  235

Qy  135 GAAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTCAGCCTGCTCTGATG  194
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  236 GAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGTTGAAGAATGCAGTCAGCCTGCTCTGATG  295

Qy  195 AAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCAGTGAGTTACAG  254
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  296 AAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCAGTGAGTTACAG  355

Qy  255 GAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCGTTGTAGGTTGTGGTCACTTT  314
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  356 GAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCGTTGTAGGTTGTGGTCACTTT  415

Qy  315 GCTGAAGTGCAGGTGGTAAGGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGATG  374
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  416 GCTGAAGTGCAGGTGGTAAGGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGATG  475

Qy  375 AAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGGAAGAGCGGGAACATA  434
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  476 AAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGGAAGAGCGGGAACATA  535

Qy  435 TTATCTCGAAGCACAGCCCGTGGAATATCAGCCTGATACAGTTTTACCTAGCTGAGCTTT  494
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  536 TTATCTCGAAGCACAGCCCGTGGAATATCAGCCTGATACAGTTTTACCTAGCTGAGCTTT  595

Qy  495 CACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGTCGTCACTTTGAATAGA  554
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  596 CACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGTCGTCACTTTGAATAGA  655

Qy  555 TATGAGGACCAGTTAGATGAATGAAAACCTGATACAGTTTTACCTAGCTGAGCTGATTTTGGCT  614
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  656 TATGAGGACCAGTTAGATGAATGAAAACCTGATACAGTTTTACCTAGCTGAGCTGATTTTGGCT  715

Qy  615 GTTCACAGGCGTTCATCTGATGGGATACGTGCATCGGATACGTGCATCAAGCCTGAGAACATTCTC  674
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  716 GTTCACAGGCGTTCATCTGATGGGATACGTGCATCGGATACGTGCATCAAGCCTGAGAACATTCTC  775

Qy  675 GTTGACCGCACAGGACACATCAAGCTGGTGTGGATCTGGTGGATTTTGGATCTGCCGCGGAAATGAATTCA  734
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  776 GTTGACCGCACAGGACACATCAAGCTGGTGTGGATCTGGTGGATTTTGGATCTGCCGCGGAAATGAATTCA  835

Qy  735 AACAAGATGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACATGGCTCCTGAAGTG  794
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  836 AACAAGATGGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACATGGCTCCTGAAGTG  895

Qy  795 CTGACTGTGATGAACGGGGATGGAAAAGGCCACCTACGGGCTGGACTGTGGTCGGTGGTGTCA  854
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  896 CTGACTGTGATGAACGGGGATGGAAAAGGCCACCTACGGGCTGGACTGTGGTCGGTGGTGTCA  955

Qy  855 GTGGGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCGCCAGAGGGGAACCTCT  914
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  956 GTGGGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCGCCAGAGGGGAACCTCT  1015

Qy  915 GCCAGAACCTTCAATAACATTATGAATTTCCAG  947
         |||||||||||||||||||||||||||||||||
Db 1016 GCCAGAACCTTCAATAACATTATGAATTTCCAG  1048
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Qy  301 GTTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  311 GTTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG  370

Qy  361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  371 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG  430

Qy  421 AAGAGCGGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCAATTACAGTATGCCT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  431 AAGAGCGGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy  481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  550

Qy  541 CACTTTGAATAGATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  551 CACTTTGAATAGATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy  601 AGCTGATTTTGGCTGTTCACAGCGTTCACAGGCGTTCATCTGATGGGATCGTGGATCTGCCG  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  611 AGCTGATTTTGGCTGTTCACAGCGTTCACAGGCGTTCATCTGATGGGATCGTGGATCTGCCG  670

Qy  661 CTGAGACAATTCTCGTTGACCGCACAGGACACAGACATCAAGCTGGTGATCTGGATCTGCCG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  671 CTGAGACAATTCTCGTTGACCGCACAGGACACAGACATCAAGCTGGTGATCTGGATCTGCCG  730

Qy  721 CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  731 CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  790

Qy  781 TGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAAGGCCACCTACGGGCTGGACT  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  791 TGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAAGGCCACCTACGGGCTGGACT  850

Qy  841 GTGACTGGTGTGTCAGTGGGGCTGTGGGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851 GTGACTGGTGTGTCAGTGGGGCTGTGGGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG  910

Qy  901 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAG  947
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  911 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAG  957
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RESULT 2
US-10-450-763-15557
; Sequence 15557, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 15557
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: (412)..(909)
; LOCATION: (412)..(909)
; OTHER INFORMATION: 77% homologous to Mus musculus Pro-Pol-dUTPase
; OTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman Score=685.
US-10-450-763-15557

RESULT 3
US-10-450-763-29273
; Sequence 29273, Application US/10450763
; GENERAL INFORMATION:

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;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 790CIP3/US
;   CURRENT APPLICATION NUMBER: US/10/450,763
;   CURRENT FILING DATE: 2003-06-11
;   PRIOR APPLICATION NUMBER: PCT/US01/08631
;   PRIOR FILING DATE: 2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
;   SEQ ID NO 29273
;   LENGTH: 1830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (1350)..(1640)
;   OTHER INFORMATION: 31% homologous to Homo sapiens Human myotonic dystrophy gene
;   OTHER INFORMATION: protein,accession number R41001,Smith-Waterman Score=77.
US-10-450-763-29273

Query Match      15.2%;    Score 225.6;  DB 7;   Length 1830;
Best Local Similarity    54.0%;   Pred. No. 5.9e-50;
Matches 534;   Conservative   0;   Mismatches 439;   Indels 15;   Gaps   3;

Qy   184 CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG 243
             |||| ||||| ||||| | |||||  ||  |||| || ||||||||| |
Db   116 CCGAACTGGCCCAGGACAAGTACGTGGCCCACTTCTTGCAGTGGGCGGAGCCCATCGTGG 175

Qy   244 CTGAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTCGAAGTCAGAAGTCTTGTAGGTT 303
             ||||     ||| |||   |||||    |||||
Db   176 TGAGGCTTAAGGAGGTCCGACTGCAGAGGACGCGACTTCGAGATTCTGAAGGTGATCGGAC 235

Qy   304 GTGGTCACTTTGCTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACATCTATGCTA 363
             |||      ||| |  ||  ||  |||  |||      |||
Db   236 GCGGGGCGTTCAGCGACTGCAGAGGTAGCGGTGAGGTGAAGATGAAGAAGCAGCAGGGTGTATGCCA 295

Qy   364 TGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGGAAG 423
             ||||    ||||  ||      || |||
Db   296 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCGTGCTTCCGTGAGG 355

Qy   424 AGCGGAACACATATTATCTCGAAGCACAAGACCCGTGGATCCCCCAATTACAGTATGCCTTTC 483
             || |   |   |||   || |||||
Db   356 AGAGGGACGTGTGGTGAATGGGACCGGCGGTGATCACGCAGCTGCACTTCGGCCTTCC 415

Qy   484 AGGACAAAAATCACCTTTATCTGGTCATGGAAATCAGCCTGAGGGGACTTGCTGTCAC 543
             ||||    |   |||   |||| ||||||   |||||
Db   416 AGGATGAGAGACTACCTGGTCACCTGGTCATGGAGTATTACGGCGGGGGGGACCTGCTGACAC 475

Qy   544 TTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTGAGC 603
             |  || | | | ||     |||   || |||   || ||  ||||| |||
Db   476 TGCTGAGCAAGTTTGGGGAGCGGATTCCGGCCGATGGGCCGCTTCTACCTGGCGGAGA 535

Qy   604 TGATTTTGGCTGCTGTTCACAGCGTTCATCTGATCGGCATCGTGCATCGAGACATCAAGCCTG 663
             ||||   || |   || ||   |||   | ||||   ||  ||  |  |||||||||| |||
Db   536 TTGTCATGGCCATAGACTGGCCATGGCATGTGCACCGGCTTGGCTGCGTGCACAGGGACATCAAACCCG 595

Qy   664 AGAACATTCTCGTTCACCGGACCACCAGGACACATCAGCATCCGCCTGGCCGA 723
             || |||| ||| | | ||  | | |  ||| |   | | |||||||| ||
Db   596 ACAACATCCTGCTGCTGACCACCGCGCTGCGCCACATCCGCCGCTGGCCTCGGCTCTTGCCTCA 655

Qy   724 AAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACATGG 783
             |  | ||  ||  || ||  |  || |   |||  ||| | ||| ||  |||
Db   656 AGCTCGCGGGGCAGATCGGAACCGGTCGCGTGGCGTGCTGTGGGCACCCAGACTACCTGT 715

Qy   784 CTCCTGAAGTGCTGA---CTGTGATGAACGGGGATGACGGCGGACCACCTACGGCCTGGACT 840
             | |||||| | |    | | ||   ||||       ||  ||   | |  ||  || |||
Db   716 CCCCCGAGATCCTGCAGGCTGTGTGGGCGGTGGCCTGGCCTGGACAGGCACGGCCGAGT 775

Qy   841 GTGACTGGTGGTCAGTGGGCGGCTGATTGCCTATGGAGATGATTATGGGAGAATCCCCTTCG 900
             |||||||||||   |||| |||||||| |||||||||                |||
Db   776 GTGACTGGTGGGCGCGTCTGGGTGTATTCGTCGATCCTATGATGAAATGTTCTATGGGCAGAGCGCCTTCT 835

Qy   901 CAGAGGGAACCTCTGCCCAGAACCTTCAATACACATTATGAATTCCAGCGCGTTTTGAAAT 960
             |  | ||| |||    ||  |  ||| |||    ||||     || ||
Db   836 ACGCGGATTCCACGGCGGGAGACCTATGGCCAAGATCGTCCACTACAACGGAGCACCTCTCTC 895

Qy   961 TTCCAGATGACCCAAAGTAGCAGT---GACTTTCTTGATCGTGATTCAAAGCTTGTGTGT 1017
             | ||||| || ||       ||     ||||| || || |  | | || |
Db   896 TGCCGCTGGTGGACGAAGGGGTCCCTGAGGAGGCTCGAGACTTCATTCAGCGGTTGCTGT 955

Qy  1018 GCGGCCAGAAAGAAGAGACTGAAGTTTGAAGGTCTTTGCTGC--------CATCCTTTCT 1068
             | |  ||| |||   |   | |||  ||||| | |     ||         |||||||||
Db   956 GTCCCCGGAGACGACACGGCTGGGCCGGGGTGGAGCAGGCGACACTTCCGGACACATCCCTTCT 1015

Qy  1069 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTGCCCCCTTCGTTCCCACCCTCA 1128
             |||   |||| | |||| | |     ||  |  |||| |||||||  || |||   |
Db  1016 TCTTTGGCCTCGACTGGTGGATGTCTCCGGCAGCAGCCGGTGCCCCCTTTACACCGGATTTCG 1075

Qy  1129 AGTCCGACGATGACACCTCCAATTTGA 1156
             |    |||||||| |||  |  |  ||
Db  1076 AAGGTGCCACCGACACCGACAACTTCGA 1103


RESULT 4
US-10-450-763-21232
;   Sequence 21232, Application US/1045076
;   GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 790CIP3/US
;   CURRENT APPLICATION NUMBER: US/10/450,763
;   CURRENT FILING DATE: 2003-06-11
;   PRIOR APPLICATION NUMBER: PCT/US01/08631
;   PRIOR FILING DATE: 2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
;   SEQ ID NO 21232
;   LENGTH: 6303
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (3137)..(5767)
;   OTHER INFORMATION: 79% homologous to Homo sapiens Human myotonic dystrophy gene
;   OTHER INFORMATION: protein,accession number R41001,Smith-Waterman Score=3811.
US-10-450-763-21232

Query Match      15.2%;    Score 225.6;  DB 7;   Length 6303;
Best Local Similarity    54.0%;   Pred. No. 8.4e-50;
Matches 534;   Conservative   0;   Mismatches 439;   Indels 15;   Gaps   3;

Qy   184 CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG 243
             |||| ||||| ||||| | |||||  ||  |||| || ||||||||| |
Db  3788 CCGAACTGGCCCAGGACAAGTACGTGGCCCACTTCTTGCAGTGGGCGGAGCCCATCGTGG 3847

Qy   244 CTGAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTCGAAGTCAGAAGTCTTGTAGGTT 303
             ||||     ||| |||   |||||    |||||
Db  3848 TGAGGCTTAAGGAGGTCCGACTGCAGAGGACGCGACTTCGAGATTCTGAAGGTGATCGGAC 3907

Qy   304 GTGGTCACTTTGCTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACATCTATGCTA 363
             |||      ||| |  ||  ||  |||  |||      |||
Db  3908 GCGGGGCGTTCAGCGAGGTAGCGGTGAGGTGAAGATGAAGAAGCAGCAGGGTGTGTATGCCA 3967

Qy   364 TGAAAGTGATGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGGAAG 423
             ||||    ||||   ||      || |||
Db  3968 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCGTGCTTCCGTGAGG 4027

Qy   424 AGCGGAACACATATTATCTCGAAGCACAAGACCCGTGGATCCCCCAATTACAGTATGCCTTTC 483
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;
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(411)
; OTHER INFORMATION: 95% homologous to Escherichia coli RF-3/Tos,accesion number
; OTHER INFORMATION: D17724,Smith-Waterman Score=665.
US-10-450-763-13871

Query Match     14.4%;    Score 213.2;   DB 7;   Length 5754;
Best Local Similarity  50.9%;   Pred. No. 1.6e-46;
Matches  590;  Conservative  0;  Mismatches 553;  Indels  15;  Gaps  3;
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Qy   135 GAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTCAGCCTGCTCTGATG 194
             |  ||||| ||||| |  |||| | |||  |||  ||||||||||| || ||||
Db    82 GAAACGTCGCTCGACGTGCGTCTGCTGCTGTACACCGAGTGCAGCCACTCGGCGCCCTGCGC 141

Qy   195 AAGATTAAGACAGTGAGCAACTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTACAG 254
         || || ||| | |  |||| |||| | ||| || | || ||| ||| |||||||| |||
Db   142 CGCGACAAGTACGTGGCCGAGTTCCTCGAGTGGCTAAACCATTTACACAGCTGGTGAAA 201

Qy   255 GAGCTCCAGCCTTCGGCACAAGGACTTCGAAGTCAGAAGTCTGTGAGGTTGTGGTCACTTT 314
         ||| |||| |||| | ||| | ||| |||| || ||||| || |||| || ||||| ||||
Db   202 GAAATGCAGCTTCATCGAGAGACTTTGAAATAATTAAAGTAATTGGAAGAGAGGTGCTTTT 261

Qy   315 GCTGAAGTGCAGGTGGTGAAGAAGAGAGAAGAGAAAGCACCGGGAGACATCTATGCTATGAAGTGATG 374
         | ||| || ||| | || || ||| | ||| | |  |||||||  |||| | ||||||  |||| ||
Db   262 GGTGAGGTTGCTGTTGTCAAAATGAAGAAGAATACTGAACGAATTATGCAATGAAAATCCTC 321

Qy   375 AAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCATTTTGTGAGGAGAGCGGAACATA 434
         || ||  || | | || ||| ||||||||| || |  | |  || |||| || || ||
Db   322 AACAAGTGGGAGATGCTGAAAAGAGCAGCAGAGACCAGCCGCGGCTTCCGGAGAGCGGCGATGTG 381

Qy   435 TTATCTGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCTTCAGGACGACAAAAAT 494
         | | || || | ||||| |||| |  || ||||  |  ||||||||||||||  |  |
Db   382 CTGGTGAACGGCGACTGCCAGTGGATCACCGGCTGCACTACGCCCTTCAGGACGAGAAC 441

Qy   495 CACCTTTATCTGGTCATGGAATATCAGCAGCCTCGGAGGGGACTTGCTGTCGTCACTTTTTGATAGA 554
         ||||| ||  | |||||||| | | |  | |  | ||| | |  || || || ||| |  | |||
Db   442 CACCTGTACTTAGTCATGGATTACTATGTGGGTGGATTTACTGACCCTGCTCAGCGAAA 501

Qy   555 TATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTTACCTGAGCTGAGTTTTGGCT 614
         | ||| || |  || ||||| |  || |  |  ||| ||| || |||| || ||| ||
Db   502 TTTGAAGACAAGCTTCGGAAGATATGGCCGAGGTTCTACATTGGTGAAATGTGCTGGCC 561

Qy   615 GTTCACAGCGTTCATCTGATGGATCACTGCCGAACTCAAGGCTGAGAACAATTCTC 674
         ||| || | |||  || | ||||||  | | || | ||||| |||| || |||| |
Db   562 ATTGACTCCATCCATCGAGCTTCATTACGTGCACAGAGACATTAAACCTGACAATGTCCTT 621

Qy   675 GTTGACCGCCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGAAAATGAATTCA 734
         ||||| || || || |||| | |||| | || || ||||| | | | || |||| | |||
Db   622 TTGGACGTGAATGGTCATATCCGCCTGGCTGACTTTGGATCATGTTTGAGATGAATGAT 681

Qy   735 AACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTACAATGGCTCCTGAAGTG 794
         || ||||| || || ||| | ||||| |||| | ||  | || | || || |  | | |
Db   682 GATGGCACTGTGCAGTCCTCCTGCCGGTGGCTGGGCCACACCTGACTACCTGGTGGTCA 741

Qy   795 CTGACTGTGATGATGAACGGGGGATGAAAAGGCACCTACGGGCTGACTGTGGTCGTCT 854
         || || | ||| ||||  |   | | | ||||||| | |||| || |||  | |  |
Db   742 CTGCAGCGGCGATG---GAGGACAGACGGATGGGGCAAATACGGGGCTTTATGCGGAGACCTC 798

Qy   855 GTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCGCAGAGGGAACCTCT 914
         || || || || || |||| | | |  |||| ||| |  | ||| || || || |||
Db   799 CTGGGTGTCTGCATGTATGAGATGTCTATGGAGAAACGGCCGTTTATGCGGCGAGTCACTC 858

Qy   915 GCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAATTTCCA---GATGAC 971
         || || || | | || || | || ||  ||||||| || |  |||  |||   ||||||
Db   859 GTGGAGACCTATGGACCATGGGAAGATCATGAACGACCATGGAAGAGCGATTCCAGTTCCCATCCCATGTC 918

Qy   972 CCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAAGCTTGTTGTGCGGGCCAGAAAGAG 1031
         || || || | ||| |||| |  || | || ||||| || | | |||| |  |  |||
Db   919 ACGGATGTATCTGAAGAAGCCAAGGACCTCATCCGAGACTGATCGTCAGTAGAGAACGC 978

Qy  1032 AGACTGAAG-------TTTGAAGGTCTTTGCTGCCATCCTTTCTTGTCTTCTCTAAAATTGAC 1082
         ||||||| |       | |  | |   |  | |||| || || |  |||| || || ||||
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Db  4028 AGAGGGACGTGTTGGTGAATGGGACCGGCGGTGATCAGCCGTCACGCAGCTCGCACTTCGCCTTCC 4087
Qy   484 AGGACAAAATCACCTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCAC 543
Db  4088 AGGATGAGAACTACCTGGTCACCTGGTCATGGAGTATTACGTGGGCGGGGACCTGCTCACAC 4147

Qy   544 TTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTGAGC 603
Db  4148 TGCTGAGCAAGTTGGGGAGCGGATTCCGGCCGAGATGGGCGGCTTCTACCTGGGCGGAGA 4207

Qy   604 TGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGTGCATCGAGACGATCAGCCTG 663
Db  4208 TTGTCATGGCCATAGACTCGGTGCACCGGCTACGGTGCACAGGGACACAAACCCG 4267

Qy   664 AGAACATTCTCGTTGACCGACGACAGGAGACATGGGGACACATGGATCTGCCGCGA 723
Db  4268 ACAACATCCTGCTGGACCGCGTGTGGCCACATCCGCGCTGGACGACTTCGCGTCTTGCCTCA 4327

Qy   724 AAATGAATTCAAACAACAAGATGTGATGGCCAAACTCCCGATTGGGACCCAGATTACATGG 783
Db  4328 AGCTGCGGGCAGATGGAACGGTGCGCGGTGCGTGGCGTGTGGGCACCCCAGACTACCTGT 4387

Qy   784 CTCCTGAAGTGCTGA---CTGTGATGAACGGGATGGAAAAGGCACCTACGGGCCTGGGACT 840
Db  4388 CCCCCAGATCCTGCGAGGCGTGTGGGCCGGTGGGCCTGGGACAGGGCAGCTACGGGCCCGAGT 4447

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900
Db  4448 GTGACTGGTGGTGGCGCGCTGGGTGTATTCGCCTATGAAATGTTCTATGGGCCAGACGCGCGTCTTCT 4507

Qy   901 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
Db  4508 ACGCCGGATTCCACGGGGAGAGACCTATGGCCAAGATCGTCCACTACAAGGAGCACCTCTCTC 4567

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCGATTCAAAAGCTTGTTGT 1017
Db  4568 TGCCCGCTGGTGGACCAAGAGGGGTCCCTGGAGGCTTCAGCTTCATTCAGCGGTTGCTGT 4627

Qy  1018 GCGGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC--------CATCCTTTCT 1068
Db  4628 GTCCCCCGGAGACACGCGTCTGGGCCGGGTGAGCGAGCCGACTTCCGGACACATCCCTTCT 4687

Qy  1069 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTTCCTCCCCCTTCGTTCCACCCCTCA 1128
Db  4688 TCTTTGGCCTCGACTCGGATGGTGCTCCCGGGACAGCCGCTGCCCCCCTTTACACCGGATTTCG 4747

Qy  1129 AGTCCGACGATGACACCTCCAATTTTGA 1156
Db  4748 AAGGTGCCACCGACACACATGCAACTTCGA 4775
```

```
;  SOFTWARE: Perl script
;  SEQ ID NO 13
;  LENGTH: 5333
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;  DATABASE ACCESSION NUMBER: Refseq / NM_053620
;  DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-13

Query Match        13.2%;   Score 196;  DB 1;  Length 5333;
Best Local Similarity 49.5%;   Pred. No. 5.5e-42;
Matches 573;  Conservative  0;  Mismatches 570;  Indels 15;  Gaps  2;
```

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Qy  135 GAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTCAGCCTGCCTCGATG 194
            |||  ||    ||| |||  | || || ||   |||  |||||| ||||  | ||| |
Db  130 GAGACCGCTGCTGGACGTGCTCGTGTGCCTTTACACCGAGTGCAGCCACTCGGCGCTCGC 189

Qy  195 AAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTACAG  254
            |||  |  |  || || |||||| | ||   || || |||  |||| || |  | |||
Db  190 CGCGACAAGTGATGTGGCGGAGTTCCTCGAGTGGCTAAGCCATTCACCCAGCTCGTGAAG 249

Qy  255 GAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTGTGTGTCACTTT 314
            || ||||||| |  || |||| |||| ||| || || |    ||| |  || ||| |
Db  250 GACATGCAGCTTCATCCGGAGGACTTTGAGATCATCAAAGTGATTGGAAGAGAGAGCTTTT 309

Qy  315 GCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACACATCATCTATGCTATGAAAGTGATG 374
            || |  || |  || | ||| |||| | || ||   |  | | ||| |  |||
Db  310 GGTGAGGTTGCTGTTGTCAAAATGATGAAGAACACTGAACGAGTTTCATTTTTTGAGGAAGAGAGCCGAACATA 369

Qy  375 AAGAAGAGGCTTTATTGGCCCAGAGACCGGTGGATCCCCAATTACAGTATGCCTTTACAGTATGCCTGCTCGTGAATAGA 434
            || | | |||  |  | |  |  | ||| | | ||   ||| || ||  |  |  |||  |  ||   |
Db  370 AACAAATGGAGATGCTAAAGAGAGACAGCAGCAGAGACAGAGACAGCAGCTTCGCTTTCGAGAAGATGAGAAC 429

Qy  435 TTATCTCGAAGCACAAGCCCGTGGGATCCCCAATTACAGTATACAGTATGCCTTTGCTCACTTTTTGAATAGA 494
            || |||||  |||| || |  |||| ||||| || ||  |  | |  | |||  |  ||||| || |  |
Db  430 CTGGTGAACGGTGACTGCCAGTGGATCATCATGCTGCTAGCTGCTACTACACGCCTTTCAAGATGAGAAC 489

Qy  495 CACCTTTATCTGGTCATGGAATATCATCAGCCTGGAGGGGACTTGCTGTCGTCTGATTTTGGCT 554
            |||  ||| | || ||| |  ||||| |  ||  |  | || | | || || |||  |  ||||
Db  490 TACCTGTACTTGGTTATGGATTACTATGTGGTGACTTGCTGACCCTGCTGAGTGAGTAAG 549

Qy  555 TATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTGAGCTGATTTTCGGCT 614
            |||  |||||||  ||| |  | |  |  || || || |   |||  || |  | ||||
Db  550 TTTGAAGACAAACTTCCAGAGACATGGCGATCATCGGGATACGTGATCAAGCGTCAGAACATTCTC 609

Qy  615 GTTCACAGGCGTTCATCTGATGGGATACGTGGTGTCAGTGGGCGTG 674
            || |  ||||  | ||  |    | |  | || || ||| |||| | |
Db  610 ATCGACTGATCCACCAGCTCCACTATGTGCACAGAGACAGCATTAAACCCGACACACGTCCTT 669

Qy  675 GTTGACCGCCACAGGACACATCAAGCTGGTGGATGTGGATTTGGATCTGCCGCCGGAAAATGAATTCA 734
            || | ||   || | || |  |  ||| || | ||   | ||| | |  | ||  || |  |||| |
Db  670 CTGGATGTCAACGGTCACATCCGCTCGGCTCGTGGCTCGTGCTTGCTGACTTTGCCTGGTCGTGGTGAAGATGAACGAT 729

Qy  735 AACAAGATGTGAATGCCAAACTCCCGATTGGGACACTCACGGCCTCCCAGATTACATGGCTCCTGAAGTG 794
            |||  || || |  ||  || |  | || ||  |  |  | || |  | |||| |  ||   |  | |||
Db  730 GACGGCACTGTTCAGTCTTCAGTCTGTGGCGCTGGGCACCACCACCTCGGCGGCTGGTGGACTGGTGGTCA 789

Qy  795 CTGACTGTGATGAACGGGGATGGAAAAGGCATGGGCAAAATACGGGCCCGAGTTGCGACTGGTGGTGGTCC 854
            |||  ||  | |  | |  | || ||   ||  | | || |   ||  | | | || || | || |  ||
Db  790 CTGCAGGCCATG- - -GAGGATGGGCATGGGCAAAATACGGGCCCGAGTTGCGACTGGTGGTGGTCC 846

Qy  855 GTGGGCGTGGATTGCCTATGAAGATGATGATTATGGAGGCATGGGAGAACGGGGATCCCCTTCGCAGAGGAGAACCTCT 914
            ||  |  ||| |   ||  || || ||   |  | | |  ||  ||  |  ||| | ||||    | || | |  |
Db  847 CTGGGCCGTCTGCATGTGATGAGATGATGATTTATGGAGAAACGCCATTTATGCAGAGTCTCTG 906

Qy  915 GCCAGAACCTTCAATAACATTATGAATTTCCAGCCGGTTTTGAAATTTCCA- - - - - - - - 965
            || | || |   | |  |  | | |  |   |  | |  || | || |  ||
Db  907 GTGGAGACATATGAAGAGATCATGAACCACCAGGAGGAGGCGGTTTCAGTTCCCATCCCCACGTC 966

Qy  966 - - -GATGACCCCAAAGTGAGCAGTGACTTTCTGACTGATCTGAATTCAAGCTTGTTGTGCGGC 1022
               |||||| ||||  |||| |  || | |  ||  || |  |  ||||  |  ||   ||
Db  967 ACTGACGTCTCTGAAGAAGCCAAAGACCTCATCCAGACTAATATGCAGACTAATATGCAGCAGAGAGCGC 1026
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Db  979 CGGCTGGGGCCAGAATGGAATGAGAGATTCAAAAAGCATGCGTTTTTGAAGGTCTAAAT 1038
            ||   | | || |  | |  |  |   || |  |  |    | ||   | || |
Qy 1083 TGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCACCCTCAAGTCCGACGATGAC 1142
            | |  |  |  | |  || ||      | | | | ||     |    || | ||| ||
Db 1039 TGGGAAATATACGGAACCTAGAAGCACCTTATATTCCTGATGTGAGCAGTCCCTCTGAC 1098

Qy 1143 ACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTG 1202
            | ||| || | ||| | | || | |  ||   | |  | |  | | || |||
Db 1099 ACATCCAACTTCGACGCTGGATGACGACGTGCTGAGAAACACGGAAATATTACCTCCTGGT 1158

Qy 1203 AGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGACGACAAGGCA 1262
            | | |  | ||| | | || |||| |  | || ||  |    | |
Db 1159 TCTCACACAGGCTTTTCTGGATTACATTTGCCATTCATTGGTTTTTACATTCACAACGGAA 1218

Qy 1263 CTGGGGATTCTTGGTAGA 1280
            ||||| |||  | |  |
Db 1219 AGCTGTTTTTCTGATCGA 1236
```

RESULT 6

PCT-US03-11189-11
```
; Sequence 11. Application PC/TUS0311189
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
; FILE REFERENCE: D0193 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11189
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745
; PRIOR FILING DATE: 2002-04-12
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 11
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-11189-11

Query Match        13.7%;   Score 202.4;  DB 1;  Length 204;
Best Local Similarity 99.5%;   Pred. No. 4.5e-44;
Matches 203;  Conservative  0;  Mismatches 1;  Indels  0;  Gaps  0;
```

```
Qy 744 GTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTG 803
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTG 60

Qy 804 ATGAACGGGATGGAAAAAGGCACCTACGGCCTGGACTGTGCGTCGACTGGTCAGTGGGCGTG 863
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 ATGAACGGGATGGAAAAAGGCACCTACGGCCTGGACTGTGCGTCGACTGGTCAGTGGGCGTG 120

Qy 864 ATTGCCTATGAGATGATTATGGGAGATCCCCTTCGCGAGAGGAACTCTGCCAGAACC 923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ATTGCCTATGAGATGATTATGGGAGATCCCCTTCGCGAGAGGAACTCTGCCAGAACC 180

Qy 924 TTCAATAACATTATGAATTTCCAG 947
           ||||||||||||||||||||||||
Db 181 TTCAATAACATTATGAATTTCCAG 204
```

RESULT 7

PCT-US04-42360-13
```
; Sequence 13. Application PC/TUS0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
```

Qy 1023 CAGAAAGAGAGACTGAGAGTTGAAGGTCTTTGCTGCCATCCTTCTTTCTCTAAAATTGAC 1082
Db 1027 CGGCTCCGGCAGAACGGGATAGAGACTTTAAGAAACATGCATTCTTTGAAGGTCTAAAT 1086

Qy 1083 TGGAACAACATTCGTAACTCTCTCCCCCCTTCGTTCCACCCTCAAGTCCGACGATGAC 1142
Db 1087 TGGGAAAATATACGGACCTGAAGCACCCTACATTCCGATGTGAGCAGCCCTTCTGAC 1146

Qy 1143 ACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCCGTGCCAGCTG 1202
Db 1147 ACGTCCAACTTCGATGTGGACGATGACGTGCTGAGAAACATCGAAATCTTACCTCCCGGAC 1206

Qy 1203 AGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCA 1262
Db 1207 TCTCACACGGGCTTCTCGGGACTGCACCACCCTTCATTGGCTTTACATTTACGACACAGAA 1266

Qy 1263 CTGGGGATTCTTGGTAGA 1280
Db 1267 AGCTGCTTTCTGACCGA 1284

RESULT 8
PCT-US03-11189-7
; Sequence 7, Application PC/TUS0311189
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
; FILE REFERENCE: D0193 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11189
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-11189-7

Query Match   11.9%; Score 176; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ATTCCGACACCATAGTGAGTTACAGGAGCTTACAGGAGCTTCGGCAAAGGACTTCGAAGTCA 288
Db   1 ATTCCGACACCATAGTGAGTTACAGGAGCTTCCAGCCTTCGGCAAAGGACTTCGAAGTCA 60

Qy 289 GAAGTCTTGTAGGTTGTGGGTCACTTTGCTGTGAAGTGCAGGTGGTAAGAGAGAAGCAACCG 348
Db 61 GAAGTCTTGTAGGTTGTGGGTCACTTTGCTGTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCG 120

Qy 349 GGGACATCATGCTATGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCCAGGAGCAG 404
Db 121 GGGACATCATGCTATGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCCAGGAGCAG 176

RESULT 9
US-10-450-763-17152
; Sequence 17152, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
SEQ ID NO 17152
; LENGTH: 4055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (3441)..(3980)
; OTHER INFORMATION: 100% homologous to Homo sapiens myotonic dystrophy protein
; OTHER INFORMATION: kinase like protein,accession number Y12337,Smith-Waterman Score=
; OTHER INFORMATION: 969.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4055)
; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-17152

Query Match   11.9%; Score 175.6; DB 7; Length 4055;
Best Local Similarity 58.4%; Pred. No. 1.3e-36;
Matches 326; Conservative 0; Mismatches 229; Indels 3; Gaps 1;

Qy 390 TTGGCCCAGGAGCAGGTTCATTTTTGAGGAAGAGCGGAACATATTATCTGAAGCACA 449
Db 3426 TTGCCCTTCCTGGAGACAGCCTGTTTCCGGAGGAGCCGGATGTGCTCGTGAAAGGGGAC 3485

Qy 450 AGCCCGTGGATCCCCAATTACAGTATGCCTTCAGGACAGAAAAATCACCTTTATCTGGTC 509
Db 3486 AGCCGGTTGGGTGACCACTCTGCACTATGCCTTCCAAGACGAGGAGTACCTGTACCTTGTG 3545

Qy 510 ATGGAATATCAGCCTGGAGGGGACTTGCGTCGTCACTTTTGAATAGATATGGGACCAGTTA 569
Db 3546 ATGGACTACTATGCTGGTGGGGACCTCCTGACGCTGCTGAGCCGTTCGAGGACCGTCTC 3605

Qy 570 GATGAAAACTGATACAGTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCAT 629
Db 3606 CCGCCCGAGCTGGCCCAGTTCTACCTGGCTGAGATGGTGCTGGCCATCCACTCGCTCGAC 3665

Qy 630 CTGATGGGATACGTGCATGCGATCGAGACATCAAGCTGAGACAATTCTCGTTGACCGCACAGGA 689
Db 3666 CAGCTGCGGTTATGTCCACAGGGATGTCAAGCCAGACAACGTCCTCTGCCGGATGTGAACGGGG 3725

Qy 690 CACATCAAGCTGGTGTGGATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGAGTGTGAAT 749
Db 3726 CACATTCGCCTGGCTGACTTCGGCCTGTCGGCTCCTGCGTCTGCGTCTGCGTCTCAACACCAACGGCATGGTGGAT 3785

Qy 750 GCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAAC 809
Db 3786 TCATCAGTGGCAGTAGGGACGCCGGACTATATCTCCCCTGAGATCCTGAGGGCCATGGA- 3844

Qy 810 GGGGATGGAAAAGGCACCTACGGCGTGGACTGGTGGTCAGTGGGCGTGATTGCC 869
Db 3845 --GGAGGGCAAGGGCCACTACGGCGTGGACTGGTGGTGGTCGTTGGAGTCCTGGACGCC 3902

Qy 870 TATGAGATGATTTATGGGACGATCCCCCTTCGCAGAGGGACCCTCTGCCAGAACCTTCAAT 929
Db 3903 TATGAGACTGCTCTTTGGGGAGGACGCGCCCTTCTATGCTGGAGTCCTTGTGTGAAAACCTACGGC 3962

Qy 930 AACATTATGAATTTCCAG 947
Db 3963 AAGATCATGAACCACGAG 3980

RESULT 10
US-11-060-756-1334
; Sequence 1334, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)

; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1334
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-1334

Query Match   11.6%;   Score 171.8; DB 8; Length 489;
Best Local Similarity   98.9%;   Pred. No. 7.2e-36;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1102 CTCCTCCCCCTTCGTTCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGATGAAC 1161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 CTCCTCCCCCTTCGTTCCACCCTCAAGTCTGACGATGACACCTCCAATTTTGATGAAC 374

Qy   1162 CAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 1221
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   375 CAAAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 434

Qy   1222 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 1276
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 489

RESULT 11
US-11-060-756-1335
; Sequence 1335, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1335
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-1335

Query Match   11.6%;   Score 171.8; DB 8; Length 489;
Best Local Similarity   98.9%;   Pred. No. 7.2e-36;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1102 CTCCTCCCCCTTCGTTCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGATGAAC 1161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 CTCCTCCCCCTTCGTTCCACCCTCAAGTCTGACGATGACACCTCCAATTTTGATGAAC 374

Qy   1162 CAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 1221
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   375 CAAAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 434

Qy   1222 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 1276
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 489

RESULT 12
US-11-060-756-5606
; Sequence 5606, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5606
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5606

Query Match   11.6%;   Score 171.8; DB 8; Length 489;
Best Local Similarity   98.9%;   Pred. No. 7.2e-36;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1102 CTCCTCCCCCTTCGTTCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGATGAAC 1161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 CTCCTCCCCCTTCGTTCCACCCTCAAGTCTGACGATGACACCTCCAATTTTGATGAAC 374

Qy   1162 CAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 1221
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   375 CAAAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGG 434

Qy   1222 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 1276
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGG 489

RESULT 13
US-11-060-756-5607
; Sequence 5607, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5607
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5607

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Best Local Similarity   98.9%;   Pred. No. 7.2e-36;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 9, Application PC/TUS0311189
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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
; FILE REFERENCE: D0193 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11189
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745

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; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-11189-9

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RESULT 15
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; Sequence 6, Application PC/TUS0311189
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;   APPLICANT: Bristol-Myers Squibb Company
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
;   TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
;   FILE REFERENCE: D0193 PCT
;   CURRENT APPLICATION NUMBER: PCT/US03/11189
;   CURRENT FILING DATE:  2003-04-11
;   PRIOR APPLICATION NUMBER: U.S. 60/372,745
;   PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
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;   LENGTH: 142
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PCT-US03-11189-6

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Search completed: March 19, 2005, 17:43:23
Job time : 349.017 secs
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OM nucleic - nucleic search, using sw model

          GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:         March 19, 2005, 07:57:47 ; Search time 5227.99 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:        91109746

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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1476.2	99.7	2066	90	US-60-215-651-9	Sequence 9, Appli
4	1388.2	93.7	1870	1	PCT-US02-31373-3	Sequence 3, Appli
5	1388.2	93.7	1870	51	US-10-262-511-3	Sequence 3, Appli
6	1388.2	93.7	5877	62	US-10-262-511A-3	Sequence 3, Appli
7	1388.2	93.7	6165	62	US-10-791-666-3	Sequence 3, Appli
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9	1388.2	93.7	8602	49	US-10-415-011-43	Sequence 43, Appl
10	1388.2	93.7	8602	49	US-10-170-235-7679	Sequence 7679, Ap
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17	1381.8	93.3	6574	52	US-10-325-430-10	Sequence 10, Appl
18	1381.8	93.3	6574	62	US-10-757-262-51	Sequence 51, Appl
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31	1110.6	75.0	7911	106	US-60-360-207-10474	Sequence 10474, A
32	947.2	64.0	2162	1	PCT-US02-01222-416	Sequence 416, App
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40	578.8	39.1	1116	31	US-09-699-998-10200	Sequence 10200, A
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ALIGNMENTS

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US-10-724-594-1
; Sequence 1, Application US/10724594
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV II
; CURRENT APPLICATION NUMBER: US/10/724,594
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-594-1

Query Match             100.0%;  Score 1481;  DB 62;  Length 1515;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1481;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db  137 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 196

Qy  181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  197 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 256

Qy  241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGAGTCTTGTAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  257 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGAGTCTTGTAG 316

Qy  301 GTTGTGTCGTCACTTTGCTGAAGTGCAGTGCGGTAAGAGAAAGCAACCGGGACATCTATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  317 GTTGTGTCGTCACTTTGCTGAAGTGCAGTGCGGTAAGAGAAAGCAACCGGGACATCTATG 376

Qy  361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  377 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG 436

Qy  421 AAGAGCCGGACAATATTATCTCGAAGCACAAGCCGTGATCCCCAATTACAGTATGCCT 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  437 AAGAGCCGGACAATATTATCTCGAAGCACAAGCCGTGATCCCCAATTACAGTATGCCT 496

Qy  481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  497 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 556

Qy  541 CACTTTTGAATAGATATGAGGACCAGTAGATGAAGAAACCTGATACAGTTTACCTAGCTG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  557 CACTTTTGAATAGATATGAGGACCAGTAGATGAAGAAACCTGATACAGTTTACCTAGCTG 616

Qy  601 AGCTGATTTGGCGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  617 AGCTGATTTGGCGTGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy  661 CTGAGAACATTCGTGACCGGCACAGGACACATCAAGCTGGTGCGCCG 720
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  677 CTGAGAACATTCGTGACCGGCACAGGACACATCAAGCTGGTGCGCCG 736

Qy  721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 780
```

APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAFALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KHAN, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GRETHER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.

TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
                          60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
                   25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 33
  LENGTH: 2066
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
  OTHER INFORMATION: Incyte ID No: 3951059CB1
US-10-311-034-33

Query Match   99.7%; Score 1476.2; DB 52; Length 2066;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1478; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 TCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCGGCCATTGCGTGCTGCCAACCGG  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     24 TCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCGGCCATTGCGTGCTGCCAACCGG  83

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT  143

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGAAGAATGCAGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGAAGAATGCAGTC  203

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAACTTGTCCGACACCA  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAACTTGTCCGACACCA  263

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  323

Qy    301 GTTGTGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGACATCTATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GTTGTGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGACATCTATG  383

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG  443

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT  503
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Db    737 CGAAATGATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTACA  796
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  856

Qy    841 GTGACTGGTGGTCAGTGGGCGTGAGTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 GTGACTGGTGGTCAGTGGGCGTGAGTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  916

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  976

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG  1036

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCGCCATCCTTCTTCTCCTAAAATTG  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCGCCATCCTTCTTCTCCTAAAATTG  1096

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG  1156

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1216

Qy   1201 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG  1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1336

Qy   1321 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGACTCTACAAGACTCTCAGGACA  1380
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Db   1337 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGACTCTACAAGACTCTCAGGACA  1396

Qy   1381 AGTGTCACAAGGTATTATTCCGCAGCCGCCTCCTTCGTTCCCTGCCTCCAGGATCCTCCCGT  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 AGTGTCACAAGGTATTATTCCGCAGCCGCCTCCTTCGTTCCCTGCCTCCAGGATCCTCCCGT  1456

Qy   1441 CCGTATATGCCAAGGGGATCCGCCCCGGGGCCCGTGCCCGTGGCTC  1481
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Db   1457 CCGTATATGCCAAGGGGATCCGCCCCGGGGCCCGTGCCCGTGGCTC  1497
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RESULT 2
US-10-311-034-33
; Sequence 33, Application US/10311034
; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BOROWSKY, Mark L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Yan
APPLICANT: GANDHI, Ameena R.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: YAO, Monique G.
APPLICANT: LU, Dyung Aina M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Danniel B.

; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Lu, Dyung Aina M.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Lal, Preeti,
; APPLICANT: Lo, Terence P.
; APPLICANT: Thornton, Michael
; APPLICANT: Lu, Yan
; APPLICANT: Bandman, Olga
; APPLICANT: Gandhi, Ameena R.
; APPLICANT: Patterson, Chandra
; APPLICANT: Burford, Neil
; APPLICANT: Khan, Farrah A.
; APPLICANT: Recipon, Shirley A.
; APPLICANT: Yao, Monique G.
; APPLICANT: Guruajan, Rajagopal
; APPLICANT: Azimzai, Yalda
; APPLICANT: Policky, Jennifer L.
; APPLICANT: Hafalia, April
; APPLICANT: Tribouley, Catherine M.
; APPLICANT: Nguyen, Danniel B.
; APPLICANT: Walia, Narinder K.
; APPLICANT: Ding, Li
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0140 P
; CURRENT APPLICATION NUMBER: US/60/215,651
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3951059CB1
US-60-215-651-9

Query Match   99.7%; Score 1476.2; DB 90; Length 2066;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1478; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TCAAATATGGAGCGCCGGAATCCTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TCAAATATGGAGCGCCGGAATCCTTGATGCTGGTGCTGCTGAACCCATTGCCAGCCGCGG   83

Qy         61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  143

Qy        121 CTCCTCTTCCCGAGAGGGATATTAGATGCACGTGAAGAATGCAGTC  180
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CTCCTCTTCCCGAGAGGGATATTAGATGCACGTGAAGAATGCAGTC  203

Qy        181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  263

Qy        241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG  323

Qy        301 GTTGTGTGTCACTTGCTGAAGTGCAGTGCAGTTGTAAGAGAGAAAGCAACCATCTATG  360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 GTTGTGTGTCACTTGCTGAAGTGCAGTGCAGTTGTAAGAGAGAAAGCAACCATCTATG  383

Qy        361 CTATGAAAGTGATGAAGAAGAGAGGCTTTATTGGCCAGGAGCAGTTTCATTTTTGAGG  420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CTATGAAAGTGATGAAGAAGAGAGGCTTTATTGGCCAGGAGCAGTTTCATTTTTGAGG  443

Qy        421 AAGAGCCGGAACATATTATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT  480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAGAGCCGGAACATATTATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT  503

Qy        481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  563

Qy        541 CACTTTTGAATAGATAGAGACCAGTTAGATGATGAAAACCTGATACAGTTTTTTACCTAGCTG  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CACTTTTGAATAGATAGAGACCAGTTAGATGATGAAAACCTGATACAGTTTTTTACCTAGCTG  623

Qy        601 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  683

Qy        661 CTGAGAACATTCTCGTTGACCGACCACAGGACACATCAAGCTGTGTGGATTTGGATCTGCCG  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CTGAGAACATTCTCGTTGACCGACCACAGGACACATCAAGCTGTGTGGATTTGGATCTGCCG  743

Qy        721 CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  803

Qy        781 TGGCTCCTGAAGTGCTGACTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TGGCTCCTGAAGTGCTGACTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  863

Qy        841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  923

Qy        901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGCGGTTTTTTGAAAT  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGCGGTTTTTTGAAAT  983

Qy        961 TTCCAGATGACCCCAAAGTGACCTGAGCAGTGACTTTCTTGATTCTGATTCAAAGCTTGTTGTGCG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 TTCCAGATGACCCCAAAGTGACCTGAGCAGTGACTTTCTTGATTCTGATTCAAAGCTTGTTGTGCG 1043

Qy       1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1103

Qy       1081 ACTGGAACAACATTCGTAACTCTCTCCCCCCTTGTTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 ACTGGAACAACATTCGTAACTCTCTCCCCCCTTGTTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1163

Qy       1141 ACACCTCCAATTTGATGAACCAGCAGAAGAATTCGTGGGTTCATCCTGTTCCGTGCCAGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 ACACCTCCAATTTGATGAACCAGCAGAAGAATTCGTGGGTTCATCCTGTTCCGTGCCAGC 1223

Qy       1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1283

Qy       1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCGGGTCTGACTCCCCTGCCAAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 CACTGGGGATCTTGGTAGATCTGAGTCTGTGTCGGGTCTGACTCCCCTGCCAAGA 1343

Qy       1321 CTAGCTCCATGGAAAAGAAAACTCTCATCAAAAGCAAAGAGTCTACAAGACTCTCAGGACA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 CTAGCTCCATGGAAAAGAAAACTCTCATCAAAAGCAAAGAGTCTACAAGACTCTCAGGACA 1403

Qy       1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTTGCTCTCCAGGATCCTCCCGT 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTTGCTCTCCAGGATCCTCCCGT 1463

Qy       1441 CCGTATATGCCAAGGGATCCGGCCCGGGGCCCGTGCTGGCTC 1481
              ||||||||||||||||||||||||||||||||||||||||||
Db       1464 CCGTATATGCCAAGGGATCCGGCCCGGGGCCCGTGCTGGCTC 1504
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RESULT 3
US-60-215-651-9
; Sequence 9, Application US/60215651
; GENERAL INFORMATION:

GENERAL INFORMATION:
; APPLICANT: Curagen Corporation
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C-061
; CURRENT APPLICATION NUMBER: PCT/US02/31373
;   CURRENT FILING DATE: 2003-09-28
; PRIOR APPLICATION NUMBER: 10/262,511
;   PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
;   PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
;   PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
;   PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
;   PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
;   PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
;   PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
;   PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
;   PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
;   PRIOR FILING DATE: 2002-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqist version 0.1
; SEQ ID NO 3
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: 268667493
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1870)
PCT-US02-31373-3

Query Match   93.7%;   Score 1388.2;   DB 1;   Length 1870;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1390;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATCGTGGTGCTGCTGAACCCATTGCAACCGG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 563

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 623

Qy   601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 683

Qy   661 CTGAGAACATTCTCGTTGACCGACCACAGGACACATCAAGCTGGTGGATCTGCCG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 CTGAGAACATTCTCGTTGACCGACCACAGGACACATCAAGCTGGTGGATCTGCCG 743

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 803

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 863

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 923

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 983

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCGTATCTGATTCAAAGCTTGTTGTGCG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCGTATCTGATTCAAAGCTTGTTGTGCG 1043

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1103

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1163

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTCATCCTCGTGCCAGC 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTCATCCTCGTGCCAGC 1223

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGTTGTGTACAGCAAGG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGTTGTGTACAGCAAGG 1283

Qy   1261 CACTGGGGATTCTTCGTAGATCTGAGTCGTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 CACTGGGGATTCTTCGTAGATCTGAGTCGTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1343

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTTACAAGACTCTCAGGACA 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTTACAAGACTCTCAGGACA 1403

Qy   1381 AGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTCGTCTCCAGATCCTCCCGT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404 AGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTCGTCTCCAGATCCTCCCGT 1463

Qy   1441 CCGTATATGCCAAGGGATCCGCCCGGGGCCCCTGCTGGCTC 1481
            |||||||||||||||||||||||||||||||||||||||||
Db   1464 CCGTATATGCCAAGGGATCCGCCCGGGGCCCCTGCTGGCTC 1504

RESULT 4
PCT-US02-31373-3
; Sequence 3, Application PC/TUS0231373

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Qy  1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1223

Qy  1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1283

Qy  1261 CACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCGGGTCGGACTCCCCTGCCCAAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 CACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCGGGTCGGACTCCCCTGCCCAAGA 1343

Qy  1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCAGACA 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCAGACA 1403

Qy  1381 AGTGTCACAAGT 1393
         ||||||||||||
Db  1404 AGTGTCACAAGAT 1416
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RESULT 5
US-10-262-511-3
; Sequence 3, Application US/10262511
; GENERAL INFORMATION:
;   APPLICANT: Smithson, Glenda
;   APPLICANT: Millet, Isabelle
;   APPLICANT: Peyman, John A.
;   APPLICANT: Kekuda, Ramesh
;   APPLICANT: Ju, Jingfang
;   APPLICANT: Li, Li
;   APPLICANT: Guo, Xiaojia (Sasha)
;   APPLICANT: Patturajan, Meera
;   APPLICANT: Spytek, Kimberly A.
;   APPLICANT: Edinger, Shlomit R.
;   APPLICANT: Ellerman, Karen
;   APPLICANT: Malyankar, Uriel M.
;   APPLICANT: Ort, Tatiana
;   APPLICANT: Gorman, Linda
;   APPLICANT: Zerhusen, Bryan D.
;   APPLICANT: Anderson, David W.
;   APPLICANT: Zhong, Mei
;   APPLICANT: Catterton, Elina
;   APPLICANT: Ji, Weizhen
;   APPLICANT: Miller, Charles E.
;   APPLICANT: Rastelli, Luca
;   APPLICANT: Stone, David J.
;   APPLICANT: Pena, Carol E. A.
;   APPLICANT: Shenoy, Suresh G.
;   APPLICANT: Shimkets, Richard A.
;   APPLICANT: Rothenberg, Mark E.
;   APPLICANT: Leach, Martin D.
;   APPLICANT: Agee, Michele L.
;   APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09

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Db    24 TCAAATATGAGCGCGGAATCCTTTGGATGCTGCGTGCTGAACCCATTGCCAGCCGGGG 83

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTGACTCAACAGCAGAGATGT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTGACTCAACAGCAGAGATGT 143

Qy   121 CTCCTCTTCCCGAGAGGGATATTAGATGCCCTCCTTGTCTCTTGAAGAATGCAGTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 CTCCTCTTCCCGAGAGGGATATTAGATGCCCTCCTTGTCTCTTGAAGAATGCAGTC 203

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 263

Qy   241 TAGCTGAGTTACAGGACCTCCAGCCTTCGGCAAGGACTCGAAGTCAGAAGTCTTGTAG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TAGCTGAGTTACAGGACCTCCAGCCTTCGGCAAGGACTCGAAGTCAGAAGTCTTGTAG 323

Qy   301 GTTGTGGTCACTTTGCTGAAGTGCCAGGTGGTAAGGAGTGGTAAGAGAAGCACCGGGACATCTATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 GTTGTGGTCACTTTGCTGAAGTGCCAGGTGGTAAGGAGTGGTAAGAGAAGCACCGGGACATCTATG 383

Qy   361 CTATGAAAGTGATGAAGAAGAAGGCTTAATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 CTATGAAAGTGATGAAGAAGAAGGCTTAATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 443

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCCCAATTACAGTATGCCT 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCCCAATTACAGTATGCCT 503

Qy   481 TTCAGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 540
         ||||||||||||||||| ||||||||||||||||||||||||||| |||||||||||
Db   504 TTCAGACAAAAATCACCCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 563

Qy   541 CACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTTTACCTAGCTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 CACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTTTACCTAGCTG 623

Qy   601 AGCTGATTTTGGCTGTCGTTCATCAGGGCGATACGTGCATCGAGACGACATCAAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 AGCTGATTTTGGCTGTCGTTCATCAGGGCGATACGTGCATCGAGACGACATCAAGC 683

Qy   661 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTGGAATTTGATCTGCCG 720
         |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   684 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTTGATCTGCCG 743

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 803

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAAGGCACCTACGGCCTGGACT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAAGGCACCTACGGCCTGGACT 863

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 923

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAAT 983

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTTGAAGTTTCTTCTTGATTCTGATTCAAAGCTTGTTGTTGCG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTTGAAGTTTCTTCTTGATTCTGATTCAAAGCTTGTTGTTGCG 1043

Qy  1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCCTAAAATTG 1103

Qy  1081 ACTGGAACAACATTCGTAACTCTCCTCCCCACCCTCGTTCCCACCCTCGTTCCCACCGTCGACGATG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104 ACTGGAACAACATTCGTAACTCTCCTCCCCACCCTCGTTCCCACCCTCGTTCCCACCGTCGACGATG 1163
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;  PRIOR APPLICATION NUMBER: 60/373,260
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/373,826
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 60/327,435
;  PRIOR FILING DATE: 2001-10-05
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: CuraSeqList version 0.1
;  SEQ ID NO 3
;  LENGTH: 1870
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (2)..(1870)
US-10-262-511-3

Query Match             93.7%;  Score 1388.2;  DB 51;  Length 1870;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1390;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy     1 TCAAATATGGAGAGGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    24 TCAAATATGGAGAGGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 83

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 143

Qy   121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC 203

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 263

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 323

Qy   301 GTTGTGGTCACTTTGCTGAAGTGCAGGTCGGTGAAGAGAAGAACCGGGACATCTATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 GTTGTGGTCACTTTGCTGAAGTGCAGGTCGGTGAAGAGAAGAACCGGGACATCTATG 383

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 443

Qy   421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGAATCCCCAATTACAGTATGCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGAATCCCCAATTACAGTATGCCT 503

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTCGGAGGGGACTTGCTGT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTCGGAGGGGACTTGCTGT 563

Qy   541 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAAACCTGATACAGTTTTACCTTAGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAAACCTGATACAGTTTTACCTTAGCTG 623

Qy   601 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGGATACGTGCATCGAGACATCAAGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGGATACGTGCATCGAGACATCAAGC 683

Qy   661 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCCCAAGCTGGTGTGATTTTGGATCTGCCG 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCCCAAGCTGGTGTGATTTTGGATCTGCCG 743

Qy   721 CGAAAATGAATTCAAACAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 CGAAAATGAATTCAAACAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 803

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAAGGCCACCTACGGCCTGGACT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAAGGCCACCTACGGCCTGGACT 863

Qy   841 GTGACTGGTGGTCAGTGGGCGTGGATTGCCTATGAGAGTGATTTATGGGAGATCCCCCTTCG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 GTGACTGGTGGTCAGTGGGCGTGGGCGTGGATTGCCTATGAGAGTGATTTATGGGAGATCCCCCTTCG 923

Qy   901 CAGAGGGAACCTTCGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTTGAAAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 CAGAGGGAACCTTCGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTTGAAAT 983

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTCTTCGATTCGATTCAGATTCAAGCTTGTTGTGCG 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTCTTCGATTCGATTCAGATTCAAAGCTTGTTGTGCG 1043

Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCTGCGTGCCATCCTTTCTTCTTCTCTAAATTG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCTGCGTGCCATCCTTTCTTCTTCTCTAAAATTG 1103

Qy  1081 ACTGGAACACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104 ACTGGAACACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1163

Qy  1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGC 1223

Qy  1201 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAAGACTGGCCGTTTGTGGGGTTTGTGCACAGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAAGACTGGCCGTTTGTGTGGGGTTTGTGCACAAGG 1283

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGAGTCGTCTGTGTGTCGGGTCTGAGCCAAGA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 CACTGGGGATTCTTGGTAGATCTGAGTCTGAGTCGTCTGTGTGTCGGGTCTGAGCCAAGA 1343

Qy  1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGACTACAAGAGTCTCAGGACA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGACAAGACTACAAGAGACTCTCAGGACA 1403

Qy  1381 AGTGTCACAAGGT 1393
           |||||||||||||
Db  1404 AGTGTCACAAGAT 1416


RESULT 6
US-10-262-511A-3
;  Sequence 3, Application US/10262511A
;  GENERAL INFORMATION:
;  APPLICANT: Smithson, Glennda
;  APPLICANT: Millet, Isabelle
;  APPLICANT: Peyman, John A.
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT: Ju, Jingfang
;  APPLICANT: Li, Li
;  APPLICANT: Guo, Xiaojia (Sasha)
;  APPLICANT: Paturajan, Meera
;  APPLICANT: Spytek, Kimberly A.
;  APPLICANT: Edinger, Shlomit R.
;  APPLICANT: Elleman, Karen
;  APPLICANT: Malyankar, Uriel M.
;  APPLICANT: Ort, Tatiana
;  APPLICANT: Gorman, Linda
;  APPLICANT: Zerhusen, Bryan D.
;  APPLICANT: Anderson, David W.
;  APPLICANT: Zhong, Mei
;  APPLICANT: Catterton, Elina
;  APPLICANT: Ji, Weizhen
;  APPLICANT: Miller, Charles E.
;  APPLICANT: Rastelli, Luca
;  APPLICANT: Stone, David J.
;  APPLICANT: Pena, Carol E. A.
```

```
;   APPLICANT:  Shenoy, Suresh G.
;   APPLICANT:  Shimkets, Richard A.
;   APPLICANT:  Rothenberg, Mark E.
;   APPLICANT:  Leach, Martin D.
;   APPLICANT:  Agee, Michele L.
;   APPLICANT:  Berghs, Constance
;   TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;   FILE REFERENCE: 21402-462C
;   CURRENT APPLICATION NUMBER: US/10/262,511A
;   CURRENT FILING DATE:  2002-10-01
;   PRIOR APPLICATION NUMBER: 60/326,483
;   PRIOR FILING DATE:  2001-10-02
;   PRIOR APPLICATION NUMBER: 60/373,815
;   PRIOR FILING DATE:  2001-10-09
;   PRIOR APPLICATION NUMBER: 60/381,642
;   PRIOR FILING DATE:  2002-04-19
;   PRIOR APPLICATION NUMBER: 60/327,917
;   PRIOR FILING DATE:  2002-05-17
;   PRIOR APPLICATION NUMBER: 60/328,029
;   PRIOR FILING DATE:  2002-10-09
;   PRIOR APPLICATION NUMBER: 60/381,038
;   PRIOR FILING DATE:  2002-05-17
;   PRIOR APPLICATION NUMBER: 60/328,056
;   PRIOR FILING DATE:  2001-10-09
;   PRIOR APPLICATION NUMBER: 60/373,260
;   PRIOR FILING DATE:  2002-04-17
;   PRIOR APPLICATION NUMBER: 60/373,826
;   PRIOR FILING DATE:  2002-04-19
;   PRIOR APPLICATION NUMBER: 60/327,435
;   PRIOR FILING DATE:  2001-10-05
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 439
;   SOFTWARE: CuraSeqlist version 0.1
;
;   SEQ ID NO 3
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1870)
US-10-262-511A-3

Query Match       93.7%;    Score 1388.2;   DB 51;   Length 1870;
Best Local Similarity 99.8%;    Pred. No. 0;
Matches 1390;  Conservative    0;   Mismatches    0;   Indels    3;   Gaps    0;
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Qy      1  TCAAATATGGAGCGCGGAATCCTTTGGATGTGGTGCTGCTGAACCCATTGCCAACCGGG    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     24  TCAAATATGGAGCGCGGAATCCTTTGGATGTGGTGCTGCTGAACCCATTGCCAGCCGGG    83

Qy     61  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT   143

Qy    121  CTCCTCTTCCCGAGAAGGAGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144  CTCCTCTTCCCGAGAAGGAGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC   203

Qy    181  AGCCTGCTCTGATGAAGATTAAGCACGTGAGCCAACTTGTCCGGAAGTATTCCGACACCA   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204  AGCCTGCTCTGATGAAGATTAAGCACGTGAGCCAACTTGTCCGGAAGTATTCCGACACCA   263

Qy    241  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGGCAAAGGACTTCAGAGTCTTTGTAG   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGGCAAAGGACTTCAGAGTCTTTGTAG   323

Qy    301  GTTGTGTCACTTGCTGAAGTGCAGTGCAGTGGTAAGAAAGCAACCGGGGACATCTATG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324  GTTGTGTCACTTGCTGAAGTGCAGTGCAGTGGTAAGAAAGCAACCGGGGACATCTATG   383

Qy    361  CTATGAAAGTGATGAAGAAGAAGGGCTTTATTGGCCCAGGCAGGTTTCATTTTTTGAGG   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384  CTATGAAAGTGATGAAGAAGAAGGGCTTTATTGGCCCAGGCAGGTTTCATTTTTTGAGG   443
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Qy    421  AAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444  AAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT   503

Qy    481  TTCAGGACAAAATCACCTTTATCTCGTCATCATGGAATATCAGCCTGGAGGGGGACTTGCTGT   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    504  TTCAGGACAAAATCACCTTTATCTCGTCATCATGGAATATCAGCCTGGAGGGGGACTTGCTGT   563

Qy    541  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    564  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG   623

Qy    601  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    624  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC   683

Qy    661  CTGAGAACATTCTCGTTGACCCGCCACAGGACACATCAAGCTCGGTGGTGGATTTTGATCTGCCG   720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    684  CTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTCGGTGGTGGATTTTGATCTGCCG   743

Qy    721  CGAAAATGAAATCAAACAAGAGTGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744  CGAAAATGAAATCAAACAAGAGTGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   803

Qy    781  TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCCACCTACGGCCTGACT   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804  TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCCACCTACGGCCTGACT   863

Qy    841  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCCTTCG   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCCTTCG   923

Qy    901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT   983

Qy    961  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTCAAAGCTTGTTGTGCG   1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTCAAAGCTTGTTGTGCG   1043

Qy   1021  GCCAGAAAGAGAGACTGAAGTTGAGGTTGAGAGGTCTTGTGCTGCCATCCTTTCTTCTTCTAAAATTG   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044  GCCAGAAAGAGAGACTGAAGTTGAGGTTGAGAGGTCTTGTGCTGCCATCCTTTCTTCTTCTAAAATTG   1103

Qy   1081  ACTGGAACAACATTCGTAACTCGTAACTCGTTCCCACCCTTCGTTCCGACGATG   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104  ACTGGAACAACATTCGTAACTCGTAACTCGTTCCCACCCTTCGTTCCGACGATG   1163

Qy   1141  ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164  ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC   1223

Qy   1201  TGAGCCCCTCAGGCTTCTCGGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGTGGGGTCTCGGACTCCCTG   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224  TGAGCCCCTCAGGCTTCTCGGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGTGGGGTCTCGGACTCCCTG   1283

Qy   1261  CACTGGGGATTCTTGGTAGATCGGAGTCGTGTGTCGGGTCTCGGACTCCCTGCCAAGA   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284  CACTGGGGATTCTTGGTAGATCGGAGTCGTGTGTCGGGTCTCGGACTCCCTGCCAAGA   1343

Qy   1321  CTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAGACTCTCAGGACA   1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344  CTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAGACTCTCAGGACA   1403

Qy   1381  AGTGTCACCAAGT   1393
           |||||||||||||
Db   1404  AGTGTCACCAAGAT   1416
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RESULT 7
US-10-791-666-3
; Sequence 3, Application US/10791666
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; GENERAL INFORMATION:
;   APPLICANT: Yu, Xuanchuan
;   APPLICANT: Miranda, Maricar
;   APPLICANT: Friddle, Carl Johan
;   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
;   FILE REFERENCE: LEX-0289-USA
;   CURRENT APPLICATION NUMBER: US/10/791,666
;   CURRENT FILING DATE:  2004-03-02
;   PRIOR APPLICATION NUMBER: US/10/028,946
;   PRIOR FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: US 60/258,335
;   PRIOR FILING DATE: 2000-12-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 5877
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-791-666-3

Query Match             93.7%;  Score 1388.2;  DB 62;  Length 5877;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1390;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      1 TCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 TCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG   70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy    121 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC  190

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy    301 GTTGTGGTCACTTTGCTGAAGTGCGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGGTCACTTTGCTGAAGTGCGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  370

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG  430

Qy    421 AAGAGGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCAATTACAGTATGCCT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCAATTACAGTATGCCT  490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGATAATCATCGCCTCGAGGGGACTTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGATAATCATCGCCTCGAGGGGACTTGCTGT  550

Qy    541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy    601 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCATGGATACGTGCATCGAGACAATCAAGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCATGGATACGTGCATCGAGACAATCAAGC  670

Qy    661 CTGAGAACAATTCTCGTTGACCGACCGCACCAGGACACATCAAGCTGGTGGATTTGGATCTGCCG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACAATTCTCGTTGACCGACCGCACCAGGACACATCAAGCTGGTGGATTTGGATCTGCCG  730

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
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Db    731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGGAAAAGGCACCTACGGCCTGGACT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGGAAAAGGCACCTACGGCCTGGACT  850

Qy    841 GTGACTGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GTGACTGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  910

Qy    901 CAGAGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGAGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT  970

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTGAAGGTCTTTGCTGATTCGATTCAAAGCTTGTGTTGTGCG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTGAAGGTCTTTGCTGATTCGATTCAAAGCTTGTGTTGTGCG  1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTCTCTAAAATTG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTCTCTAAAATTG  1090

Qy   1081 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTTCGTTCTCCGTGCCAGC  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTTCGTTCTCCGTGCCAGC  1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCGTCCCGTGCCAGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCGTCCCGTGCCAGC  1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGTACAGCAAGG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGTACAGCAAGG  1270

Qy   1261 CACTGGGGATTCTTGGTAGATCGGAGTCGAGTCGTGTGTGCGGGCTCGGACTCCCCGCCAAGA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271 CACTGGGGATTCTTGGTAGATCGGAGTCGAGTCGTGTGTGCGGGCTCGGACTCCCCGCCAAGA  1330

Qy   1321 CTAGCTCCATGAGAAAGAAACTTCTCATCAAAAGCAAAGACTCTCAGGACA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 CTAGCTCCATGAGAAAGAAACTTCTCATCAAAAGCAAAGACTCTCAGGACA  1390

Qy   1381 AGTGTCACAAGGT  1393
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Db   1391 AGTGTCACAAGAT  1403
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RESULT 8
US-10-791-666-1
; Sequence 1, Application US/10791666
; GENERAL INFORMATION:
;   APPLICANT: Yu, Xuanchuan
;   APPLICANT: Miranda, Maricar
;   APPLICANT: Friddle, Carl Johan
;   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
;   FILE REFERENCE: LEX-0289-USA
;   CURRENT APPLICATION NUMBER: US/10/791,666
;   CURRENT FILING DATE:  2004-03-02
;   PRIOR APPLICATION NUMBER: US/10/028,946
;   PRIOR FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: US 60/258,335
;   PRIOR FILING DATE: 2000-12-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6165
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-791-666-1

Query Match             93.7%;  Score 1388.2;  DB 62;  Length 6165;
Best Local Similarity   99.8%;  Pred. No. 0;
```

Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     1 TCAAATATGAGGCGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11 TCAAATATGAGGCGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCTGATGAAGATAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACCACCA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACCACCA 250

Qy   241 TAGCTGAGTTACAGGAGACTTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGACTTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 310

Qy   301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTTAAGAGAGAAAGCAACCGGGGACATCTATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTTAAGAGAGAAAGCAACCGGGGACATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 430

Qy   421 AAGAGCGGGAACATATTATTCTCGAAGCACAAGCCCGTGGAATCCCCAATTACAGTATGCCT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGGAACATATTATTCTCGAAGCACAAGCCCGTGGAATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy   541 CACTTTTGAATAGATATGAGGACCAGTAGTGAGTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGATATGAGGACCAGTAGTGAGTAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy   601 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy   661 CTGAGAACATTCTCGTTGACCGTGACCGACAGGACACATCAAGCTGGTGTGTTGGATCTGCCG 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCTCGTTGACCGTGACCGACAGGACACATCAAGCTGGTGTGTTGGATCTGCCG 730

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGAGCTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGAGCTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 850

Qy   841 GTGACTGGTGTGCAGTGGCGCTGGGCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGTGCAGTGGCGCTGGGCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG 910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCCAGACTTTCCAGCCGGTTTTTTGAAAT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGAACCTCTGCCAGAACCTTCCAGACTTTCCAGCCGGTTTTTTGAAAT 970

Qy   961 TTCCAGATGACCCCAAAGTGACGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTCGCG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGACCCCAAAGTGACGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTCGCG 1030

Qy  1021 GCCAGAAAGAGAGAGACTGAAGTTTGAAGCGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1031 GCCAGAAAGAGAGAGACTGAAGTTTGAAGCGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1090
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Qy  1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTTCAAGTCCGACGATG 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTTCAAGTCTGACGATG 1150

Qy  1141 ACACCCCAATTTGATGAACCAGCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151 ACACCCCAATTTGATGAACCAGCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy  1201 TGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGG 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211 TGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGG 1270

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1330

Qy  1321 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGACTTCAGCACA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1331 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGACTTCAGCACA 1390

Qy  1381 AGTGTCACAAGGT 1393
         ||||||||||||
Db  1391 AGTGTCACAAGAT 1403
```

RESULT 9
US-10-415-011-43
; Sequence 43, Application US/10415011
; GENERAL INFORMATION:
;   APPLICANT: INCYTE CORPORATION
;   APPLICANT: GURURAJAN, Rajagopal
;   APPLICANT: BAUGHN, Mariah R.
;   APPLICANT: CHAWLA, Narinder K.
;   APPLICANT: ELLIOTT, Vicki S.
;   APPLICANT: XU, Yuming
;   APPLICANT: ARVIZU, Chandra S.
;   APPLICANT: YAO, Monique G.
;   APPLICANT: RAMKUMAR, Jayalaxmi
;   APPLICANT: DING, Li
;   APPLICANT: TANG, Y. Tom
;   APPLICANT: HAFALIA, April J.A.
;   APPLICANT: NGUYEN, Danniel B.
;   APPLICANT: GANDHI, Ameena R.
;   APPLICANT: LU, Yan
;   APPLICANT: YUE, Henry
;   APPLICANT: BURFORD, Neil
;   APPLICANT: BANDMAN, Olga
;   APPLICANT: TRIBOULEY, Catherine M.
;   APPLICANT: LAL, Preeti G.
;   APPLICANT: RECIPON, Shirley A.
;   APPLICANT: LU, Dyung Aina M.
;   APPLICANT: BOROWSKY, Mark L.
;   APPLICANT: THORNTON, Michael B.
;   APPLICANT: SWARNAKER Anita
;   APPLICANT: THANGAVELU, Kavitha
;   APPLICANT: KHAN, Farrah A.
;   APPLICANT: ISON, Craig H.
;   TITLE OF INVENTION: HUMAN KINASES
;   FILE REFERENCE: PI-0262 USN
;   CURRENT APPLICATION NUMBER: US/10/415,011
;   CURRENT FILING DATE: 2003-04-18
;   PRIOR APPLICATION NUMBER: PCT/US01/47728
;   PRIOR FILING DATE: 2001-10-20
;   PRIOR APPLICATION NUMBER: US 60/242,410
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: US 60/244,068
;   PRIOR FILING DATE: 2000-10-27
;   PRIOR APPLICATION NUMBER: US 60/245,708
;   PRIOR FILING DATE: 2000-11-03
;   PRIOR APPLICATION NUMBER: US 60/247,672
;   PRIOR FILING DATE: 2000-11-09
;   PRIOR APPLICATION NUMBER: US 60/249,565

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;   PRIOR FILING DATE: 2000-11-16
;   PRIOR APPLICATION NUMBER: US 60/252,730
;   PRIOR FILING DATE: 2000-11-22
;   PRIOR APPLICATION NUMBER: US 60/250,807
;   PRIOR FILING DATE: 2000-12-01
;   NUMBER OF SEQ ID NOS: 44
;   SOFTWARE: PERL Program
;   SEQ ID NO 43
;   LENGTH: 6298
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: Incyte ID No: 7484498CB1
US-10-415-011-43

Query Match             93.7%;     Score 1388.2;   DB 54;   Length 6298;
Best Local Similarity   99.8%;     Pred. No. 0;
Matches 1390;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy     1 TCAAATATGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG    60
           ||||||||| ||||| | ||||| ||| ||||||||||||||||||||||||| |||||
Db    65 TCAAATATGGAGCGCGGCGGAATCGTTTCTGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 124

Qy    61 CCTCCAGGCTGAATCGTTCTTCCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
           |||||  |||||||||||||||||||| || |||||||||||||||||||||||||||||
Db   125 CCTCCGGGCTGAATCGTTCTTCCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 184

Qy   121 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 244

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 304

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGGAGTCTTGTAG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGGAGTCTTGTAG 364

Qy   301 GTTGTGGTCACTTTGCTCAGGTGCAGGTGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365 GTTGTGGTCACTTTGCTCAGGTGCAGGTGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 424

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 484

Qy   421 AAGAGCGGAACATATTCTCGAAGCACAAGCGCCCGTGGATCCCCAATTACAGTATGCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485 AAGAGCGGAACATATTCTCGAAGCACAAGCGCCCGTGGATCCCCAATTACAGTATGCCT 544

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 604

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGAATGAAAATCTGATACAGTTTACCTAGCTG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605 CACTTTTGAATAGATATGAGGACCAGTTAGAATGAAAATCTGATACAGTTTACCTAGCTG 664

Qy   601 AGCTCGATTTTGGCTGTCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   665 AGCTCGATTTTGGCTGTCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 724

Qy   661 CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGAATTTGGATCTGCCG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   725 CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGAATTTGGATCTGCCG 784

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   785 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 844

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCCTGGACT 840
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Db   845 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCCTGGACT 904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 GTGACTGGTGGTCAGTGGGCGTGGGCGTGGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900

Db   905 GTGACTGGTGGTCAGTGGGCGTGGGCGTGGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 CAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960

Db   965 CAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 1024
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGACGTCTTTCTTGATCGATCCGATTCAAAGCTGTGTTGTCG 1020

Db  1025 TTCCAGATGACCCCAAAGTGAGCAGTGACGTCTTTCTTGATCGATCCGATTCAAAGCTGTGTTGTCG 1084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCAAAAATTG 1080

Db  1085 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCAAAAATTG 1144
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081 ACTGGAACAACATTCGTAACTCTCCCTCCCACCCTTCGTTCCACGATG 1140

Db  1145 ACTGGAACAACATTCGTAACTCTCCCTCCCACCCTTCGTTCCACGATG 1204
           ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141 ACACCTTCCAATTTGATGAACCAGCAGAAGAATTCGTTGGGGTTTCATCCTCTCCGTGCCAGC 1200

Db  1205 ACACCTTCCAATTTGATGAACCAGCAGAAGAATTCGTTGGGGTTTCATCCTCTCCGTGCCAGC 1264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTGTGGGGTTTGTGGGG 1260

Db  1265 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTGTGGGGTTTGTGGGG 1324
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261 CACTGGGATTCTTGTAGATCTGAGTCTGTGTGTCGGGGTCTGGACTCCCCTGCCAAGA 1320

Db  1325 CACTGGGATTCTTGTAGATCTGAGTCTGTGTGTCGGGGTCTGGACTCCCCTGCCAAGA 1384
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1321 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAAGCTACAAGACTCTCAGGACA 1380

Db  1385 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAAGCTACAAGACTCTCAGGACA 1444
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 AGTGTCACAAGT 1393

Db  1445 AGTGTCACAAGAT 1457
           ||||||||||||
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RESULT 10
US-10-170-235-7679
;   Sequence 7679, Application US/10170235
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig
;   TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
;   TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;   FILE REFERENCE: CL001380
;   CURRENT APPLICATION NUMBER: US/10/170,235
;   CURRENT FILING DATE: 2003-03-17
;   NUMBER OF SEQ ID NOS: 42514
;   SEQ ID NO 7679
;   LENGTH: 8602
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-7679

Query Match             93.7%;     Score 1388.2;   DB 49;   Length 8602;
Best Local Similarity   99.8%;     Pred. No. 0;
Matches 1390;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy     1 TCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG    60
           ||||||||| |||||| |||||| ||||||||||||||||||||||||||||| |||||
Db    67 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 126

Qy    61 CCTCCAGGCTGAATCGTTCTTCCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
           |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   127 CCTCCCAGGCTGAATCGTTCTTCTTCCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 186
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RESULT 11
US-10-017-216-3
; Sequence 3, Application US/10017216
; GENERAL INFORMATION:
;   APPLICANT: KAPELLER-LIBERMANN, Rosana
;   TITLE OF INVENTION: 13245, A Novel Human Myotonic Dystrophy Type Protein
;   TITLE OF INVENTION: Kinase and Uses Therefor
;   FILE REFERENCE: 10147-57U1
;   CURRENT APPLICATION NUMBER: US/10/017,216
;   CURRENT FILING DATE: 2001-10-23
;   PRIOR APPLICATION NUMBER: US 60/242,429
;   PRIOR FILING DATE: 2000-10-23
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 6159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-216-3

  Query Match             93.3%;  Score 1381.8;  DB 46;  Length 6159;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches  1386;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 TCAAATATGGAGGCGGAATCCTTTGGATGTGGTGCTGCTGAACCCATTGCCAACCGGGG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 TCAAATATGGAGGCGGAATCCTTTGGATGTGGTGCTGCTGAACCCATTGCCAGCCGGGG 70

Qy         61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy        121 CTCCTCTTCCCGAGAAGGGGATATTAGAGCACGTGAGCAACTTCTTGTCTCTTTGAAGAATGCAGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CTCCTCTTCCCGAGAAGGGGATATTAGAGCACGTGAGCAACTTCTTGTCTCTTTGAAGAATGCAGTC 190

Qy        181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTCCGACACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTCCGACACCA 250

Qy        241 TAGCTGAGTTACAGGAGCTCGAAGTGCAGGTGCAGGTGGTTAAGAGAAAGCAACCGGGGACATCTATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TAGCTGAGTTACAGGAGCTCGAAGTGCAGGTGCAGGTGGTTAAGAGAAAGCAACCGGGGACATCTATG 310

Qy        301 GTTGTGTCACTTGCTGAAGTGCAGTGCAGTGGTTTATTGGCCATCATGAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTTGTGTCACTTGCTGAAGTGCAGTGCAGTGGTTTATTGGCCATCATGAAATTG 370

Qy        361 CTATGAAGTGATGAAGAAGAAGAGGCTTATTTGAGG 420
              ||||||||||||||||||||||||||||||||||||
Db        371 CTATGAAGTGATGAAGAAGAAGAGGCTTATTTGAGG 430

Qy        421 AAGAGGCGGAACATATTATCTCGAAGCACAGACAAGCCCGTGATCCCCAATTACAGTATGCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AAGAGGCGGAACATATTATCTCGAAGCACAGACAAGCCCGTGATCCCCAATTACAGTATGCCT 490

Qy        481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 606

Qy        541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 666

Qy        601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGTCATCGAGACATCAAGC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGTCATCGAGACATCAAGC 726

Qy        661 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGTGTGGATCTGCCG 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGTGTGGATCTGCCG 786

Qy        721 CGAAAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CGAAAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 846

Qy        781 TGGCCTCCTGAAGTGCTGACTGCTGATGAACGGGATGGAAAAGGCACCTACGGCCTCGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TGGCCTCCTGAAGTGCTGACTGCTGATGAACGGGATGGAAAAGGCACCTACGGCCTCGACT 906

Qy        841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 966

Qy        901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 1026

Qy        961 TTCCAGATGACCCCAAAGTGAGCAGTGACACTTCTCAAAGCTTGTTGTGCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 TTCCAGATGACCCCAAAGTGAGCAGTGACACTTCTCAAAGCTTGTTGTGCG 1086

Qy       1021 GCCAGAAGAGAGACAACAACATTCGTAACTCGTAACTCCTCCCCCCTTGCTGCCATCCTTCTCTTCAAAATTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GCCAGAAGAGAGACAACAACATTCGTAACTCGTAACTCCTCCCCCCTTGCTGCCATCCTTCTCTTCAAAATTG 1146

Qy       1081 ACTGGAACAACATTCGTAACTCGTAACTCCTCCCCCCTTCGTTCCCACCCTTCGTTCATTTTTCATTTTTGAGG 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ACTGGAACAACATTCGTAACTCGTAACTCCTCCCCCCTTCGTTCCCACCCTTCGTTCATTTTTCATTTTTGAGG 1206

Qy       1141 ACACTTCCAATTTTGATGAACGGAAGAGATTCGTGGGTTTCATCCTCCGTTGCCAGC 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 ACACTTCCAATTTTGATGAACGGAAGAGATTCGTGGGTTTCATCCTCCGTTGCCAGC 1266

Qy       1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTCGTACAGCAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTCGTACAGCAAGG 1326

Qy       1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTCGGG 1320
              ||||||||||||||||||||||||||||||||||||
Db       1327 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTCGGG 1386

Qy       1321 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAAGACTACAGAGACTTCAGGACA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAAGACTACAGAGACTTCAGGACA 1446

Qy       1381 AGTGTCACAAGT 1393
              ||||||||||||
Db       1447 AGTGTCACAAGAT 1459
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; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPI01-294P1RNWOM
; CURRENT APPLICATION NUMBER: PCT/US02/41011
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentSeq for Windows Version 4.0
;
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)

PCT-US02-41011-11

Query Match   93.3%;   Score 1381.8;   DB 1;   Length 6162;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1386; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

```
Qy       1 TCAAAATATGGAGCGCGGAATCCTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 TCAAAATATGGAGCGCGGAATCCTTGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG   70

Qy      61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy     121 CTCCTCTTCCCGAGAAGGGGATATTAGATAGCATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 CTCCTCTTCCCGAGAAGGGGATATTAGATAGCATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC  190

Qy     181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy     241 TAGCTGAGTTACAGAGACTCCAGCTTCGGCGAAAGACTTCGAAGTCAGAAGTCTTGTAG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 TAGCTGAGTTACAGAGACTCCAGCTTCGGCGAAAGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy     301 GTTGTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGCAACCGGGGACATCTATG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 GTTGTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGCAACCGGGGACATCTATG  370

Qy     361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGGTTCATTTTTGAGG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGGTTCATTTTTGAGG  430

Qy     421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT  490

Qy     481 TTCAGGACAAAAATCACCTTTATCTGCTGATGGAAGAATATCAGCCTGAGGGGGACTTGCTGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 TTCAGGACAAAAATCACCTTTATCTGCTGATGGAAGAATATCAGCCTGAGGGGGACTTGCTGT  550

Qy     541 CACTTTTGAATAGATAGAGGAACCAGTTAGATAGAAAACCTGATACAGTTTACCTAGCTG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     551 CACTTTTGAATAGATAGAGGAACCAGTTAGATAGAAAACCTGATACAGTTTACCTAGCTG  610

Qy     601 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGGATACGTGCATCGAGACATCAAGC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     611 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGGATACGTGCATCGAGACATCAAGC  670

Qy     661 CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTCGGTGGATTTTGGATCTGCCG  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTCGGTGGATTTTGGATCTGCCG  730

Qy     721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  790
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Db     491 TTCAGGACAAAAATCACCTTTATCTGCTGATGGAAGAATATCAGCCTGAGGGGGACTTGCTGT  550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     541 CACTTTTGAATAGATGATGATGAGGACCAGTTAGATGAAAACCTGATGAAACTGATGGAATCAGCGGATACGTGCATCGGATACGTGCATCGAGACATCAAGCTGCTGT  550

Db     551 CACTTTTGAATAGATGATGATGAGGACCAGTTAGATACAGTTTTGGATCTGCCG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     611 CACTTTTGAATAGATGATGATGAGGACCAGTTAGATACAGTTTTGGATCTGCCG  610

Db     601 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGATCATCGAGACATCAAGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     661 AGCTGATTTTGGTCGTGTTCATCTGATGGGATACGTGCATCGTGCATCGAGACATCAAGC  670

Db     661 AGCTGATTTTGGCTCATCTGACAGGGATCATCTGATCATCGAGACATCAAGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||
Qy     721 CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTCGGTGGATTTTGGATCTGCCG  730

Db     721 CGAAAATGAATTCAAACAAGATGGTGAATGGCCAAACTCCCAGATTACA  780
           ||||||||||||||||||||||||||||||||||||||||||||
Qy     731 CGAAAATGAATTCAAACAAGATGGTGAATGGCCAAACTCCCAGATTACA  790

Db     781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAGGCACCTACGGCCTGGACT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAGGCACCTACGGCCTGGACT  850

Db     841 GTGACTGGTGGTCAGTGGGGCGTGAGTTCGGGGGCGTGAGATGAGATGATTATGGGAGAT  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     851 GTGACTGGTGGTCAGTGGGGCGTGAGTTCGGGGGCGTGAGATGAGATGATTATGGGAGAT  910

Db     901 CAGAGGGAACCTCGCCAGAACCTTCAATACATTATGAATTCCAGCGGTTTTGAAAT  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     911 CAGAGGGAACCTCGCCAGAACCTTCAATACATTATGAATTCCAGCGGTTTTGAAAT  970

Db     961 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTCTTGATCTGATTCAAAGTTGTTGTGCG  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     971 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTCTTGATCTGATTCAAAGTTGTTGTGCG  1030

Db    1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCGTGCCATCCTTTCTTCTTCCTAAAATTG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCGTGCCATCCTTTCTTCTTCCTAAAATTG  1090

Db    1081 ACTGGAACAACACATTCGTAACTCGTAACTCGTCCCCCCTTCGTTCCCACCCTCAGTCCGACGATG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1091 ACTGGAACAACACATTCGTAACTCGTAACTCGTCCCCCCTTCGTTCCCACCCTCAGTCCGACGATG  1150

Db    1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||
Qy    1151 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC  1210

Db    1201 TGAGCCCCTCCAGGCTTCTCCGGTGAAGAACTGCCGTTGTGTGGGGTTTCGTACAGCAAGG  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1211 TGAGCCCCTCCAGGCTTCTCCGGTGAAGAACTGCCGTTGTGTGGGGTTTCGTACAGCAAGG  1270

Db    1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCTCGGACTCCCCGCCAAGA  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCTCGGACTCCCCGCCAAGA  1330

Db    1321 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTCTCAGGACA  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1331 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTCTCAGGACA  1390

Db    1381 AGTGTCACAAGGT  1393
           |||||||||||||
Qy    1391 AGTGTCACAAGAT  1403
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RESULT 12

PCT-US02-41011-11
; Sequence 11, Application PC/TUS0241011
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,

Matches 1386;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

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Qy     1 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCGAACCCGGG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCGAACCCGGG   70

Qy    61 CCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCCTTATGACTCAACAGCAGATGT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCCTTATGACTCAACAGCAGATGT  130

Qy   121 CTCCTCTTTCCCGAGAAGGGATATTAGGATGCCCTCTTGTCTCTTTGAAGAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTTCCCGAGAAGGGATATTAGGATGCCCTCTTGTCTCTTTGAAGAATGCAGTC  190

Qy   181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCGATGAAGATTAAGCACGTGAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy   301 GTTGTGGTCACTTGCTGAAGTGCAGTGCAGTGGTGTAAGGACAACCGGGACAATCCATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGGTCACTTGCTGAAGTGCAGTGCAGTGGTGTAAGGACAACCGGGACAATCCATG  370

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGACCAGGTTCATTTTTTGAGG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGACCAGGTTCATTTTTTGAGG  430

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy   481 TTCAGACAAAAATCACCTTTATCTGGTCATGTGAGGAATATCAGCGTGGTGGCTTGCTGT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGACAAAAATCACCTTTATCTGGTCATGTGAGGAATATCAGCGTGGTGGCTTGCTGT  550

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAATGAAAACCTGATACAGTTTTACCTAGCTG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy   601 AGCTGATTTTGCTGTTCATCTGATACGTGCATCTGATGGGATACGTGCATCTGAGACATCAAGC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTTGCTGTTCATCTGATACGTGCATCTGATGGGATACGTGCATCTGAGACATCAAGC  670

Qy   661 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTCGTGTGATCTGCCG  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTCGTGTGATCTGCCG  730

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT  850

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTTATGGGAGATCCCCCTTCG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTTATGGGAGATCCCCCTTCG  910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  970

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTGAGGTCTTCAAGCTTGTTGTGCG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGACCCCAAAGTGAGCAGTCAGTTGAGGTCTTCAAGCTTGTTGTGCG 1030

Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1090

Qy  1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1150

Qy  1141 ACACCTCCAATTTGATGAACCAGACCAGGAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151 ACACCTCCAATTTGATGAACCAGACCAGGAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGC 1210

Qy  1201 TGAGCCCCTGAAGGCTTCTCGGGTGAAGAACTGCGGTCGGTTGTGTGTGGGCTCGACTCCGCAAGA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211 TGAGCCCCTGAAGGCTTCTCGGGTGAAGAACTGCGGTCGGTTGTGTGTGGGCTCGACTCCGCAAGA 1270

Qy  1261 CACTGGGGATTCTTGGTAGATCGAGTCGTCGTTGTGTGTGTCGGGTCTCGACTCCCTGCCAAGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1271 CACTGGGGATTCTTGGTAGATCGAGTCGTCGTTGTGTGTGTCGGGTCTCGACTCCCTGCCAAGA 1330

Qy  1321 CTAGCTCCATGGAAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGACTCTCAGGACA 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1331 CTAGCTCCATGGAAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGACTCTCAGGACA 1390

Qy  1381 AGTGTCACAAGGT 1393
         |||||||||||||
Db  1391 AGTGTCACAAGAT 1403
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RESULT 13
US-10-325-430-11
; Sequence 11, Application US/10325430
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
;   32838,336 and 52908
; FILE REFERENCE: MPI01-294P1RNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match   93.3%;   Score 1381.8;   DB 52;   Length 6162;
Best Local Similarity 99.5%;   Pred. No. 0;

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Qy   301  GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACGGGGACATCTATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   329  GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACGGGGACATCTATG  388

Qy   361  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTCATTTTTGAGG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   389  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTCATTTTTGAGG   448

Qy   421  AAGAGGCGGAACATATATCTGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449  AAGAGGCGGAACATATATCTGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT   508

Qy   481  TTCAGGACAAAAATCACCTTTATCTGCATGGAATATCAGCCTGAGGGGGACTTGCTGT  540
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   509  TTCAGGACAAAAATCACCTTTATCTGACTGGAGGAATATCAGCCTGAGGGGGACTTGCTGT  568

Qy   541  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   569  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG  628

Qy   601  AGCTGATTTTGGCTGTGTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   629  AGCTGATTTTGGCTGTGTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  688

Qy   661  CTGAGAACATTCTCGTTGACCGTGACCGCACAGAGCACACATCAAGCTGGTGGATTTTGGATCTGCCG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   689  CTGAGAACATTCTCGTTGACCGTGACCGCACAGAGCACACATCAAGCTGGTGGATTTTGGATCTGCCG  748

Qy   721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  808

Qy   781  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTACGGCCTGGACT  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTACGGCCTGGACT  868

Qy   841  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  928

Qy   901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCAGCGCGTTTTTGAAAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   929  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCAGCGCGTTTTTGAAAT  988

Qy   961  TTCCAGATGACCCCAAAGTGACTCAGTCGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG  1020
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   989  TTCCAGATGACCCCAAAGTGAGTCAGTCGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG  1048

Qy  1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCGCCATCCTTTCTTCTCTAAAATTG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1049  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCGCCATCCTTTCTTCTCTAAAATTG  1108
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Qy  1081  ACTGGAACAACATTGTAACTCTCCTCCCCCCTTCGTTCCACCCTTCGTTCCACCGACGATG  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091  ACTGGAACAACATTGTAACTCTCCTCCCCCCTTCGTTCCACCCTTCGTTCCACCGACGATG  1150

Qy  1141  ACACCTCCAATTTGATGACCAGCAGAGAATTCGTGGGGTTTCATCCTCCGTGCCAGC  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151  ACACCTCCAATTTGATGACCAGCAGAGAATTCGTGGGGTTTCATCCTCCGTGCCAGC  1210

Qy  1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTGTGCGGCAAGG  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTGTGCGGCAAGG  1270

Qy  1261  CACTGGGGATTCTTGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1271  CACTGGGGATTCTTGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1330

Qy  1321  CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGCAAAGACTACAAAGACTCTCAGGACA  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1331  CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGCAAAGACTACAAAGACTCTCAGGACA  1390

Qy  1381  AGTGTCACAAGGT  1393
          |||||||||||
Db  1391  AGTGTCACAAGAT  1403
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Query Match 93.3%; Score 1381.8; DB 1; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches 0; Indels 7; Gaps 0;

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Qy     1  TCAAATATGAGCGGCGGAATCCTTGGATGCTGGTGCTGCTCAGGGAACCCATTGCCAACCGGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    29  TCAAATATGAGCGGCGGAATCCTTGGATGCTGGTGCTGCTCAGGGAACCCATTGCCAGCCGGG   88

Qy    61  CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89  CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  148

Qy   121  CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTGTTCTCTTTGAAGAATGCAGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149  CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTGTTCTCTTTGAAGAATGCAGTC  208

Qy   181  AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGGAAGTATTCCGACACCA  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   209  AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGGAAGTATTCCGACACCA  268

Qy   241  TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269  TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  328
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Db   1409 AGTGTCACAAGAT 1421
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RESULT 15
PCT-US04-00750-51
; Sequence 51, Application PC/TUS0400750
; GENERAL INFORMATION:
;   APPLICANT: Karicheti, Venkateswarlu
;   APPLICANT: Silos-Santiago, Inmaculada
;   APPLICANT: Eliasof, Scott D.
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;   TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 51810, 211, 5687, 884,
;   TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
;   TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
;   TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
;   TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
;   TITLE OF INVENTION: 32720, 4805, 14303, 16816, 17827, 32620, 577, 619, 1423,
;   TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
;   TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
;   TITLE OF INVENTION: 55053
;   FILE REFERENCE: MPI03-007
;   CURRENT APPLICATION NUMBER: PCT/US04/00750
;   CURRENT FILING DATE: 2004-01-14
;   PRIOR APPLICATION NUMBER: US 60/440,318
;   PRIOR FILING DATE: 2003-01-15
;   PRIOR APPLICATION NUMBER: US 60/444,783
;   PRIOR FILING DATE: 2003-02-04
;   PRIOR APPLICATION NUMBER: US 60/457,901
;   PRIOR FILING DATE: 2003-03-27
;   PRIOR APPLICATION NUMBER: US 60/468,775
;   PRIOR FILING DATE: 2003-05-08
;   PRIOR FILING DATE: 2003-05-19
;   PRIOR APPLICATION NUMBER: US 60/478,742
;   PRIOR FILING DATE: 2003-06-16
;   PRIOR APPLICATION NUMBER: US 60/488,529
;   PRIOR FILING DATE: 2003-07-18
;   PRIOR APPLICATION NUMBER: US 60/491,156
;   PRIOR FILING DATE: 2003-07-30
;   PRIOR APPLICATION NUMBER: US 60/499,594
;   PRIOR FILING DATE: 2003-09-02
;   PRIOR APPLICATION NUMBER: US 60/506,332
;   PRIOR FILING DATE: 2003-09-26
;   NUMBER OF SEQ ID NOS: 136
;   SOFTWARE: FastSEQ for Windows Version 4.0
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;   LENGTH: 6574
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (19)...(6180)
PCT-US04-00750-51

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Best Local Similarity  99.5%;
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Score 1381.8;   DB 2;   Length 6574;
Pred. No. 0;
Indels  0;   Gaps  0;
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Sequence alignment (Qy / Db):

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Qy   241 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 328

Qy   301 GTTGTGTGTCACTTGCTGAAGTGCGCAGGTGGTAAGAGAAAGCAACCGGGACATCTATG 360
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Db   329 GTTGTGTGTCACTTGCTGAAGTGCGCAGGTGGTAAGAGAAAGCAACCGGGACATCTATG 388

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTGAGG 420
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Db   389 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTGAGG 448

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT 480
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Qy   481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 540
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us-10-724-594-1_copy_17_1497.rnpm

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Search completed: March 19, 2005, 17:31:32
Job time : 5230.99 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         March 19, 2005, 11:54:37 ; Search time 810.2 Seconds
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5544816 seqs, 297661598 residues

Total number of hits satisfying chosen parameters:      11089632

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
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                           SUMMARIES
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2	1481	100.0	1515	14	US-10-238-709-1	Sequence 1, Appli
3	1481	100.0	1515	17	US-10-724-594-1	Sequence 33, Appli
4	1476.2	99.7	2066	17	US-10-311-034-33	Sequence 3, Appli
5	1388.2	93.7	1870	17	US-10-262-511-3	Sequence 3, Appli
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38	234.6	15.8	2785	19	US-10-848-755A-116	Sequence 116, App
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41	234.6	15.8	7151	17	US-10-433-794-39	Sequence 39, Appli
42	231.4	15.6	2621	16	US-10-252-157-179	Sequence 179, App
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                                ALIGNMENTS

RESULT 1
US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. US2002013232A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1515
;  TYPE: DNA
;  ORGANISM: Human
US-09-804-471A-1

  Query Match             100.0%;  Score 1481;  DB 9;  Length 1515;
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Db   977   TTCCAGAAAGTGACCCCCAAAGTGAGCAGTGACTTTCTTCGTGCTGCCATCCTTTCTTCCTTCTTCTTCTTAAAGCTTGTTGTGCG   1036

Qy   1021   GCCAGAAAGAGAGACTGAAGTTTGAAGGGTCTTTGCTGCCATCCTTCGTTCCCATCCTTCTTCTTCTTCTTCTTCTAAAATTG   1080
Db   1037   GCCAGAAAGAGAGACTGAAGTTTGAAGGGTCTTTGCTGCCATCCTTCGTTCCCATCCTTCTTCTTCTTCTTCTTCTTCTAAAATTG   1096

Qy   1081   ACTGGAACAACATTCGTAACTCGTCCTCTCCCCTTCGTTCCCACCCTGTTCCCAAGTCCGACGATG   1140
Db   1097   ACTGGAACAACATTCGTAACTCGTCCTCTCCCCTTCGTTCCCACCCTGTTCCCAAGTCCGACGATG   1156

Qy   1141   ACACCTCCAATTTGATGAACCAGAGAAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC   1200
Db   1157   ACACCTCCAATTTGATGAACCAGAGAAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC   1216

Qy   1201   TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGGTGTGGGGTTTTCGTACAGCAAGG   1260
Db   1217   TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGGTGTGGGGTTTTCGTACAGCAAGG   1276

; Publication No. US20040091993A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV II
; CURRENT APPLICATION NUMBER: US/10/724,594
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-594-1

Query Match   100.0%;   Score 1481;   DB 17;   Length 1515;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1481;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGTCGAACCCATTGCCAACCGGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGTCGAACCCATTGCCAACCGGG 76

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACACCCTTTATGACTCAAACGACAGAGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACACCCTTTATGACTCAAACGACAGAGT 136

Qy   121 CTCCTCTTTCCCGAGAAGGGGATATTAGATAGATGCCCTCTTCTGTTCTCTTTGAAGAATGAGTCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   137 CTCCTCTTTCCCGAGAAGGGGATATTAGATAGATGCCCTCTTCTGTTCTCTTTGAAGAATGAGTC 196

Qy   181 AGCCTGCTCTGATGAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   197 AGCCTGCTCTGATGAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 256

Qy   241 TAGCTGAGTTACAGGAGCTCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   257 TAGCTGAGTTACAGGAGCTCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 316

Qy   301 GTTGTGTGCTCACTTGCTGCAGGTGGTAAGCAGAAAGCAACGGGGACAATCTATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   317 GTTGTGTGCTCACTTGCTGCAGGTGGTAAGCAGAAAGCAACGGGGACAATCTATG 376

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGCCCGTGGATCCCCAATTACAGTATGCCT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   377 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGCCCGTGGATCCCCAATTACAGTATGCCT 436

Qy   421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGCGAATATCAGCTCATGGAATATCAGCTGCTGT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   437 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGCGAATATCAGCTCATGGAATATCAGCTGCTGT 496

Qy   481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCTCGAGGGGACTTGCTGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   497 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCTCGAGGGGACTTGCTGT 556

Qy   541 CACTTTTGAATAGATATGAGGACACCAGTTAGATGACAGAAAACCTGATACAGTTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   557 CACTTTTGAATAGATATGAGGACACCAGTTAGATGACAGAAAACCTGATACAGTTTTACCTAGCTG 616

Qy   601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy   661 CTGAGAACATTCGTTGACCGGTCACCAGGACACACATCAAGCTGGTGGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   677 CTGAGAACATTCGTTGACCGGTCACCAGGACACACATCAAGCTGGTGGATCTGCCG 736

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 780
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Db   737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 796

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCGGTGGGACCTGCTGT 540
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Db   497 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCGGTGGGACCTGCTGT 556

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   557 CACTTTTGAATAGATATGAGGACCAGTTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 616

Qy   601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy   661 CTGAGAACATTCGTTGACCGGTCACCAGGACACACATCAAGCTGGTGGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   677 CTGAGAACATTCGTTGACCGGTCACCAGGACACACATCAAGCTGGTGGATCTGCCG 736

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 796

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGGCCTGGACT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   797 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGGCCTGGACT 856

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   857 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG 916

Qy   901 CAGAGGGAACCTCTGCCAGAACCTCAATAACAATATGAGAATTTCCAGCGGTGTTTTGAAAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   917 CAGAGGGAACCTCTGCCAGAACCTCAATAACAATATGAGAATTTCCAGCGGTGTTTTGAAAT 976

Qy   961 TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTGTGTTGTGCG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   977 TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTGTGTTGTGCG 1036

Qy   1021 GCCAGAAAGAGAGACTGAAGGTCTTGAAGGTCTTCGTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGGTCTTGAAGGTCTTGAAGGTCTTCGTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1096

Qy   1081 ACTCGGAACACACATTCGTAACCTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACTCGGAACACACATTCGTAACCTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1156

Qy   1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGTGGGGTTTTGTCTACAGCAAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGTGGGGTTTTGTCTACAGCAAGG 1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCTGTGTCGGGTCTGAGACTCCCCTGCCAAGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCTGTGTCGGGTCTGAGACTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAAGAGCTACAAGAGCTCTCAGGACA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAAGAGCTACAAGAGCTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCCGGCCTCCTTCCGTTGCTCCAGCATCCTCCCGT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 AGTGTCACAAGGTATTTATTTCCGCAGCCCGGCCTCCTTCCGTTGCTCCAGCATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGATCCGCCCGGGGGCCCGTGCTGGCTC 1481
          ||||||||||||||||||||||||||||||||||||||||||
Db   1457 CCGTATATGCCAAGGGATCCGCCCGGGGGCCCGTGCTGGCTC 1497

RESULT 3
US-10-724-594-1
; Sequence 1, Application US/10724594

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;   APPLICANT:  BAUGHN, Mariah R.
;   APPLICANT:  HE, Ann
;   APPLICANT:  THORNTON, Michael
;   APPLICANT:  HAFALIA, April
;   APPLICANT:  ARVIZU, Chandra S.
;   APPLICANT:  GURURAJAN, Rajagopal
;   APPLICANT:  LO, Terence P.
;   APPLICANT:  KHAH, Farrah A.
;   APPLICANT:  RECIPON, Shirley A.
;   APPLICANT:  AZIMZAI, Yalda
;   APPLICANT:  POLICKY, Jennifer L.
;   APPLICANT:  DING, Li
;   APPLICANT:  GRETHER, Megan
;   APPLICANT:  ELLIOTT, Vicki S.
;   APPLICANT:  THANGAVELU, Kavitha
;   APPLICANT:  BATRA, Sajeev
;   APPLICANT:  ISON, Craig H.
;   TITLE OF INVENTION: HUMAN KINASES
;   FILE REFERENCE: PI-0125 PCT
;   CURRENT APPLICATION NUMBER: US/10/311,034
;   CURRENT FILING DATE: 2002-12-10
;   PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
    60/228,056
;   PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
    25
;   NUMBER OF SEQ ID NOS: 52
;   SOFTWARE: PERL Program
;   SEQ ID NO 33
;   LENGTH: 2066
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US2004002324A1 3951059CB1
US-10-311-034-33

Query Match             99.7%;  Score 1476.2;  DB 17;  Length 2066;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1478;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TCAAAATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     24 TCAAAATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 83

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTCTTGTTCTCTTTATGACTCAACAGCAGAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTCTTGTTCTCTTTATGACTCAACAGCAGAGATGT 143

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGAATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144 CTCCTCTTTCCCGAGAAGGGATATTAGAATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 203

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 263

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGAAGACTTCGAAGTCAGAAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGAAGACTTCGAAGTCAGAAGTCTTGTAG 323

Qy    301 GTTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGACATCTATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GTTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGACATCTATG 383

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTTGAGG 443

Qy    421 AAGAGCGGAACTATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    444 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 503

Qy    481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCGGAATATCAGCCTGGAGGGGGACTTGCTGT 540

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACACGGGGATGGAAAAGGCACCTACGGCCTGGACT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 TGGCTCCTGAAGTGCTGACTGTGATGAACACGGGGATGGAAAAGGCACCTACGGCCTGGACT 856

Qy    841 GTGACTGGTGGTCAGTGGGCCTGATTGCCATGAGATGATTTATGGGAGATCCCCCCTTCG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 GTGACTGGTGGTCAGTGGGCCTGATTGCCATGAGATGATTTATGGGAGATCCCCCCTTCG 916

Qy    901 CAGAGGGAACCTCGCCAGAACCTTCAATAACACATTATGAGCGGGTTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGAGGGAACCTCGCCAGAACCTTCAATAACACATTATGAGCGGGTTTTTGAAAT 976

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTGTGCG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTGTGCG 1036

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1096

Qy   1081 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCGTCCGTCCAGTCCGACGATG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCGTCCGTCCAGTCCGACGATG 1156

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216

Qy   1201 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGGGGTTTTGTGTACAGCAAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGGGGTTTTGTGTACAGCAAGG 1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTTGTGGTCGGTCTGAGACTCCCCTGCCAAGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTTGTGGTCGGTCTGAGACTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTACAAGACTTCTCAGGACA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTACAAGACTTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTCCGTTGCTCCAGATCCTCCCGT 1440
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Db   1397 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTCCGTTGCTCCAGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGATCCGCCGGGGGGCCGGGGGGCCGGGGGGCCGCTGCGGCTC 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457 CCGTATATGCCAAGGGATCCGCCGGGGGGCCGGGGGGCCGGGGGGCCGCTGCGGCTC 1497
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RESULT 4
US-10-311-034-33
; Sequence 33, Application US/10311034
; Publication No. US2004002324A1
GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: YUE, Henry
;   APPLICANT: LAL, Preeti
;   APPLICANT: BANDMAN, Olga
;   APPLICANT: BOROWSKY, Mark L.
;   APPLICANT: AU-YOUNG, Janice
;   APPLICANT: LU, Yan
;   APPLICANT: GANDHI, Ameena R.
;   APPLICANT: TRIBOULEY, Catherine M.
;   APPLICANT: CHAWLA, Narinder K.
;   APPLICANT: YAO, Monique G.
;   APPLICANT: LU, Dyung Aina M.
;   APPLICANT: GREENWALD, Sara R.
;   APPLICANT: RAMKUMAR, Jayalaxmi
;   APPLICANT: GRIFFIN, Jennifer A.
;   APPLICANT: KEARNEY, Liam
;   APPLICANT: BURFORD, Neil
;   APPLICANT: NGUYEN, Danniel B.
;   APPLICANT: TANG, Y. Tom

```
Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     504    TTCAGGACAAAAATCACCTTTATCTGGTCATGCATGGAATATCAGCCTGGAGGGGACTTGCTGT   563
Qy   541    CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG   600
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Db   564    CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG   623
Qy   601    AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATCGGATACGTGCATCGAGACATCAAGC   660
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Db   624    AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATCGGATACGTGCATCGAGACATCAAGC   683
Qy   661    CTGAGAACATTCTCGTGACCGCACAGGACACATCAAGCTGGTGGATCTGGATCTGCCG   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684    CTGAGAACATTCTCGTGACCGCACAGGACACATCAAGCTGGTGGATCTGGATCTGCCG   743
Qy   721    CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   780
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Db   744    CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   803
Qy   781    TGGCTCCTGAAGTGCTGACTGTGATGAACAGGCACCTACGGCCTGGACT   840
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Db   804    TGGCTCCTGAAGTGCTGACTGTGATGAACAGGCACCTACGGCCTGGACT   863
Qy   841    GTGACTGGTGTGTCAGTGGGCGTGAGTTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG   900
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Db   864    GTGACTGGTGTGTCAGTGGGCGTGAGTTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG   923
Qy   901    CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924    CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT   983
Qy   961    TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGCTTGTTGTGCG   1020
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Db   984    TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGCTTGTTGTGCG   1043
Qy   1021   GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG   1080
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Db   1044   GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG   1103
Qy   1081   ACTGGAACAACAATTCGTAACTCTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG   1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104   ACTGGAACAACAATTCGTAACTCTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG   1163
Qy   1141   ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC   1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164   ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC   1223
Qy   1201   TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCGTACAGCAAGG   1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224   TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCGTACAGCAAGG   1283
Qy   1261   CACTGGGGATTCTTCGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA   1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284   CACTGGGGATTCTTCGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA   1343
Qy   1321   CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA   1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344   CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA   1403
Qy   1381   AGTGTCACAAGGTATTTATTTCCCGCACGCGGCCTCCTTCCTTGCCTCCCAGGATCCTCCCGT   1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404   AGTGTCACAAGGTATTTATTTCCCGCACGCGGCCTCCTTCCTTGCCTCCCAGGATCCTCCCGT   1463
Qy   1441   CCGTATATGCCAAGGGATCCGCCCGGGGCCGCTGCTGGCTC   1481
            |||||||||||||||||||||||||||||||||||||||||
Db   1464   CCGTATATGCCAAGGGATCCGCCCGGGGCCGCTGCTGGCTC   1504
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; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBBR: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
;
; SEQ ID NO 3
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3

Query Match   93.7%;   Score 1388.2;   DB 17;   Length 1870;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    1   TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
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Db   24   TCAAATATGGAGCGCGGAATCCTTTGCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAGCGCCCGGG   83
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RESULT 5
US-10-262-511-3
; Sequence 3, Application US/10262511
; Publication No. US2004038223A1
; GENERAL INFORMATION:

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Qy    61  CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84  CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  143

Qy   121  CTCCTCTTTCCCGAGAAGGGATATTAGACGTGACGAAGAATGCAGTC                180
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   144  CTCCTCTTTCCCGAGAAGGGATATTAGACGTGACGAAGAATGCAGTC                203

Qy   181  AGCCTGCTCTGATGAGACGTAAGCACGTGACCTTCGGCGAACAACTTGTCGGAGTATTCCGACACCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204  AGCCTGCTCTGATGAGACGTAAGCACGTGACCTTCGGCGAACAACTTGTCGGAGTATTCCGACACCA  263

Qy   241  TAGCTGAGTTACAGGAGCTCAGCTGGTAAGAGACTTCGAGAGTCTTGTAG             300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264  TAGCTGAGTTACAGGAGCTCAGCTGGTAAGAGACTTCGAGAGTCTTGTAG             323

Qy   301  GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGGTAAGAGAGAACACCGGGGACATCTATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324  GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGGTAAGAGAGAACACCGGGGACATCTATG  383

Qy   361  CTATGAAAGTGATGAAGAGAGAGAGGCTTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTTGAGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384  CTATGAAAGTGATGAAGAGAGAGAGGCTTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTTGAGG  443

Qy   421  AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT        480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444  AAGAGCGGAACACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT        503

Qy   481  TTCAGGACAAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504  TTCAGGACAAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT  563

Qy   541  CACTTTTGAATAGATATGAGGACCAGTTGAGTAGTTTACCTAGCTG                 600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   564  CACTTTTGAATAGATATGAGGACCAGTTGAGTAGTTTACCTAGCTG                 623

Qy   601  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC   683

Qy   661  CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGGATCTGGTGGATCTGCCG   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684  CTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGGATCTGGTGGATCTGCCG   743

Qy   721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   744  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA   803

Qy   781  TGGCTCCTGAAGTGCTGACTGTGATGGAAAGGCACTCACGGCCTGGACT             840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   804  TGGCTCCTGAAGTGCTGACTGTGATGGAAAGGCACTCACGGCCTGGACT             863

Qy   841  GTGACTGGTGTCAGTGGGCGTGATTGCCTATGGAGATGATTATGGGAGATCCCCCTTCG   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864  GTGACTGGTGTCAGTGGGCGTGATTGCCTATGGAGATGATTATGGGAGATCCCCCTTCG   923

Qy   901  CAGAGGGAACCTCTGCCAGGAACCTTCAATAACATTCCAGCCGGTTTTTTGAAAT         960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924  CAGAGGGAACCTCTGCCAGGAACCTTCAATAACATTCCAGCCGGTTTTTTGAAAT         983

Qy   961  TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTGATTCAAAGCTTGTGTTGTGCG     1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984  TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTGATTCAAAGCTTGTGTTGTGCG     1043

Qy  1021  GCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTGCTAAAATTG    1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044  GCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTGCTAAAATTG    1103

Qy  1081  ACTGGAACAACAATTCGTAACCTCTGCCGTGTTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104  ACTGGAACAACAATTCGTAACCTCTGCCGTGTTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1163

Qy  1141  ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCCAGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164  ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCCAGC  1223

Qy         TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTCGGTTTGTGGGGTTTGTGGGGTTTCGTACAGCAAGG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224  TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTCGGTTTGTGGGGTTTGTGGGGTTTCGTACAGCAAGG  1283

Qy  1261  CACTGGGGATTCTTGTAGATCTGGTAGATCTGAGTCGTGTCGGGTCTCGGACTCCCTGCCCAAGA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284  CACTGGGGATTCTTGTAGATCTGGTAGATCTGAGTCGTGTCGGGTCTCGGACTCCCTGCCCAAGA  1343

Qy  1321  CTAGCTCCATGAGAAAAGAAACTTCTCATCAAAAGCAAAAGAGACTACAAGACTCTCAGGACA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344  CTAGCTCCATGAGAAAAGAAACTTCTCATCAAAAGCAAAAGAGACTACAAGACTCTCAGGACA  1403

Qy  1381  AGTGTCACAAGGT   1393
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Db  1404  AGTGTCACAAGAT   1416
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RESULT 6
US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match 93.7%;   Score 1388.2;   DB 13;   Length 5877;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1390;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

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Qy     1  TCAAATATGGAGCGGGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGCGG    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11  TCAAATATGGAGCGGGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGCGG    70

Qy    61  CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71  CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT   130

Qy   121  CTCCTCTTTCCCGAGAAGGGATATTAGACGTGACGAAGAATGCAGTC                180
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   131  CTCCTCTTTCCCGAGAAGGGATATTAGACGTGACGAAGAATGCAGTC                190

Qy   181  AGCCTGCTCTGATGAATGAAGATTAAGCACGTGACGTGACGTGAGCAACTTGTCCGGAGTATTCCGACACCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191  AGCCTGCTCTGATGAATGAAGATTAAGCACGTGACGTGACGTGAGCAACTTGTCCGGAGTATTCCGACACCA  250

Qy   241  TAGCTGAGTTACAGAGACTCAGAGAGCTCGAAGTCGAAGTCAGAAGTCTTGTGTAG        300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   251  TAGCTGAGTTACAGAGACTCAGAGAGCTCGAAGTCGAAGTCAGAAGTCTTGTGTAG        310

Qy   301  GTTGTGGTCACTTTGCTGAAGTGGAAGTGGACAGGCACCGCGGGGGACATCTATG         360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311  GTTGTGGTCACTTTGCTGAAGTGGAAGTGGACAGGCACCGCGGGGGACATCTATG         370

Qy   361  CTATGAAAGTGATGAAGAGAAGAAGGCTTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTTGAGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371  CTATGAAAGTGATGAAGAGAAGAAGGCTTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTTGAGG  430
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;   Publication No. US20040209297A1
;   GENERAL INFORMATION:
;   APPLICANT: Yu, Xuanchuan
;   APPLICANT: Miranda, Maricar
;   APPLICANT: Friddle, Carl Johan
;   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
;   FILE REFERENCE: LEX-0289-USA
;   CURRENT APPLICATION NUMBER: US/10/791,666
;   CURRENT FILING DATE: 2004-03-02
;   PRIOR APPLICATION NUMBER: US/10/028,946
;   PRIOR FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: US 60/258,335
;   PRIOR FILING DATE: 2000-12-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn for Windows Version 4.0
;   SEQ ID NO 3
;     LENGTH: 5877
;     TYPE: DNA
;     ORGANISM: homo sapiens
US-10-791-666-3

Query Match             93.7%;    Score 1388.2;   DB 18;   Length 5877;
Best Local Similarity   99.8%;    Pred. No. 0;
Matches 1390;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 70

Qy       61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy      121 CTCCTCTTCCCGAGAAGGGATATTAGACGTGAGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      131 CTCCTCTTCCCGAGAAGGGATATTAGACGTGAGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 190

Qy      181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy      241 TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAGGACTTCGAAGTCGAGAGTCTTGTAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      251 TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAGGACTTCGAAGTCGAGAGTCTTGTAG 310

Qy      301 GTTGTGGTCACTTGCTGAAGTGCAGTGCGTAAGAGAAAGCAACCGGGACATCTATG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311 GTTGTGGTCACTTGCTGAAGTGCAGTGCGTAAGAGAAAGCAACCGGGACATCTATG 370

Qy      361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTGAGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTTCATTTTTGAGG 430

Qy      421 AAGAGCCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      431 AAGAGCCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy      481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy      541 CACTTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      551 CACTTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy      601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy      661 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      671 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730
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(continued)

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Qy      421 AAGAGCCGGAACATATTATTCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      431 AAGAGCCGGAACATATTATTCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy      481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy      541 CACTTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      551 CACTTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy      601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy      661 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      671 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730

Qy      721 CGAAATGAATTCAAACAGAGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      731 CGAAATGAATTCAAACAGAGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy      781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAGGAAAAGGCACCTACGGCGGCTGGACT 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAGGAAAAGGCACCTACGGCGGCTGGACT 850

Qy      841 GTGACTGGTGGTCAGTGGCGTGATGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      851 GTGACTGGTGGTCAGTGGCGTGATGCCTATGAGATGATTATGGGAGATCCCCCTTCG 910

Qy      901 CAGAGGGAACCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      911 CAGAGGGAACCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 970

Qy      961 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTTGAGTCAAAGCTTGTTGTGCG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      971 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTTGAGTCAAAGCTTGTTGTGCG 1030

Qy     1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGGTCTTCGCCATCCTTTCTTCTTCTCTAAAATTG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGGTCTTCGCCATCCTTTCTTCTTCTCTAAAATTG 1090

Qy     1081 ACTGGAACAACATTCGTAACCTCTCCCCCTTCGTTCCCACCCTCAGTCCGACGATG 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1091 ACTGGAACAACATTCGTAACCTCTCCCCCTTCGTTCCCACCCTCAGTCCGACGATG 1150

Qy     1141 ACACCTCCAATTTTGATGACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1151 ACACCTCCAATTTTGATGACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy     1201 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGCGGGTTTGTGTACAGCAAGG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1211 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGCGGGTTTGTGTACAGCAAGG 1270

Qy     1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1330

Qy     1321 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGCTCTCAGGACA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1331 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGCTCTCAGGACA 1390

Qy     1381 AGTGTCACAAGGT 1393
            ||||||||||||
Db     1391 AGTGTCACAAGAT 1403
```

```
RESULT 7
US-10-791-666-3
; Sequence 3, Application US/10791666
```

Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    1  TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG    60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11  TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGCGGG   70

Qy   61  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy  121  CTCCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTCTTCTTGAAGAAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  131  CTCCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTCTTCTTGAAGAAATGCAGTC  190

Qy  181  AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA    240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  191  AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA    250

Qy  241  TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAAGTCTTGTAG         300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  251  TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAAGTCTTGTAG         310

Qy  301  GTTGTGTGTCACTTGCTGAGTGCGCAGTGGTGTAAGGACGAAGCAACCGGGACATCATG   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  311  GTTGTGTGTCACTTGCTGAGTGCGCAGTGGTGTAAGGACGAAGCAACCGGGACATCATG   370

Qy  361  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCAGGAGCAGTTCATTTTTGAGG      420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  371  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCAGGAGCAGTTCATTTTTGAGG      430

Qy  421  AAGAGCGGAACATATATCTCGAAGCACAGCCGTGATCCCCAATTACAGTATGCCT      480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  431  AAGAGCGGAACATATATCTCGAAGCACAGCCGTGATCCCCAATTACAGTATGCCT      490

Qy  481  TTCAGGACAAAAATCACCTTTATCTGTCGTCATGGAATATCAGCGTGGACTTGCTGT    540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  491  TTCAGGACAAAAATCACCTTTATCTGTCGTCATGGAATATCAGCGTGGACTTGCTGT    550

Qy  541  CACTTTTGAATAGATGAGGACCAGTAGTAGAAAACCTGAAGCGTGATTTTGGATCTGCCG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  551  CACTTTTGAATAGATGAGGACCAGTAGTAGAAAACCTGAAGCGTGATTTTGGATCTGCCG  610

Qy  601  AGCTGAATTTGCGTGTTCATCGTGATGGGATACGTGCATCGAGACATCAAGC        660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  611  AGCTGAATTTGCGTGTTCATCGTGATGGGATACGTGCATCGAGACATCAAGC        670

Qy  661  CTGAGAACATTCTCGTTGACCGGCCACAGGACACATCAAGCTGGTGGTGGATTTTGGATCTGCCG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  671  CTGAGAACATTCTCGTTGACCGGCCACAGGACACATCAAGCTGGTGGTGGATTTTGGATCTGCCG  730

Qy  721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA             780
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  731  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA             790

Qy  781  TGGCTCCTGAAGTGCTGACTGTGATGACTGAACGGGATGAACGGGACT             840
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  791  TGGCTCCTGAAGTGCTGACTGTGATGACTGAACGGGATGAACGGGACT             850

Qy  841  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG   910

Qy  901  CAGAGGGAACCTCGCCAGAACCTTCAATACACATTATGAATTTCCAGCGGTTTTGAAAT   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  911  CAGAGGGAACCTCGCCAGAACCTTCAATACACATTATGAATTTCCAGCGGTTTTGAAAT   970

Qy  961  TTCCAGATGACCCCAAAGTGACTTTCTTGATTCAGTGCCATCCTTTTCTTCTCTAAAATTG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  971  TTCCAGATGACCCCAAAGTGACTTTCTTGATTCAGTGCCATCCTTTTCTTCTCTAAAATTG 1030

Qy 1021  GCCAGAAAGAGAGACTGAAGTTTGAAGGTTTGAAGGTCTTTGCTGCCATCCTTTTCTCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1031  GCCAGAAAGAGAGACTGAAGTTTGAAGGTTTGAAGGTCTTTGCTGCCATCCTTTTCTCTAAAATTG 1090

Qy 1081  ACTGGAACAACATTCGTAACTCTCCCCCCTTGTTCCCACCCTCGTTGACGATG       1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1091  ACTGGAACAACATTCGTAACTCTCCCCCCTTGTTCCCACCCTCGTTGACGATG       1150

Qy 1141  ACACCTCCAATTTTGATGACCAGGAAGAATTCGTGGGTTTCATCGTCCTCTCCGTTGCCAGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1151  ACACCTCCAATTTTGATGACCAGGAAGAATTCGTGGGTTTCATCGTCCTCTCCGTTGCCAGC 1210

Qy 1201  TGAGCGCCCTCCAGGCTTCTCGGTGAACTGCCGTTGTGTGGGGTTTCGTACAGCAAGG   1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1211  TGAGCGCCCTCCAGGCTTCTCGGTGAACTGCCGTTGTGTGGGGTTTCGTACAGCAAGG   1270

Qy 1261  CACTGGGGATTCTTGTGTAGATCGAGTCTGTGTGTCGGGGTCTGCGACTCCCCTGCCAAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1271  CACTGGGGATTCTTGTGTAGATCGAGTCTGTGTGTCGGGGTCTGCGACTCCCCTGCCAAGA 1330

Qy 1321  CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTCTACAGACTCTCAGGACA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1331  CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTCTACAGACTCTCAGGACA 1390

Qy 1381  AGTGTCACAAGGT 1393
         ||||||||||| |
Db 1391  AGTGTCACAAGAT 1403
```

RESULT 8
US-10-028-946-1
; Sequence 1, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
;   APPLICANT: Yu, Xuanchuan
;   APPLICANT: Miranda, Maricar
;   APPLICANT: Friddle, Carl Johan
;   TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding
;   FILE REFERENCE: LEX-0289-USA
;   CURRENT APPLICATION NUMBER: US/10/028,946
;   CURRENT FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: US 60/258,335
;   PRIOR FILING DATE: 2000-12-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6165
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-028-946-1

Query Match   93.7%; Score 1388.2; DB 13; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;

Qy   301 GTTGTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAGCAACCGGGCAGCATCTATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAGCAACCGGGCAGCATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCAGGAGTTTCATTTTTGAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCAGGAGTTTCATTTTTGAGG 430

Qy   421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCTTATCTGTCATGGAATATCAGCCTGAGGGGACTGCTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTATCTGTCATGGAATATCAGCCTGAGGGGACTGCTGT 550

Qy   541 CACTTTTGAATAGTATATGAGGACCAGTTAGATACACAGTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGTATATGAGGACCAGTTAGATACACAGTTTACCTAGCTG 610

Qy   601 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy   661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGGATTTTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGGATTTTGGATCTGCCG 730

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGCACCTACGGCCTGGACT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGCACCTACGGCCTGGACT 850

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGGATGATTTATGGGAGATCCCCCTTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGGATGATTTATGGGAGATCCCCCTTCG 910

Qy   901 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGCGGTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGCGGTTTTGAAAT 970

Qy   961 TTCCAGATGAGACCCCAAAGTGAGCAGTGACTTTCTGATCTGGATTCAAAGCTTGTTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGAGACCCCAAAGTGAGCAGTGACTTTCTGATCTGGATTCAAAGCTTGTTGTGCG 1030

Qy 1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCTCTAAAATTG 1090

Qy 1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTGCCAACCGGG 1140
          |||||||||||||||||||||||||||||||||||||||||||||
Db 1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTGCCAACCGGG 1150

Qy 1141 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1151 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy 1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCCGTTTGTGCGGGTTTTGTGGGGTTTTCGTACAGCAAGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCCGTTTGTGCGGGTTTTGTGGGGTTTTCGTACAGCAAGG 1270

Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTCGTTGTGTGTCGGGTCGGGAGTCCCCTGCCAAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1271 CACTGGGGATTCTTGGTAGATCTGAGTCGTCGTTGTGTGTCGGGTCGGGAGTCCCCTGCCAAGA 1330

Qy 1321 CTAGCTGAGTTGACAGGACTTCTCATCAAAAGCAAAGAGTACAAGACTTCAGGACA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1331 CTAGCTGAGTTGACAGGACTTCTCATCAAAAGCAAAGAGTACAAGACTTCAGGACA 1390

Qy 1381 AGTGTCACAAGGT 1393
          |||||||||||||
Db 1391 AGTGTCACAAGAT 1403

RESULT 9
US-10-791-666-1

; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-1

Query Match   93.7%; Score 1388.2; DB 18; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy   1 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTGCTGGATGCTGCTGAACCATTGCCAACCGGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTGCTGGATGCTGCTGAACCATTGCCAACCGGG 70

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTGTTCTTCTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTGTTCTTCTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGGAAGTATTCCGACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGGAAGTATTCCGACACCA 250

Qy   241 TAGCTGAGTTACAGGAGCTTCCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTTCCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

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Qy   1381 AGTGTCACAAGT 1393
          ||||||||| |
Db   1391 AGTGTCACAAGAT 1403
```

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Qy      1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     65 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG  124

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 CCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 184

Qy    121 CTCCCTCTTCCCGAGAAGGGATATTAGGATGCCCTCTTCTTGTTCTCTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 CTCCCTCTTCCCGAGAAGGGATATTAGGATGCCCTCTTCTTGTTCTCTTGAAGAATGCAGTC 244

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 304

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCCAAAGACTTCGAAGTCAGAAGTCTTGTAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCCAAAGACTTCGAAGTCAGAAGTCTTGTAG 364

Qy    301 GTTGTGGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCACCGGGACATCTATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GTTGTGGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCACCGGGACATCTATG 424

Qy    361 CTATGAAAGTGATGAAGAAGAAGAGGCTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTGAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 CTATGAAAGTGATGAAGAAGAAGAGGCTTATTGGCCCAGGAGGAGCAGGTTTCATTTTTGAGG 484

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 544

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 604

Qy    541 CACTTTTGAATAGTATGAGACACCAGTTAGATGAGATGAAAACCTGATACAGTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 CACTTTTGAATAGTATGAGACACCAGTTAGATGAGATGAAAACCTGATACAGTTTACCTAGCTG 664

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 724

Qy    661 CTGAGAACAATTCTCGTTGACCGCCACAGGACACATCAAGCTCGGTGGTGGATTTTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CTGAGAACAATTCTCGTTGACCGCCACAGGACACATCAAGCTCGGTGGTGGATTTTGGATCTGCCG 784

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 844

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACCGGGATGGAAAAGGCACCTACGGCCTGGACT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGCTCCTGAAGTGCTGACTGTGATGAACCGGGATGGAAAAGGCACCTACGGCCTGGACT 904

Qy    841 GTGACTGGTGGTCAGTGGGCGGTGAGTTTGAAGGTCTTGCGCCATCCTTCTTTGCTCGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 GTGACTGGTGGTCAGTGGGCGGTGAGTTTGAAGGTCTTGCGCCATCCTTCTTTGCTCGCC 964

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT 1024

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCGAAAGCTTGTTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCGAAAGCTTGTTGTGCG 1084

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTCTTCTTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTCTTCTTCTAAAATTG 1144

Qy   1081 ACTGGACAACATTCGTAACTCTCCCCCCTTCGTTCCCACCCTCCAAGTCCGACGATG 1140
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Db   1145  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
           ACTGAACAACATTCGTAACTCTCTCCCCCCTTCGTTCCCACCCTCAAGTCTCGACGATG  1204

Qy   1141  ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205  ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1264

Qy   1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGG  1260
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1265  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGG  1324

Qy   1261  CACTGGGGATTCTTGGTAGATCTGAGTCGTCTGTGTCGGGTCTGGACTCCCGTGCCAAGA  1320
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1325  CACTGGGGATTCTTGGTAGATCTGAGTCGTCTGTGTCGGGTCTGGACTCCCGTGCCAAGA  1384

Qy   1321  CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGCAAAGAGCTACAAGAGCTCTCAGGACA  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1385  CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGCAAAGAGCTACAAGAGCTCTCAGGACA  1444

Qy   1381  AGTGTCACAAGGT  1393
           |||||||||||||
Db   1445  AGTGTCACAAGAT  1457
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RESULT 11
US-10-017-216-3
; Sequence 3, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
;   APPLICANT: KAPELLER-LIBERMANN, Rosana
;   TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
;   TITLE OF INVENTION: Kinase and Uses Therefor
;   FILE REFERENCE: 10147-57U1
;   CURRENT APPLICATION NUMBER: US/10/017,216
;   CURRENT FILING DATE: 2001-10-23
;   PRIOR APPLICATION NUMBER: US 60/242,429
;   PRIOR FILING DATE: 2000-10-23
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 6159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-216-3

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Query Match       93.3%;   Score 1381.8;   DB 13;   Length 6159;
Best Local Similarity   99.5%;   Pred. No. 0;
Matches 1386;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy      1  TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11  TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG  70

Qy     61  CCTCCAGGCTGAATCGTTCTTCCAGCGGGAAAACCACCCTTTATGACTCAACAGCAGATGT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71  CCTCCAGGCTGAATCGTTCTTCCAGCGGGAAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy    121  CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTTGTCTCTTTGAAGAATGCAGTC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131  CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTTGTCTCTTTGAAGAATGCAGTC  190

Qy    181  AGCCTGCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191  AGCCTGCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy    241  TAGCTGAGTTGACAGGAGCTACAGAGAGCTTCGGCAAAAGGACTTCGAAGTCTTGTAG  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251  TAGCTGAGTTGACAGGAGCTACAGAGAGCTTCGGCAAAAGGACTTCGAAGTCTTGTAG  310

Qy    301  GTTGTGGTCACTTTGCTGGAGTGCAGGTGCAGGTGGTAAGAGAAAAGCAACCGGGACATCTATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311  GTTGTGGTCACTTTGCTGGAGTGCAGGTGCAGGTGGTAAGAGAAAAGCAACCGGGACATCTATG  370
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(also for the upper alignment, query/db numbering 361–1030)

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Qy    361  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCAGGAGCAGGTTCATTTTTGAGG  420
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Db    371  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCAGGAGCAGGTTCATTTTTGAGG  430

Qy    421  AAGAGCGGACACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431  AAGAGCGGACACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy    481  TTCAGGACAAAAATCACCTTTATCTGTCATGGAGAAATATCAGCCTGGAGGGACTTGCTGT  540
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    491  TTCAGGACAAAAATCACCTTTATCTGTCATGGAGAAATATCAGCCTGGAGGGACTTGCTGT  550

Qy    541  CACTTTTGAATAGTATGAGGACCAGTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551  CACTTTTGAATAGTATGAGGACCAGTAGATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy    601  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATAGTGCATCGAGACATCAAGC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATAGTGCATCGAGACATCAAGC  670

Qy    661  CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGTGGATTTTGGATCTGCCG  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671  CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGTGGATTTTGGATCTGCCG  730

Qy    721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  790

Qy    781  TGGCTTCCTGAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791  TGGCTTCCTGAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT  850

Qy    841  GTGACTGGTGTGTCAGTGGCGTGGGCGTGATTGCCATGGAGATGATTATGGGAGATCCCCTTCG  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851  GTGACTGGTGTGTCAGTGGCGTGGGCGTGATTGCCATGGAGATGATTATGGGAGATCCCCTTCG  910

Qy    901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT  970

Qy    961  TTCCAGTGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTCG  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971  TTCCAGTGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTCG  1030

Qy   1021  GCCAGAAAGAGAGCGAAGTTGAAGGTCTTGCCCATCCTTTCTTCCTTCTCTAAAATTG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCCCATCCTTTCTTCCTTCTCTAAAATTG  1090
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RESULT 12
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: MPI01-294P1RNM
; TITLE OF INVENTION: 32838,336 and 52908
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
US-10-325-430-11

Query Match   93.3%;   Score 1381.8;   DB 16;   Length 6162;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1386;   Conservative 0;   Mismatches 0;   Indels 7;   Gaps 0;

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Qy     1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCTGCTGCCACCGGG   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCTGCTGCCAGCGGG   70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGCTCAACAGCAGATGT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGCTCAACAGCAGATGT  130

Qy   121 CTCCTCTTTCCCGAGAGGGGATATTAGATGCGCCTCTTGTCTCTTTGAAGAATGCAGTC  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTTCCCGAGAGGGGATATTAGATGCGCCTCTTGTTCTCTTTGAAGAATGCAGTC  190

Qy   181 AGCCTGCTCTGATGGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy   301 GTTGTGTGCACTTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGTGCACTTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  370

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTAATTGGCCCAGGAGGCAGGTTTCATTTTTTGAGG  420
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGGCTTTAATTGGCCCAGGAGGCAGGTTTCATTTTTTGAGG  430

Qy   421 AAGAGGGGAACATATATATCTCGAAGCACAGCACCCGTGGAATCCCCAATTACAGTATGCCT  480
         |||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGGCGGAACATATTATCTCGAAGCACAGCACCCGTGGAATCCCCAATTACAGTATGCCT  490

Qy   481 TTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGATGGAGGAATATCAGCCTGGAGGGGACTTGCTGT  550

Qy   541 CACTTTTGAATAGATGAGGACCAGTTAGTGAATGAAAACCTGATACAGTTTTACCTAGCTG  600
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGATGAGGACCAGTTAGTGAATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy   601 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATA  660
         ||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  670

Qy   661 CTGAGAACAATTCTCGTTGACCGCCACAGGACACATCAAGCTGCTGGTGGATTTGGATCTGCCG  720
         ||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACAATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTTGGATCTCGCCG  730

Qy   721 CGAAAATGAATCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
         ||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATGAATCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACTGGCCTGGACT  840
         |||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACTGGCCTGGACT  850

Qy   841 GTGACTGGTGGTCAGTGGGCCGTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG  900
         |||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCCGTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG  910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAT  960
         |||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAT  970

Qy   961 TTCCAGTGACCCCCAAAGTGAGCAGTGACTTTCCTTGATCTGATTCAAAGCTTGTTGTGCG  1020
         |||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGTGACCCCCAAAGTGAGCAGTGACTTTCCTTGATCTGATTCAAAGCTTGTTGTGCG  1030

Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCTCTAAAATTG  1080
         ||||||||||||||||||||||||||||||||||||
Db  1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTCTTCTCTAAAATTG  1090

Qy  1081 ACTGGAACAACATTGTAACTCTCCCCCCTTCGTTCGTCCAAGTCCGACGATG  1140
         ||||||||||||||||||||||||||||||||||||||||
Db  1091 ACTGGAACAACATTGTAACTCTCCCCCCTTCGTTCGTCCAAGTCTGACGATG  1150

Qy  1141 ACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1200
         ||||||||||||||||||||||||||||||||||||||||
Db  1151 ACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1210

Qy  1201 TGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCGGTTGTGGGGTTTGTGTACAGCAAGGG  1260
         ||||||||||||||||||||||||||||||||||||||||
Db  1211 TGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCGGTTGTGGGGTTTGTGTACAGCAAGGG  1270

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCGGACTCCCCGCCAAGA  1320
         ||||||||||||||||||||||||||||||||||||||||
Db  1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCGGACTCCCCGCCAAGA  1330

Qy  1321 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGACTACAAGACTCTCAGGACA  1380
         ||||||||||||||||||||||||||||||||||||||||
Db  1331 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGACTACAAGACTCTCAGGACA  1390

Qy  1381 AGTGTCACAAGGT  1393
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Db  1391 AGTGTCACAAGAT  1403
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RESULT 13
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match   93.3%;   Score 1381.8;   DB 13;   Length 6574;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1386;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCGCGGG 88

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 148

Qy   121 CTCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149 CTCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 208

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   209 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 268

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG 328

Qy   301 GTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAACCACCGGGACAATCTATG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   329 GTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAACCACCGGGACAATCTATG 388

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   389 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 448

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 508

Qy   481 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   509 TTCAGGACAAAATCACCTTTATCTGATGGAGGAATATCAGCCTGGAGGGGACTTGCTGT 568

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   569 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 628

Qy   601 AGCTGATTTTGGCTGTTCCACGGTTCATCTGATGGGATACGTGCATCGAGACACATCAAGC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   629 AGCTGATTTTGGCTGTTCCACAGCGTTCATCTGATGGGATACGTGCATCGAGACACATCAAGC 688

Qy   661 CTGAGAACATTCTCGTTGACCGCACAGGACACACAAGCTGGTGATTTGGATCTGCCG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   689 CTGAGAACATTCTCGTTGACCGCACAGGACACACAAGCTGGTGATTTGGATCTGCCG 748

Qy   721 CGAAAATGATTCAAACAACAGATGTGAATGCCAAACTCCCAGATTACA 780
            |||||||||||||||||||||||||||||||||||||||||||||||||
Gdb   749 CGAAAATGATTCAAACAACAGATGGTGAATGCCAAACTCCCAGATTACA 808

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCCACTACGGGCCTGGACT 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCCACTACGGGCCTGGACT 868

Qy   841 GTGACTGGTCGTGTCAGTGGCGTGGCGTGATTGCCTATGACGATGATTATGGGAGATCCCTCG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869 GTGACTGGTCGTGTCAGTGGCGTGGCGTGATTGCCTATGACGATGATTATGGGAGATCCCTCG 928

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAAATTTCCAGCGGTTTTGAAAT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   929 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAAATTTCCAGCGGTTTTGAAAT 988

Qy   961 TTCCAGATGACGACCCCAAAGTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   989 TTCCAGATGACGACCCAAAGTGAGCAGTGACTTTCTTGATCGTCGATTCGATTCAAAGTCTTGTTGTGTGCG 1048

Qy   1021 GCCAGAAAGAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTCTAAAATTG 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 GCCAGAAAGAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTCTAAAATTG 1108

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCTGTTCCCACCCTCAAGTCCGACGATG 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 ACTGGAACAACATTCGTAACTCTCCTCCCCTGTTCCCACCCTCAAGTCTGACGATG 1168

Qy   1141 ACACCTCCAATTTGATGAACCAGAAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 ACACCTCCAATTTGATGAACCAGAAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC 1228

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGTGGGGTTTGTGGGGTTTCGTACAGCAAGG 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGTGGGGTTTGTGGGGTTTCGTACAGCAAGG 1288

Qy   1261 CACTGGGGATTCTTCGGTAGATCTGAGTCTGTCTGTGTCGGGTCTCGGACTCCCCTGCCAAGA 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 CACTGGGGATTCTTCGGTAGATCTGAGTCTGTCTGTGTCGGGTCTCGGACTCCCCTGCCAAGA 1348

Qy   1321 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAAGAGTACAAAAGCAAAGAGAGACTCTCAGGACA 1380
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Db   1349 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAAGAGTACAAAAGCAAAGAGAGACTCTCAGGACA 1408

Qy   1381 AGTGTCACAAGGT 1393
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Db   1409 AGTGTCACAAGAT 1421

RESULT 14
US-10-325-430-10
; Sequence 10, Application US/10325430
; Publication No. US2003015325A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPI01-294PIRNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-430-10

Query Match   93.3%;   Score 1381.8;   DB 16;   Length 6574;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1386;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCGCGGG 88

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 148

Qy   121 CTCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149 CTCCTCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 208

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Qy   1321 CTAGCTCCATGAGAAAGAAACTTCTCATCAAAAGCAAAGAGAGTACAAGAGACTCTCAGGACA 1380
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Qy   1381 AGTGTCACAAGT 1393
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RESULT 15
US-10-757-262-51
; Sequence 51, Application US/10757262
; Publication No. US2004019782SA1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPIO3-007P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)...(6180)
US-10-757-262-51

Query Match   93.3%; Score 1381.8; DB 18; Length 6574;
Best Local Similarity   99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy   241 TAGCTGAGTTACAGAGGAGCTCCAGCCTTCGGCCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
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Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Qy   961 TTCCAGATGACCCCCAAAGTGAGACTTTGAAGGTCTTGATTCAGTCAAAGCTTCAAAGTG 1020
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Qy   1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTCATCCTCCTTCGCGTCCTCGTGTCGCCAGC 1200

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Qy 1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGG 1260
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Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGAGTCCCCTGCCAAGA 1320
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Qy 1381 AGTGTCACAAGGT 1393
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Db 1409 AGTGTCACAAGAT 1421

Search completed: March 19, 2005, 18:10:57
Job time : 813.2 secs

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Qy 661   CTGAGAACATTCTCGTTGACCGGACGACATCAAGTCTGGTGATTTTGGATCTGCCG 720
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Db 689   CTGAGAACATTCTCGTTGACCGGACGACATCAAGTCTGGTGATTTTGGATCTGCCG 748

Qy 721   CGAAAATGATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
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Db 809   TGGCTCCTGAAGTGCTGACTGCTGATGGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 868

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Db 1049 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCCTCTAAAATTG 1108

Qy 1081 ACTCGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCCCCTTCGTTCCCACCCTCGTCTGACGATG 1140
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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      March 19, 2005, 07:56:21 ; Search time 261.498 Seconds
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Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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2	1481	100.0	1515	4	US-10-238-709-1	Sequence 1, Appl
3	1388.2	93.7	5877	4	US-10-028-946-3	Sequence 3, Appli
4	1388.2	93.7	6165	4	US-10-028-946-1	Sequence 1, Appli
5	947.2	64.0	2162	4	US-09-774-528-419	Sequence 419, App
6	744.8	50.3	1133	4	US-09-916-204-1	Sequence 1, Appli
7	744.8	50.3	1133	4	US-10-282-048-1	Sequence 1, Appli
8	234.6	15.8	2423	4	US-09-949-016-2640	Sequence 2640, Ap
9	225.6	15.2	2726	2	US-08-422-699A-12	Sequence 12, Appl
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11	218.8	14.8	2511	2	US-08-422-699A-8	Sequence 8, Appli
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16	194	13.1	2706	2	US-08-630-822A-61	Sequence 61, Appl
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18	194	13.1	2706	3	US-09-171-156A-20	Sequence 20, Appl
19	194	13.1	2706	4	US-09-004-730A-20	Sequence 20, Appl
20	194	13.1	2706	4	US-09-981-799A-20	Sequence 20, Appl
21	186	12.6	4363	2	US-08-685-576-5	Sequence 5, Appli
22	184.4	12.5	4848	4	US-09-976-594-295	Sequence 295, App
23	178.8	12.1	48763	4	US-09-916-204-3	Sequence 3, Appli
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28	156.4	10.6	3323	2	US-08-422-699A-10	Sequence 10, Appl
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33	125.4	8.5	1498	3	US-09-509-902A-6	Sequence 6, Appli
34	125.4	8.5	1961	3	US-09-509-902A-15	Sequence 15, Appl
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                            ALIGNMENTS

RESULT 1
US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1515
;  TYPE: DNA
;  ORGANISM: Human
US-09-804-471A-1

Query Match           100.0%;  Score 1481;  DB 4;  Length 1515;
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Qy     301 GTTGTGGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGGACATCTATG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 GTTGTGGTCACTTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG 376

Qy     361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCTGCAGAGGTTTCATTTTTGAGG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    377 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCAGGGTTTCATTTTTTGAGG 436

Qy    421 AAGAGCGGAACATATATATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 AAGAGCGGGAACATATATATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 496

Qy    481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGCT 556

Qy    541 CACTTTTGAATAGATAGATGAGGACCTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 CACTTTTGAATAGATAGATGAGGACCTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 616

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGGTGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGGTGATCTGCCG 736

Qy    721 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796

Qy    781 TGGCTCCTGAGACTGCTGACTGTGATGATGAACGGCACCTACGGCCTGGACT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 TGGCTCCTGAGACTGCTGACTGTGATGATGAACGGCACCTACGGCCTGGACT 856

Qy    841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGAGATTATGGGAGATCCCCCTTCG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGAGATTATGGGAGATCCCCCTTCG 916

Qy    901 CAGAGGGAACCTCTGCCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGAGGGAACCTCTGCCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 976

Qy    961 TTCCAGATGACCCCCAAAGTGAGCTGACTGACTTCTTCTGATCTGATTCGATCTGAGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 TTCCAGATGACCCCCAAAGTGAGCTGACTGACTTCTTCTGATCTGATTCGATCTGAGC 1036

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCGCCATCCTTTCTTCTTCTAAAATTG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCGCCATCCTTTCTTCTTCTAAAATTG 1096

Qy   1081 ACTGGAACAACATTGCTAACTCGTCCTCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACTGGAACAACATTGCTAACTCGTCCTCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1156

Qy   1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTCATCCTCCTCCGTCGTACAGCAAGG 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTCATCCTCCTCCGTCGTACAGCAAGG 1216

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCGTTGTGTGGGGTTTCGTACAGCAAGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCGTTGTGTGGGGTTTCGTACAGCAAGG 1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAGAAAGCAAGACTCTACAAGAGACTTCTCTCAGGACA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGGAAAAGAAACTTCTCATCAAAGAAAGCAAGACTCTACAAGAGACTTCTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGCCTCCTTGCTTCGCCGGATCCTCCCGT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 AGTGTCACAAGGTATTTATTTCCGCAGCCGCCTCCTTGCTTCGCCGGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGATCCGCCCGGGGCCGGGGCCCGGTGCCTGCTGGCTC 1481
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457 CCGTATATGCCAAGGGATCCGCCCGGGGCCGGGGCCCGGTGCCTGCTGGCTC 1497
```

RESULT 2
US-10-238-709-1
; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
;   APPLICANT: WEBSTER, Marion et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001164DIV
;   CURRENT APPLICATION NUMBER: US/10/238,709
;   CURRENT FILING DATE: 2002-09-11
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1515
;   TYPE: DNA
;   ORGANISM: Human
US-10-238-709-1

  Query Match   100.0%; Score 1481; DB 4; Length 1515;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1481; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      1 TCAAATATGGAGCGCGAACCTCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17 TCAAATATGGAGCGCGAACCTCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 76

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 136

Qy    121 CTCCTCCTTTCCCGAGAAGGGGATATTAGACGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 CTCCTCCTTTCCCGAGAAGGGGATATTAGACGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 196

Qy    181 AGCCTGCTCGATGAAGATTAAGCACCTGAGCAACTTGTCCGGAGTATTCCGAGCACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 AGCCTGCTCGATGAAGATTAAGCACCTGAGCAACTTGTCCGGAGTATTCCGAGCACCA 256

Qy    241 TAGCTGAGTTACAGGAGCTCGAGTCGAAGGACTTCGAAGTCGAAGAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 TAGCTGAGTTACAGGAGCTCGAGTCGAAGGACTTCGAAGTCGAAGAGTCTTGTAG 316

Qy    301 GTTGTGTGGTCACTTGCTGAAGCGGCAGTGGCAGTGGTAAGGAGAAAGCAACCGGGGACATCCATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 GTTGTGTGGTCACTTGCTGAAGCGGCAGTGGCAGTGGTAAGGAGAAAGCAACCGGGGACATCCATG 376

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCAGGGTTTCATTTTTTGAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCAGGGTTTCATTTTTTGAGG 436

Qy    421 AAGAGCGGAACATATATATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 AAGAGCGGAACATATATATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 496

Qy    481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGCTGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGCTGT 556

Qy    541 CACTTTTGAATAGATAGATGAGGACCTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 CACTTTTGAATAGATAGATGAGGACCTAGATGAGAAACCTGATACAGTTTTACCTAGCTG 616

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 CTGAGAACATTCTCGTTGACCGCACAGGACACACATCAAGCTGGTGGATTTTGGATCTGCCG 736
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; ORGANISM: homo sapiens
US-10-028-946-3

Query Match          93.7%;  Score 1388.2;  DB 4;  Length 5877;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1390;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 TCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 TCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG  70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy    121 CTCCCTCTTCCCGAGAAGGGATATTAGACACTGAGAATGCCCTCTCTTGTCTCTTGAAGAATGCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCCTCTTCCCGAGAAGGGATATTAGACACTGAGAATGCCCTCTCTTGTCTCTTGAAGAATGCAGTC 190

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 250

Qy    241 TAGCTGAGTTACGAGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TAGCTGAGTTACGAGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy    301 GTTGTGGTCACTTGCTGAGTGCAGGTGCAGGTGTAAGAGAAGCAACCCGGGACACATCTATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGGTCACTTGCTGAGTGCAGGTGCAGGTGTAAGAGAAGCAACCCGGGACACATCTATG 370

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCACGAGGAGCCAGGTTTCATTTTTGAGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCACGAGGAGCCAGGTTTCATTTTTGAGG 430

Qy    421 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy    541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG 610

Qy    601 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGATACTCGTGCATCGAGACATCAAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGATACTCGTGCATCGAGACATCAAGC 670

Qy    661 CTGAGAACATTCTCGTTGACCGACACAGGACACATCAAGCTCGTGTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACATTCTCGTTGACCGACACAGGACACATCAAGCTCGTGTGGATCTGCCG 730

Qy    721 CGAAATGAATTCAAACAAGATGGTCAAACTCCCAGATTACA 780
          |||||||||||||||||||||||||||||||||||||||||
Db    737 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 796

Qy    781 TGGCTTCCGAAGTGCTGACTGCTGACTGGGGCGGATGAAGGCACCTACGGCCTGGACT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 TGGCTTCCGAAGTGCTGACTGCTGACTGGGGCGGATGAAGGCACCTACGGCCTGGACT 856

Qy    841 GTGACTGGTGGTCGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 GTGACTGGTGGTCGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTCG 916

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 976

Qy    961 TTCCAGATGACCCCAAAGTGACTTTCTTGATTCAATTCAAAGCTTGTTGTTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 TTCCAGATGACCCCAAAGTGACTTTCTTGATTCAATTCAAAGCTTGTTGTTGCG 1036

Qy   1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1096

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1156

Qy   1141 ACACCTCCAATTTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216

Qy   1201 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGGTTTGTGTCGGGT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGGTTTGTGTCACAGCAAGG 1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCGCCTTCCTTGCTCCAGGATCCTCCCGT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 AGTGTCACAAGGTATTTATTTCCGCAGCCGGCCGCCTTCCTTGCTCCAGGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGATCCGCCCCGGGGCCCGGGGCCCTGCTGGCTC 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457 CCGTATATGCCAAGGGATCCGCCCCGGGGCCCGGGGCCCTGCTGGCTC 1497
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RESULT 3
US-10-028-946-3
; Sequence 3. Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA

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Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGCTCAGAAGTCTTGTAG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGCTCAGAAGTCTTGTAG  310

Qy    301 GTTGTGGTCACTTGCTGAAGTCGCAGTGGTGGTCAGTGGTGTAAGAGAAAGCAACCGGGGACATCTATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGGTCACTTGCTGAAGTCGCAGTGGTGGTCAGTGGTGTAAGAGAAAGCAACCGGGGACATCATG  370

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTTATGGCCAGGAGGAGCAGTTTCATTTTTGAGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTATGAAAGTGATGAAGAAGAAGGCTTTATGGCCAGGAGGAGCAGTTTCATTTTTGAGG  430

Qy    421 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  550

Qy    541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  670

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTCGGATCTGCCG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTCGGATCTGCCG  730

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  790

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT  850

Qy    841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTCG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTCG  910

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGATGAATTTCCAGCGGTTTTGAAAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGATGAATTTCCAGCGGTTTTGAAAT  970

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGTCGTTGTTGTGCG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGTCGTTGTTGTGCG  1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG  1090

Qy   1081 ACTGGAACAACATTCGTAACTCTCGTTCCCACCCTCCAAGTCCGACGATG  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 ACTGGAACAACATTCGTAACTCTCGTTCCCACCCTCCAAGTCCGACGATG  1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC  1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTGTCGGGTTTCGTACAGCAAGG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTGTCGGGTTTCGTACAGCAAGG  1270

Qy   1261 CACTGGGATTCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271 CACTGGGATTCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA  1330

Qy   1321 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGACTCTCAGGACA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAGACTCTCAGGACA  1390

Qy   1381 AGTGTCACAAGGT  1393
          ||||||||||||
Db   1391 AGTGTCACAAGAT  1403
```

RESULT 4
US-10-028-946-1
; Sequence 1, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-1

Query Match   93.7%; Score 1388.2; DB 4; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy      1 TCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGCG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     11 TCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGGG   70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy    121 CTCCTCTTTCCCGAGAAGGGGGATATTAGATGCCCTCTTGTCTTCTTTGAAGAATGCAGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTTCCCGAGAAGGGGGATATTAGATGCCCTCTTGTCTTCTTTGAAGAATGCAGTC  190

Qy    181 AGCCTGCTCTCGATGAAGATTAAGCACGTGACCACTTTGTCCGGAAGTATTCCGACACCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 AGCCTGCTCTCGATGAAGATTAAGCACGTGACCACTTTGTCCGGAAGTATTCCGACACCA  250
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Db   1331 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CTAGCTCCATGCAGGAAAGAAACTTCTCATCAAAGCAAAGAGCTACAAGAGACTTCAGGACA 1390

Qy   1381 AGTGTCACAAGGT 1393
          |||||||||||||
Db   1391 AGTGTCACAAGAT 1403


RESULT 5
US-09-774-528-419
; Sequence 419, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: Goodrich, Ryle
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Zhang, Jie
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Yang, Yonghong
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION:  No. 6743619el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE:  802
;  CURRENT APPLICATION NUMBER: US/09/774,528
;  CURRENT FILING DATE: 2001-01-30
;  NUMBER OF SEQ ID NOS: 441
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 419
;  LENGTH: 2162
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (364)..(2010)
US-09-774-528-419;

Query Match       64.0%;  Score 947.2;  DB 4;  Length 2162;
Best Local Similarity   99.7%;  Pred. No. 8e-310;
Matches  949;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCGTCGCTGAACCCATTGCCAACCGGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCGTCGCTGAACCCATTGCCAGCCGGG 433

Qy     61 CCTCCAGGCTGAATCTGTTCTTCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 CCTCCAGGCTGAATCTGTTCTTCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 493

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 553

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCGAACTTGTCCGGAAGTATTCCGACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCGAACTTGTCCGGAAGTATTCCGACACCA 613

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGAGACTTCGAAGTCAGGAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGAGACTTCGAAGTCAGGAGTCTTGTAG 673

Qy    301 GTTGTGGTCACTTTGCTGGAGTGCAGGTGGTAAGAGAGAAGCACCGGGACATCTATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 GTTGTGGTCACTTTGCTGGAGTGCAGGTGGTAAGAGAGAAGCACCGGGACATCTATG 733

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCCAGGAGGACGCAGGTTTCATTTTTGAGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    734 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCCAGGAGGACGCAGGTTTCATTTTTGAGG 793

Qy    421 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCATCTGATCATCAGTATGCT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCATCTGATCATCAGTATGCT 853

Qy    481 TTCAGGAGCAAAAATCACCTTTATCTGGTCATGGAGAATATCAGCTGAGGGGACTTGCTGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 TTCAGGAGCAAAAATCACCTTTATCTGGTCATGGAGAATATCAGCTGAGGGGACTTGCTGT 913

Qy    541 CACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 CACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG 973

Qy    601 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    974 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 1033

Qy    661 CTGAGAACATTCTCGTTGACCCGACCACAGGACACATCAAGCTGGTGCAGTTGGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1034 CTGAGAACATTCTCGTTGACCCGACCACAGGACACATCAAGCTGGTGGATTTGGATCTGCCG 1093

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1094 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 1153

Qy    781 TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGATGGATGAAAAGCGCACCTACGGCCTGGACT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1154 TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGATGGATGAAAAGCGCACCTACGGCCTGGACT 1213

Qy    841 GTGACTGGTGTGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1214 GTGACTGGTGTGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 1273

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTT 952
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1274 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTT 1325


RESULT 6
US-09-916-204-1
; Sequence 1, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164CIP
;  CURRENT APPLICATION NUMBER: US/09/916,204
;  CURRENT FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1133
;  TYPE: DNA
;  ORGANISM: Human
US-09-916-204-1

Query Match       50.3%;  Score 744.8;  DB 4;  Length 1133;
Best Local Similarity   99.7%;  Pred. No. 2.2e-241;
Matches  746;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCGTCGCTGAACCCATTGCCAACCGGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCGTCGCTGAACCCATTGCCAGCCGGG 123

Qy     61 CCTCCAGGCTGAATCTGTTCTTCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CCTCCAGGCTGAATCTGTTCTTCGAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 183

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  184 CTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 243
                                                                          Db  124 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 183
Qy  181 AGCCTGCTCTGATGAAGTAAGCACGTCCGGAAGTCTTGTCCGACACCA 240                  Qy  121 CTCCTCTTCCCGAGAAGGGATATTAGATGCGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 AGCCTGCTCTGATGAAGTAAGCACGTCCGGAAGTATTCCGACACCA 303                    Db  184 CTCCTCTTCCCGAGAAGGGATATTAGATGCGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 243

Qy  241 TAGCTGAGTTACAGGAGCTCAGGTGGTAAGAGAAGCAACCGGGACATCTATG 300              Qy  181 AGCCTGCTCTGATGAAGTAAGCACGTCGGCAACTTGTCGGAAGTATTCCGACACCA 240
        |||||||||||||||||||||||||||||||||||||||||||||                               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  304 TAGCTGAGTTACAGGAGCTCAGGTGGTAAGAGAAGCAACCGGGACATCTTGTAG 363            Db  244 AGCCTGCTCTGATGAAGTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 303

Qy  301 GTTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAGCAGGTTTCATTTTTTGAGG 360         Qy  241 TAGCTGAGTTACAGGAGCTCGGCAAAGGACTTCGAAGACTTCAGAAGTCTTGTAG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||                     ||||||||||||||||||||||||||||||||||||||||||||||
Db  364 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGCACAAGCCGTGGATCCCCAATT 423    Db  304 TAGCTGAGTTACAGGAGCTCCGGCAAAGGACTTCGAAGAAGTATTCAGAAGTCTTGTAG 363

Qy  361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGCACAAGCCGTGGATCCCCAATT 420    Qy  301 GTTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAGCAACCGGGACATCTATG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                 |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  424 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 483   Db  364 GTTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAGCAACCGGGACATCTATG 423

Qy  421 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480   Qy  361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGCAGGTTTCATTTTTTGAGG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  484 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 543  Db  424 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGCAGGTTTCATTTTTTGAGG 483

Qy  481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540  Qy  421 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  544 CACTTTTGAATAGATATGAGGACCAGTTAGATGCGTCATCTGAGACATCAAGC 603          Db  484 AAGAGGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 543

Qy  541 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGAGACATCAAGC 660                     Qy  481 TTCAGGACAAAAATCACCTTTATCTGGTAGATATGAGGACCAGTTTACCTAGCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||                                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  604 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGAGACATCAAGC 723                     Db  544 TTCAGGACAAAAATCACCTTTATCTGGTAGATATGAGGACCAGTTTACCTAGCTG 603

Qy  601 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATCTGCCG 720          Qy  541 CACTTTTGAATAGATATGAGGACCAGTTAGATGCGTCATCGAGACATCAAGC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||                       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  724 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATCTGCCG 783         Db  604 CACTTTTGAATAGATATGAGGACCAGTTAGATGCGTCATCGAGACATCAAGC 663

Qy  721 CGAAAATGAATTCAAACAAGATGGTGAA 748                                    Qy  601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGAGACATCAAGC 660
        ||||||||||||||||||||||||||||                                                ||||||||||||||||||||||||||||||||||||||||||||
Db  784 CGAAAATGAATTCAAACAAGATGGTAAA 811                                    Db  664 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGAGACATCAAGC 723

                                                                          Qy  661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATCTGCCG 720
                                                                                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                          Db  724 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATCTGCCG 783

                                                                          Qy  721 CGAAAATGAATTCAAACAAGATGGTGAA 748
                                                                                  ||||||||||||||||||||||||||| |
                                                                          Db  784 CGAAAATGAATTCAAACAAGATGGTAAA 811
```

RESULT 7
US-10-282-048-1

; Sequence 1, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Human
US-10-282-048-1

Query Match　　　50.3%;　　Score 744.8;　DB 4;　Length 1133;
Best Local Similarity　99.7%;　Pred. No. 2.2e-241;
Matches 746;　Conservative　0;　Mismatches　2;　Indels　0;　Gaps　0;

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Qy    1 TCAAATATGGAGCGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 TCAAATATGGAGCGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 123

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 8
US-09-949-016-2640

; Sequence 2640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2640
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2640

Query Match　　　15.8%;　　Score 234.6;　DB 4;　Length 2423;

RESULT 9
US-08-422-699A-12
; Sequence 12, Application US/08422699A
; Patent No. 595265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   STREET: Two Militia Drive
;   CITY: Lexington
;   STATE: Massachusetts
;   COUNTRY: US
;   ZIP: 02713
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/422,699A
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/422,706
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/023,612
;   FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/839,255
;   FILING DATE: 20-FEB-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/01545
;   FILING DATE: 19-FEB-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB93/00253
;   FILING DATE: 05-FEB-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: GB9202485.0
;   FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Granahan, Patricia
;   REGISTRATION NUMBER: 32,227
;   REFERENCE/DOCKET NUMBER: MIT-5830A2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-861-6240
;   TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2726 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-422-699A-12

Query Match   15.2%;   Score 225.6; DB 2; Length 2726;
Best Local Similarity 54.0%; Pred. No. 5.3e-65;
Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;

Db   2038 ATTTGATGTAGATGATGATTGTTTAAAAAATTCTGAAACGATGCCCCACCAACACATA 2097

Qy   1210 CAGGCTTCTCGGTGAAGAACTGCCGTTTGTGTGGGGTTTTCGTACA 1254
          |||||||||||||||||||||||||||||||||||||||| ||||||
Db   2098 CTGCATTTTCTGCCACCATCTGCCATTTGTTGTTTTTACATATA 2142

Best Local Similarity 52.5%;   Pred. No. 4.3e-68;
Matches 591; Conservative   0; Mismatches 519; Indels 15; Gaps   3;

Qy   142 TATTAGATGCCCTCCTTGTTCTCTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTA 201
          || ||| ||| ||| ||| ||||||||||||| |||||||
Db   1021 TACTGGATATCTCATCTGCCTTTATGATGAATGCAATAATTCTCCATTGAAGAAGAGA 1080

Qy   202 AGCACGTGAGCAAACTTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCC 261
          | | ||| ||||| ||||||||||| ||||||||||| |||||||||||||||
Db   1081 AGAACATTCTCGATACCTAGAAATGGGCTAAACCATTTACTTCTAAAGTGAAACAAATGC 1140

Qy   262 AGCCTTCGGCAAAGGACTTCGAAGTCAGAGAGTCTTGTAGGTTGTGGTCACTTGCTGAAG 321
          ||||| ||| || |
Db   1141 GATTACATAGAGAAGACTTTGAAATATTAAAGGTGATTGGTCGAGGAGCTTTTGGGGAGG 1200

Qy   322 TGCAGGTGGTAAGAGAGAAAGCAACCCGGGGACAATCTATGCTATGAAAGTGATGAAGAAGA 381
          | ||| ||||||||||| |
Db   1201 TTGCTGTGTAAAACTAAAAAAATGCAGATAAAGTGTTTGCCATGAAAATATTGAATAAAT 1260

Qy   382 AGGCTTTATTGGCCCAGGAGCAGAGTTTCATTTTTGAGGAAGAGCGGAACATATTATCTC 441
          |||||| |
Db   1261 GGGAAATGCTGAAAAGAGCTGAGACAGCATGTTTTCCGTGAAGAAAGGATGTATTAGTGA 1320

Qy   442 GAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCTTTCAGACAAAAAATCACCTTT 501
          |||||
Db   1321 ATGGAGACAATAAATGGATTACAACCTTGCACTATGCTTTCCAGGATGACAATAACTTAT 1380

Qy   502 ATCTGGTCATGGAATATCAGCGCTGAGGGGACTTGCTCGTGTCACTTTTGAATAGATATGAGG 561
          | ||| ||| |||||
Db   1381 ACCTTGGTTTATGGATTATTATGTTGGTGGGGATTTTGCTTACTCCTACTCAGCAAAATTTGAAG 1440

Qy   562 ACCAGTTAGATGAAAAACCTGATAACAGTTTTACCTCATGGCTGTTTTTGGCTGTTCACA 621
          | ||| | |
Db   1441 ATAGATTGCCTGAAGATATGGCTAGATTTTTACTTGGCTGAGATGGTGATAGCAATTGACT 1500

Qy   622 GCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACC 681
          ||||||
Db   1501 CAGTTCATCAGCTACATTATGTACACAGAGACACATTAAACCTGACAATATACTGATGGGATA 1560

Qy   682 GCACAGGACACATCAAGCTCGTGGATTTTCGGATCTGCCGCGAAAATGAATTCAAACAAGA 741
          ||||| |
Db   1561 TGAATGGACATATTCGGTTAGCAGATTTTGGTTCTTGTCTGTCGAACGTGATGGAAGATGGAA 1620

Qy   742 TGGTGAATGCCAAACTCCCGATTGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTG 801
          ||||| |
Db   1621 CGGTTCAGTCCTCAGTGGCTGTGTAGGAACTCCAGATTATATCTCTCCTGAAATCCTTCAAG 1680

Qy   802 TGATGAACGGGGATGGAAAAGCGCACCTCACGGCCTGACTGTGACTGTCAGTGGGGCG 861
          ||| |
Db   1681 CCATGGAAG--ATGGAAAGAGGAGATATGGACCTGAATGGACTGGTCTTTGGGGGG 1737

Qy   862 TGATTGCCTATGAGATGATTATGGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAA 921
          |
Db   1738 TCTGTATGTATGGAAATGCTTTACGGAGAAATCCTTTATGCAGAAATCGCTCGTGGTGGGAGA 1797

Qy   922 CCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAATTTCCAG---ATGACCCCAAAG 978
          | | | |
Db   1798 CATACGGAAAAATCATGAACCACAAAGAGAGGTTTCAGTTTCCAGCCCAGTGACTGATG 1857

Qy   979 TGAGCAGTGACTTTCTTGATTCTGATCTGATTCAAAGCTTTGTGTGCGGCCAGAAGAGAGACT-- 1036
          || |
Db   1858 TGTCTGAAAATGCTAAGGATCTTATTCGGAAGGCTCATTTGTAGCAGAGAACATCGACTTG 1917

Qy   1037 ------GAAGTTTGAAGGTCTTTCGCTGCCATCGTTCTTCTTCTAAAATTGACTGGAACA 1089
          | ||| |
Db   1918 GTCAAAATGGAATAGAAGACTTTAAGAAACACCCCATTTTTCAGTTGAATTGATTGGGATA 1977

Qy   1090 ACATTCGTAACTCTCCTCCCCCCCTCGTTCCCACCCTCCAGTCGCGACGATGACACCTCCA 1149
          |||||
Db   1978 ATATTTCGGAACTGTGAAGCACCTTATATTCCAGAAGTTAGTAGCCCAACAGATACATCGA 2037

Qy   1150 ATTTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCCTCCCTCGGTCGTGAGCCCCT 1209
          |||||||| | || ||

GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-422-706B-12

Query Match   15.2%;   Score 225.6; DB 2;   Length 2726;
Best Local Similarity   54.0%;   Pred. No. 5.3e-65;
Matches 534;   Conservative   0;   Mismatches 439;   Indels   15;   Gaps   3;

Qy   184 CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGGAAGCCATAG 243
           ||||| ||||| ||||||||||||||||
Db   243 CCGAACTGGCCCAGGACAACTACGTGGCCACTTCTTGCAGTGCAGTGACCTTCCGAGTGGTGGCCGGAGCCATCGTGG 302

Qy   244 CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCAGAAGTCTTGTAGGTT 303
           |||||||| ||||||
Db   303 TGAGGCTTAAGGAGGTCCGAGTGGTAGCCGGTAGTGAAGGTGATCGGAC 362

Qy   304 GTGGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAGAAAGCAACCGGGACACATCTATGCTA 363
           ||||||
Db   363 GCGGGGCGTTCAGCGAGGTAGCCGTAGTGAAGATGAAGCAGCAGGGTGATGCGGAC 422

Qy   364 TGAAAGTGATGAAGAGAAGAGGCTTTATTGCCCAGGAGCAGGTTTCATTTTTGAGGAAG 423
           ||||||
Db   423 TGAAGATCAATGAACAAGTGCTGAAGACAATGGGACATGGGAGAGGGGCGGAGGTGTCTGTGCGTTCCCGTGAGG 482

Qy   424 AGCGGAACATATTATTCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCTTTC 483
           ||||||
Db   483 AGAGGACGTGTTGGTGAATGGGGACCGGCGGCGTGGATCACGCAGCTGCACTTCGCCTTCC 542

Qy   484 AGGACAAAAATCACCTTTATCTGCTGGTCATGATGGAATATCAGCCTCGAGGGGGACTTGCTGTCAC 543
           |||||| ||||||
Db   543 AGGATGAGAACTACCTGTACCTGGTCATGAGGATTACGTGGCGCGGGGGACCTGCTGACAC 602

Qy   544 TTTTGAATAGTATGATGAGGACCAGTTAGATGAGTGAAAAACCTGATACAGTTTACCTAGCTGAGC 603
           |||||| ||||||
Db   603 TGCTCAGCCAAGTTTGGGGAGGCGGATTCCGGCGGACGGATGGGCGCGCTTCTACCTGGCGGGAGA 662

Qy   604 TGATTTTGGCTGTTCACAGCGTTCATCTGATGGAATACCGTGCATCGAGACATCAAGCCTG 663
           ||||||
Db   663 TTGTCATGGCCATAGACTCGGTGCACCGGCTTGGCTACGGTCACGGGCGCGGGACCATCAAACCCG 722

Qy   664 AGAACATTCTCGTTGACCGGACAGCAGGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGA 723
           |||||| ||||||
Db   723 ACAACATCCTGCTGGACCTGTGGCCACATCCCGCCTGCCTGCCTGCGGCTTCGGCCTTCGGCTTGCCCTCA 782

Qy   724 AAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGG 783
           ||||||
Db   783 AGTCGCGGCAGATGGAACGGCGTGCGGTGCTCGTCGTGGGCACCCCAGACTACCTGT 842

Qy   784 CTCCTGAAGTGCTGA---CTGTGATGAACCGGGATGGAAAAGGCACCTACGGGCCTGGACT 840
           |||||| ||||||
Db   843 CCCCCGAGATCCTGCGAGGTTCGAGGCGGTGGCCTGGACAGGCGCAGCTACGGGCCCAGT 902

Qy   841 GTGACTGGTCGTGGTCAGTGGGCGTGATTGCCATGAGAATGATTTATGGGAGATCCCCTTCG 900
           |||||| ||||||
Db   903 GTGACTGGTCGGGCGCTGGGGTGTATTCGCCCATGAAAATGTTCTATGGACGCAGCGCCCTTCT 962

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
           ||||||
Db   963 ACGCGGATTCCACGCGGCGGACCTATGCGAGACCTATCGCTCCACTACAGGGAGCACCTCTCTC 1022

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAGCTTGTTGT 1017
           ||||||
Db   1023 TGCCGCTCGGTGGACGGAAGGGGTCCCTGAGGAGGGCTCGAGACTTCATTCAGCCGGTTCGTGT 1082

Qy   1018 GCGGGCCAGAAAGAGAGACTGAAGTTTGAAGCTCTGC--------CATCCTTTCT 1068
           ||||||
Db   1083 GTCCCCCGGAGACAACGGGCTGGGCGTGACGGCCGGGGTGAAGAGGAGAAAGCAACCGGGACACATCTATGCTA 1142

Qy   1069 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCACCCCTCA 1128
           ||||||
Db   1143 TCTTTGGCTTCGACTGGGATGGTCTCCGGGACAGCGTGCCCCCCTTTACACCGGATTTCG 1202

Qy   1129 AGTCCGACGATGACACCTCCAATTTTGA 1156
Db   1203 AAGGTGCCACCGACACACATGCAACTTCGA 1230

RESULT 10
US-08-422-706B-12
; Sequence 12, Application US/08422706B
; Patent No. 5977333

; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,699A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,706
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,612
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/839,255
; FILING DATE: 20-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01545
; FILING DATE: 19-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00253
; FILING DATE: 05-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB9202485.0
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5830A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1746
US-08-422-699A-8

Query Match   14.8%; Score 218.8; DB 2; Length 2511;
Best Local Similarity 54.5%; Pred. No. 1e-62;
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;

Qy   364 TGAAAGTGATGAAGAAGAGAGGCTTTATTGGCCCAGGAGGCAGTTTCATTTTTGAGGAAG 423
           |||| || | |||| ||| | ||||||| |||||||||||||||||| ||||||||
Db   423 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCGTGCTTCCGTGAGG 482

Qy   424 AGCGGAACATATTATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCTTTC 483
           |||| | | || ||| | ||| |||||||| |||||| ||| | ||| |||||
Db   483 AGAGGGACGTGTTGGTGAATGGGACCGGCGGGGTGATCACGCAGCTGCACTTCGCCTTCC 542

Qy   484 AGGACAAAAATCACCTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCAC 543
           |||| | || || || ||| | ||| | ||| ||| | || ||| | |||||
Db   543 AGGATGAGAACTACCTGTCATGGAGTATTACGTGGCGGGGACCTGCTGACAC 602

Qy   544 TTTTGAATAGATATGAGGACCAGTTAGATGAAAAACCTGATACAGTTTTACCTAGCTGAGC 603
           || | ||| |||| || |||||| ||||| ||| ||| | ||| ||| | |||||
Db   603 TGCTGAGCAAGTTTGGGGAGGCGGATTCCGGCCGGATGGGACGCCGCTTCTCACCTGGCGGAGA 662

Qy   604 TGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGCCTG 663
           || | || || || || | ||| || || ||| || | | || ||||| |||||
Db   663 TTGTCATGGCCATAGACTCCGTGCACCGGCTTGGCTACGTGCACAGGGACATCAAACCCG 722

Qy   664 AGAACATTCTCGTTGACCGCACCAGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGA 723
           | | ||||| | |||||| |||| | ||||||| ||| |||| || | || | ||||
Db   723 ACAACATCCTGCTGACCCGCTGTGCCACATCCCGCCGACTTCGGCTCTTGCCTCA 782

Qy   724 AAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGG 783
           || |||| || || |||| | || | ||| ||| |||| | ||| | |||||||
Db   783 AGCTGCGGGCAGATGGAACGGTGCGGTGCCTCGCGGTCTGGGCCACCCCAGACTACCTGT 842

Qy   784 CTCCTGAAGTGCTGA---CTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
           | || || || | |||| || || || ||| | || |||| | ||||||
Db   843 CCCCCGAGATCCTGCAGGCTGTGGGGCGGTGGGCCTGGACAGGCAGCTACGCGGCCCGAGT 902

Qy   841 GTGACTGGTTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
           |||||||||| || | | | | |||||| | | ||| | | ||| | ||||| |||
Db   903 GTGACTGGTTGGTGGGCCGCTGGGGTGTATTCGCCTATGAAATGTTCTATGGCAGAGCGCCCTTCT 962

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCCGGTTTTTGAAAT 960
           ||||| || || | ||||| ||| | |||| | ||| || ||| ||| | |||||||
Db   963 ACGGGGATTCCACGCGGCGGAGACCTATGGCAAGATCGTCCACTACAAGAGAGCACCTCTCTC 1022

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAGCTTGTTGT 1017
           || || | | ||| | |||| | ||| | ||| || || | ||| | |||
Db   1023 TGCCGCTGGTGGACGAAGGGGTCCCTGAGGAGGTCTCGAGACTCATTCAGCGGTTGCGT 1082

Qy   1018 GCGGGCCAGAAAGAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC--------CATCCTTCT 1068
           |||| | ||||| ||||| || ||| ||||||| | |||| ||| |||||||||
Db   1083 GTCCCCCGGAGACACGGGTGGGCCCGGCCCGGGTGGGAGCAGAGGGGCGAGCTCGGACATCCCTTCT 1142

Qy   1069 TCTCTAAAATTGACTGGACAACATTCGTAACTCTCTCCTCCCCCCTTCGTTCCCACCCTCA 1128
           ||| | | || ||||| | ||| | | ||||||||||||| ||| | ||||||| |
Db   1143 TCTTTGGCCTTCGACTGGGATGGTCTTCCGGGACAGCGCTGCCCCCCTTTACACCGGATTTCG 1202

Qy   1129 AGTCCGACGATGACACCTCCAATTTGA 1156
           |||| || | || ||||| |||||
Db   1203 AAGGTGCCACCGACACATGCAACTTCGA 1230

RESULT 11
US-08-422-699A-8
; Sequence 8, Application US/08422699A
; Patent No. 5955265
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

Qy   234 GACACCATAGTGAGTTACGAGCTCCAGCTTCCGGCAAAGGACTTCGAAGTCAGAAGT 293
           |||||||| ||| | | |||||||||||||| |||| |||||||| ||| ||||||
Db   43   GCCATCGTGGTGGAGGCTTAAGGAGGTCCGACTTGCGAGAGGGACGACGACTTCGAGATTCTCGAAG 102

Qy   294 CTTGTAGGTTGGTCGTCACTTTGCTACGGAGTCGAGGTCGAGGTGGTAAGAGAGAAGGACTTCGAAGAGAAGCAACCGGGGAC 353
           | | || | | | | ||| |||||| ||| | ||||| |||| |||||||||||| |||||||||| ||||||||
Db   103 GTGATCGGACGCGCGGGCGTTCAGCGAGGTAGCGGTAGTGAGTGAAGATGAAGAGAGGGCGGAGGTGTCGTGC 162

Qy   354 ATCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAACGCTGAGAAGCGCCCCCAATTACATT 413
           || | |||| || |||||||| ||||| ||||| ||| | ||| ||| | | || | || | |||||||
Db   163 GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCGTGC 222

Qy   414 TTTGACGAAGAGCGAACACATATTATCTCGAAGCACAAGCACCGCCCTGGATCCCCCAATTACAG 473
           |||| | |||||| | ||| |||||||| ||||||||| || || | ||| | | ||||||
Db   223 TTCCGTGAGGAGAGGGACGTGTTGGTGAATGGGACCGGCGGGGTGATCACGCAGCTGCAC 282

Qy   474 TATGCCTTTCAGGACAAAAATCACCTTATCTGGTCATGGTCATGGAATATCAGCCTGGAGGGGAC 533
           | |||||| | ||| |||| || ||| | | |||||| |||| ||| | ||||||||

APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746
US-08-422-706B-8

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Query Match          14.8%;    Score 218.8;    DB 2;    Length 2511;
Best Local Similarity 54.5%;    Pred. No. 1e-62;
Matches  511;  Conservative    0;  Mismatches  412;  Indels   15;  Gaps    3;

Qy   234 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGT 293
          |||||  |||||| ||  |||| ||||||  |||||||| | |||||||||||
Db    43 GCCATCGTGGTGAGGCTTAAGGAGGTCCGACTGCAGAGGGACGACTTCGAGATTCTGAAG 102

Qy   294 CTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGAGGTAGCAGGAGAAGCAACCGGGAC 353
          |||| ||||||||| ||   |||||||||| |||| |||||| | |||||| |||| ||
Db   103 GTGATCGGACGCGGGGGCGTTCAGCGAGGTAGCGGTAGTGAAGAGGCAGACGGGCCAG 162

Qy   354 ATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGAGACAGCAGTTTCATTT 413
          ||| ||  |||| || ||| ||  |||||| ||| | ||||| |||||| ||||||||
Db   163 GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGATGTGAAGACCCGGGTGTCGTGC 222

Qy   414 TTTGAGGAAGAGCGGAACATATTATCTCGAAGCAAGACCCGTGATCCCCAATTACAG 473
          |||| ||||| |||||||  ||||  ||| || |||||| ||||| |  | |  |
Db   223 TTCCGTGAGGAGGAGCGTGTTGGTGAATGGGACGGCCGGTGGATCACGCAGCTGCAC 282

Qy   474 TATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGAC 533
          ||  ||||| |||| |   |   |||  |||| |||||| ||||||  ||||||| |||
Db   283 TTCGCCCTTCCAGGATGACGAACTACCTGTACCTGGTCATGGAGTATTACGTGGGCGGGGAC 342

Qy   534 TTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACTGATACAGTTTTAC 593
          |||| |||||||| |||||||| ||||||| |||||||| ||||||  ||||| |||
Db   343 CTGCTGACACTGCTGAGCAAGTTTGGGGAGCCGGATTCCGGGCCGAGATGGGCGGCTTCTAC 402

Qy   594 CTAGCTGAGCTGATTTGGCTGTTCACAGGTTCATCTGATGGGATACGTCGATCGAGAC 653
          || || || |  | |||| ||||||||   ||||||  |||||  |   |||||| ||
Db   403 CTGGCCGAGATTGTCATGGCCCATAGACTCGGTGCCACCGGCTTGGCTACGTGCACAGGGAC 462

Qy   654 ATCAAGCCTGAGAACATTCTCGTTGACCGACCACAGGACACATCAAGCGTGGTGGATTTTCGA 713
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                                                                    TELEFAX:   713/651-5246
                                                                    TELEX:     762829
                                                                 INFORMATION FOR SEQ ID NO:  11:
                                                                 SEQUENCE CHARACTERISTICS:
                                                                    LENGTH:  3182 base pairs
                                                                    TYPE:  nucleic acid
                                                                    STRANDEDNESS:  double
                                                                    TOPOLOGY:  linear
                                                                    MOLECULE TYPE:  DNA (genomic)
                                                              US-08-484-044-11

                                          Query Match      14.7%;    Score 218.4;   DB 1;   Length 3182;
                                          Best Local Similarity   54.5%;    Pred. No. 1.6e-62;
                                          Matches  510;   Conservative     0;   Mismatches  411;   Indels  15;   Gaps    3;

Db   463 ATCAAACCCGACAACACATCCTGCTGGACCGCTGTGGCCACATCCGCCTGGCCGACTTCGGC 522

Qy   236 CACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGTCAGAGAGTCT 295
         ||||||||||| |  |||| ||||  ||||||||  ||| ||||||||||||||
Db   743 CATCGTGGTGAGGCTTAAGGAGGTCCGACTGCACTGACTTCGAGATTCGAAGGT 802

Qy   714 TCTGCCCGCGAAAATGAATTCAAACAACAAGATGGTGAACGATCCCGGATTGGGACCCCA 773
         |||  || || |  || |||||||||||||||||||||||||
Db   523 TCTTGCCTCAAGCTGCGGGACGATGGAACGGTGCCGTCGCGTCGGTGTGGGCACCCCA 582

Qy   774 GATTACATGGCTCCTGA---AGTGCTGACTGTGATGAAACGGGGATGGAAAAAGGCACCTAC 830
         ||| | |||| |||||      ||||||||||||||||||| |||
Db   583 GACTACCCTGTCCCCCGAGATCCTGCAGCGCTGTGGGCCGGTGGCCTGGGACAGGCAGCTAC 642

Qy   831 GGCCTGGACTGTGACTGGTGTCAGTGGGCGCTGATTGCCTATGAGATGATTTATGGGAGA 890
         |||||||||||||||||||||||||||||
Db   643 GGGGCCCGAGTGTGACTGGTGACGGCGCTGGGTGTATTCGCCTATGAAATGTTCTATGGGCAG 702

Qy   891 TCCCCCTTCGCAGAGGAGGCGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGG 950
         | |||||||||||||||||||  ||||||||||||||
Db   703 ACGCCCTTCTACGCCGATTCCACGGCGGCAACATGAATCGTCCACTACAAGGAG 762

Qy   951 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAA 1007
         ||||||||  |||| |||||||||||||
Db   763 CACCTCTCTCGCCGTGGACGAAGGGGTCCCTGAGGAGGGCTCGAGACTTCATTCAG 822

Qy   1008 AGCTTGTGTGCGGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC--------- 1058
          ||||||||||||||||||||||||||||||
Db   823 CGGTTGCTGTGTCCCCGGAGACACAGCTGGCCTGGGGTGGAGCAGGCGACTTCCGGACA 882

Qy   1059 CATCCTTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTT 1118
          ||||||||||||||||||
Db   883 CATCCCTTCTTCTTTGGCCCTGACGTCCCGGACAGCGTGCCCGGGACAGCGTGCCCCCCTTTACA 942

Qy   1119 CCACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1156
          |||||||||||||||||||||||
Db   943 CCGGATTTCGAAGGTGCCACCGGACCACCGACAACTTCGA 980

Qy   476 TGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGGAGGGGACTT 535
         | |||||||||||| ||||||||||
Db   983 CGCCTTCCAGGATGGAGAACTACCTGTACCTGTCATCGGTCATGGGGCGGGGGACCT 1042

Qy   536 GCTGTCACTTTGAATAGATATGAGGACGCCAGTTAGATGAAAACCTGATACAGTTTTACCT 595
         |||||||||||||||||||||||||
Db   1043 GCTGACACTGCTGAGCAAGTTTGGGGAGCGGATTCCGGCGATGGGATACGTGCATCGAGACAT 1102

Qy   596 AGCTGAGCTGATTTGCGTGTTCACAGCGTTCATCTGATGGGGATACGTGCACTACGG 655
         |||||||||||||||||||||||||
Db   1103 GGGCGAGAGATTGTCATGCGCCATAGACTTCGGTGCGCTTGGCTGCGTCACTGTGCACCAGCGGGACAT 1162

Qy   656 CAAGGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGGATTTTGATC 715
         ||||||||||||||||||||||||||
Db   1163 CAAACCCGACAACATCCTCGTCGTGGCCACATCCCGCTGCCGCCATCCCGCCTGGCCGACTTCGGCTC 1222

Qy   716 TGCCGGCGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGA 775
         ||||||||||||||||||||||||
Db   1223 TTGCCTCAAGCTGCGGGACGATGGAACGGTGCCGGTCGCGTCGGTGTGGGCACCCCAGA 1282

Qy   776 TTACATGGCTCCTGA---AGTGCTGACTGTGATGAAACGGGGATGGAAAAAGGCACCTACGG 832
         ||||||| |||||     ||||||||||||||||||||
Db   1283 CTACCTGTCCCCCGAGATCCTGCAGCGCTGGGGCCGGTGTGGGCCTGGGACAGGCAGCTACGG 1342

Qy   833 CCTGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATAGAGATGATTTATGGGAGATC 892
         |||||||||||||||||||||||
Db   1343 GCCCGAGTGTGACTGGTGGGCGCTGGGTGTATTCGCCTATGAAATGTTCTATGGGCAGAC 1402

Qy   893 CCCCTTCGCGAGGGAGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTT 952
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Db   1403 GCCCTTCTACGCCGATTCCACGGCGGCAACATCGTCCACTACAAGGAGCACCTCTCTCGCC 1462

Qy   953 TTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAG 1009
         |||||||||||||||||||
Db   1463 CCTCTCTCGCCGTCGGTGGACGAAGGGGTCCCTGAGGAGGGCTCGAGACTTCATTCAGCGG 1522

Qy   1010 CTTGTTGTGCGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC--------CA 1060
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Db   1523 GTTGCTGTGTCCCCCGGAGACACAGCGCTGGGGCGGGGTGGAGCAGGCGACTTCCGGACACA 1582

Qy   1061 TCCTTTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCC 1120
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RESULT 13
US-08-484-044-11
; Sequence 11, Application US/08484044
; Patent No. 5552282
; GENERAL INFORMATION:
;   APPLICANT: Caskey, C. T.
;   APPLICANT: Fu, Ying-Hui
;   APPLICANT: Friedman, David L.
;   APPLICANT: Pizzuti, Antonio
;   APPLICANT: Fenwick, Raymond G.
;   TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
;   NUMBER OF SEQUENCES: 13
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fulbright & Jaworski, L.L.P.
;   STREET: 1301 McKinney, Suite 5100
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: U.S.A.
;   ZIP: 77010-3095
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/484,044
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/019,940
;   FILING DATE: 19-FEB-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Paul, Thomas D.
;   REGISTRATION NUMBER: 32,714
;   REFERENCE/DOCKET NUMBER: D-5443
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 713/651-5325

Db   1583 TCCCTCTTCTTTGGCCTCGACTGGGATGGTCTCCGGGACAGCGTGCCCCCCTTTACACC 1642

Qy   1121 CACCCTCAAGTCCGACGATGACACCTCCAATTTGA 1156
               ||| || | | ||| ||| || ||
Db   1643 GGATTTCGAAGGTGCCACCGACACATGCAACTTCGA 1678

RESULT 14
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match   13.8%; Score 205; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   743 GGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGT 802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130289 GGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGT 130348

Qy   803 GATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGGTCGTGGTCAGTGGGCGT 862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130349 GATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGGTCGTGGTCAGTGGGCGT 130408

Qy   863 GATTGCCTATGAGATGATGATTTATGGGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAAC 922
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130409 GATTGCCTATGAGATGATGATTTATGGGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAAC 130468

Qy   923 CTTCAATAACATTATGAATTTCCAG 947
           |||||||||||||||||||||||||
Db 130469 CTTCAATAACATTATGAATTTCCAG 130493

RESULT 15
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Query Match   13.8%; Score 205; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   743 GGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGT 802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130289 GGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGT 130348

Qy   803 GATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGGTCGTGGTCAGTGGGCGT 862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130349 GATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGGTCGTGGTCAGTGGGCGT 130408

Qy   863 GATTGCCTATGAGATGATGATTTATGGGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAAC 922
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 130409 GATTGCCTATGAGATGATGATTTATGGGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAAC 130468

Qy   923 CTTCAATAACATTATGAATTTCCAG 947
           |||||||||||||||||||||||||
Db 130469 CTTCAATAACATTATGAATTTCCAG 130493

Search completed: March 19, 2005, 14:35:03
Job time : 264.498 secs

GenCore version 5.1.6

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.OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:45:41 ; Search time 4489.47 Seconds
                                     (without alignments)
                                     12556.766 Million cell updates/sec

Title: US-10-724-594-1_COPY_17_1497
Perfect score:. 1481
Sequence: 1 tcaaatatggagcgcggaat.........cccgggccgctgctggctc 1481

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

Database :   EST:*
          1: gb_est1:*
          2: gb_est2:*
          3: gb_htc:*
          4: gb_est3:*
          5: gb_est4:*
          6: gb_est5:*
          7: gb_est6:*
          8: gb_gss1:*
          9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	602.6	40.7	698	5	BP146990	BP146990 BP146990
2	521.2	35.2	1085	9	BM904785	BM904785 AGENCOURT
3	478	32.3	492	7	CR746615	CR746615 CR746615
4	438.4	29.6	600	4	BG808196	BG808196 2082-86 M
5	423.8	28.6	427	4	BG944539	BG944539 ax51f11.x
6	409.4	27.6	485	7	CR746792	CR746792 CR746792
7	400.4	27.0	617	5	BQ417810	BQ417810 ik51b06.y
8	380	25.7	481	7	CN682405	CN682405 E0164B04-
9	378	25.5	479	7	CN678533	CN678533 E0112C12-
10	337	22.8	490	4	BF562826	BF562826 UI-R-BJ0p
11	329.8	22.3	821	9	BI654262	BI654262 603280370
12	327	22.1	449	9	CG501399	CG501399 OST45249
13	325	21.9	450	9	CG501400	CG501400 OST45250
14	318.2	21.5	512	9	CG652891	CG652891 OST417039
c 15	314.2	21.2	340	2	BF380737	BF380737 IL2-UT007
16	312.8	21.1	423	2	BF344814	BF344814 602014091
17	312.6	21.1	582	5	BX516291	BX516291 BX516291
18	281.6	19.0	521	1	AI882189	AI882189 u131e08.y
19	281.4	19.0	355	8	CC325092	CC325092 XL068 Bay
20	278.8	18.8	539	9	AW525215	AW525215 UI-R-BJ0p
c 21	272.6	18.4	336	9	CG869028	CG869028 AB0155 Sa
c 22	270.8	18.3	321	2	BF932611	BF932611 RC5-NT018
23	262.4	17.7	335	2	BF763211	BF763211 IL2-CS004
c 24	262.4	17.7	524	7	CK841805	CK841805 UI-R-BJ0p

25	260.4	17.6	325	3	BC008127	BC008127 Homo sapi
26	251.8	17.0	423	2	BB27314	BB27314 BB27314
27	246.4	16.6	385	9	CG655761	CG655761 OST426725
28	246.2	16.6	289	4	BF944809	BF944809 PM3-NN117
29	245.8	16.6	547	7	CF744826	CF744826 UI-M-GV0-
30	245.8	16.6	647	7	CF744580	CF744580 UI-M-GV0-
31	240.8	16.3	401	6	BY602044	BY602044 BY602044
32	238.2	16.1	2688	3	BC024150	BC024150 Mus muscu
33	237.2	16.0	2862	3	BC056615	BC056615 Mus muscu
34	237	16.0	398	5	BY018641	BY018641 BY018641
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36	235.6	15.9	807	7	CK147448	CK147448 AGENCOURT
37	233.6	15.8	605	5	BP168081	BP168081 BP168081
38	233.4	15.8	563	6	CD310916	CD310916 StrPu691.
39	233.4	15.8	801	5	BU475240	BU475240 60384406g
40	233.4	15.8	847	5	BU467302	BU467302 60373635
41	231.4	15.6	423	2	BB823725	BB823725 BB823725
42	231.2	15.6	508	6	CB783081	CB783081 AMGNNUC:N
43	225.2	15.2	1600	3	BC038993	BC038993 Homo sapi
44	218.4	14.7	1472	9	AY408840	AY408840 Homo sapi
45	217.2	14.7	370	5	BY021399	BY021399 BY021399

ALIGNMENTS

RESULT 1
BP146990

LOCUS   BP146990   698 bp   mRNA   linear   EST 30-DEC-2003
DEFINITION   BP146990 full-length enriched swine cDNA library, adult ovary Sus
             scrofa cDNA clone OVRM10025B09 5', mRNA sequence.
ACCESSION   BP146990
VERSION   BP146990.1 GI:40396461
KEYWORDS   EST.
SOURCE   Sus scrofa (pig)
ORGANISM   Sus scrofa
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 698)
AUTHORS   Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
             Okumura,N., Hamasima,N. and Awata,T.
TITLE   PEDE (Pig EST Data Explorer): construction of a database for ESTs
             derived from porcine full-length enriched cDNA libraries
JOURNAL   Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT   Contact: Hirohide Uenishi
             Animal Genome Laboratory, Genome Research Department
             National Institute of Agrobiological Sciences
             2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
             Tel: +81-29-838-8627
             Fax: +81-29-838-8627
             Email: huenishi@affrc.go.jp
             EST project with full-length enriched cDNA libraries carried out in
             Animal Genome Research Program (Japan) by National Institute of
             Agrobiological Sciences and STAFF-Institute
             Single pass sequencing of clones derived from oligo-capped cDNA
             library
             Vector sequences were eliminated by RepeatMasker version 2002/07/13
             and crossmatch version 0.990319
             Low quality bases were trimmed based on the quality values.
FEATURES   Location/Qualifiers
     source   1..698
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="OVRM10025B09"
                     /tissue_type="ovary"
                     /dev_stage="adult"
                     /clone_lib="full-length enriched swine cDNA library, adult
                     ovary"
ORIGIN

Query Match   40.7%; Score 602.6; DB 5; Length 698;
Best Local Similarity   91.4%; Pred. No. 7.9e-172;

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Matches 638; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy  396 CAGGAGCAGGTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCG 455
        ||||||||||||||||||||||||||||| ||||| ||||| || ||||||||||||
Db    1 CAGGAGCAGGTTCATTTTTGAGGAAGAGCAGAACATCTTATCCCGGAGCACAAGCCCT 60

Qy  456 TGGATCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA 515
        |||||||||| |||||||||||||||||||||||  || |||||||||||||||||
Db   61 TGGATCCCCAGTTACAGTATGCCTTTCAGGACAAACAACATAACCTTTATCTGGTCATGGAA 120

Qy  516 TATCAGCCTGAGGGGACTTGCTGTCACTTTTGAATAGAATGAGGACCAGTTAGTGAA 575
        |||||||||||||| |||||||||| |||||||||||||||||||||| ||||| |||
Db  121 TATCAGCCTGAGGGGGATTTGCTGTCATTTTGAATAGAATGAGGACCAATTAGTAGAA 180

Qy  576 AACCTGATACAGTTTTACCTAGCTGACGTGCTGATTTGGCTGATTTGGCTTCACAGCGTTCATCTGATG 635
        || |||||||||||||||||||||||  ||||||||||| |||||||||||||||||||| |
Db  181 AATATGATACAGTTTTACCTAGCTGAAATGATTTTGGCTGTTTCACAGCGTTCATCAGATG 240

Qy  636 GGATACGTGCATCGAGACATCAAGCCTGAGACATTCTCGTTGACCGCACAGGACACATC 695
        ||||| ||| |||||||| |||||||||||||||||||| ||| |||||||||||||
Db  241 GGATATGTACATCGAGACAATCAAGCCTGAGACATTCTCATCGAACGGGACACATC 300

Qy  696 AAGTCTGGTGGATTTGGATCTGCCCGCGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAA 755
        ||| |||||||| ||||||| || |  ||||||||| || ||||  ||||||||||||||||||
Db  301 AAGCTGGTGGACTTTGGATCAGCTGCTAAGATGAACTCAAATAAGATGGTGAATGCCAAA 360

Qy  756 CTCCCGATTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGGACGGGGAT 815
        ||||| |||||||||||||||||||||||||||||||||||||||||| |||||
Db  361 CTCCCCGGTTGGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGGAATGGGGAT 420

Qy  816 GGAAAAGGCACCTACGGCCTGACTGTGACTGGTGGTCGTCAGTGGGCGCTGATTGCCTTATGAG 875
        |||||||| ||||| ||||| |||||||| |||||||||||||||||| |||| |||||||||
Db  421 GGAAAAGGTGCCTATGGCCTAGACTGTGATTGGTGGTCGTCAGTGGGCGAGTTATTGCTTTATGAG 480

Qy  876 ATGATTTATGGAGATCCCCCTTCACTGAGGGAACCTCGCCAGAGAACCTTCAATAACATT 935
        ||| ||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db  481 ATGGTTTATGGAAGGTCCCCATTCACTGAGGGAACCTCAGCCAGCAGAACCTTCAATAACATC 540

Qy  936 ATGAATTCCAGCGCGGTTTTTGAAATTTCCAGATGACCCAAAGTGAGCAGTGAGTTCTT 995
        |||||| ||||||   |||||||||||||||||||||||||||| ||||||| | |||
Db  541 ATGAATTTCCAGCGTTCCAGATGACCCAAAGTTAGCAGTGAGTGAATTGCTT 600

Qy  996 GATCTGATTCAAAGCTTGTGTGTGCGGCCAGAAAAGAGACTTGAAGGTCTTTGC 1055
        ||||||| |||||| | |||||||||||||||||||||||||||||| | ||||
Db  601 GATCTGATCCAAAGNTTATTGTGTGCGGCCAGAAAAGAGACTTGAAGGTTTGAAGGCCCTTTGC 660

Qy 1056 TGCCATCCTTTCTTCTCTAAAATTGACTGAACAACAT 1093
        || ||||||||||||||||||| |||||| || |||||
Db  661 TGTCATCCTTTCTTCTCTAAAAATCGACTGGAATAACAT 698
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RESULT 2
BM904785
LOCUS   BM904785   1085 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6699306 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557590
            5', mRNA sequence.
ACCESSION   BM904785
VERSION   BM904785.1 GI:19355164
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1085)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation

---

            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12279 row: d column: 07
            High quality sequence stop: 510.
            Location/Qualifiers

FEATURES
     source   1..1085
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5557590"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
                     Average insert size 2 kb. Library constructed by Life
                     Technologies."

ORIGIN

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Query Match 35.2%; Score 521.2; DB 5; Length 1085;
Best Local Similarity 99.3%; Pred. No. 6.5e-147;
Matches 534; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy  857 GGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCGCAGAGGAACCTCTGC 916
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Db    1 GGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCGCAGAGGAACCTCTGC 60

Qy  917 CAGAACCTTCAATAACATTAACAACATTCCAGCGGTTTTCAGAATTTCCAGATGACCCCAA 976
        ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   61 CAGAACCTTCAATAACATTAACAACATTCCAGCGGTTTTCAGAATTTCCAGATGACCCCAA 120

Qy  977 AGTGAGCAGTGACTTCTTCTTGATTGATCTGATTCAAAGCTTCAAGCTGGTTGTCGTGCGGCGGCCAGAAAAGAGAGAGACT 1036
        |||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  121 AGTGAGCAGTGACTTCTTGATTGATCTGATTCAAAGCTCAAGCTGGTTGTCGTGCGGCGGCCAGAAAAGAGAGAGACT 180

Qy 1037 GAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTCTAAAATGACTGGAACAACATTCG 1096
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTCTAAAATGACTGGAACAACATTCG 240

Qy 1097 TAACTCTCCTCCCCCTTCCGTTCCCACCCTCAAGTCGACGATGACCTCCAATTTTGA 1156
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Db  241 TAACTCTCCTCCCCCTTCCGTTCCCACCCTCAAGTCGACGATGACCTCCAATTTTGA 300

Qy 1157 TGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGCTGAGCCCCTCAGCTT 1216
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Db  301 TGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGCTGAGCCCCTCAGCTT 360

Qy 1217 CTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTCGGGATTCTTGG 1276
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Db  361 CTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTCGGGATTCTTGG 420

Qy 1277 TAGATCTGAGTCTGTGTGTCGGGTCGGACTCCCCTGCCAAGACTAGCTCCATGGAAAA 1336
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TAGATCTGAGTCTGTGTGTCGGGTCGGACTCCCCTGCCAAGACTAGCTCCATGGAAAA 480

Qy 1337 GAAACTTCTCATCATCAAAA-GCAAAGAGAGCTACAAGAGCTACAAGTGTCACAAGT 1393
        ||||||||||||||||||||| |||||||||||||  |||| ||||||||||||| |
Db  481 GAAACTTCTCATCATCAAAAGGCAAAGAGAGCTACCAGACTACCAGTGTCACAAGAT 538
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RESULT 3
CR746615
LOCUS   CR746615   492 bp   mRNA   linear   EST 30-AUG-2004
DEFINITION CR746615 NIH_MGC_72 Homo sapiens cDNA clone IMAGp998D712279 ;
            IMAGE:5557590 5', mRNA sequence.
ACCESSION   CR746615
VERSION   CR746615.1 GI:51659741
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 492)
AUTHORS   Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
             Peters,M., Radelof,U. and Schneider,D.
TITLE   I.M.A.G.E. cDNA Clone Collection
JOURNAL   Unpublished (2004)
COMMENT   Contact: Inge Arlart
             RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Heubnerweg 6, D-14059 Berlin, Germany
             Email: www.rzpd.de
             RZPD; IMAGp998D0712279;
             RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
             Contact: Inge Arlart
             RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Heubnerweg 6, D-14059 Berlin, Germany
             Tel: +49 30 32639 100
             Fax: +49 30 32639 111
             www.rzpd.de
             This clone is available royalty-free from RZPD;
             contact RZPD (clone@rzpd.de) for further information. Seq primer:
             M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES   Location/Qualifiers
     source 1..492
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGp998D0712279 ; IMAGE:5557590"
             /tissue_type="melanotic melanoma"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_72"
             /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
             Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 2 kb. Library constructed by Life
             Technologies."

ORIGIN

Query Match   32.3%;   Score 478;   DB 7;   Length 492;
Best Local Similarity 98.6%;   Pred. No. 7.3e-134;
Matches 481;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   848 GTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCTTCGCAGAGGG 907
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Db   5 GCGGTNNGCGCGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCTTCGCAGAGGG 64

Qy   908 AACCTCTGCCAGAACCTTCAATACACATTATGAATTTCCAGCGCGGTTTTGAAATTTCCAGA 967
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   65 AACCTCTGCCAGAACCTTCAATACACATTATGAATTTCCAGCGCGGTTTTGAAATTTCCAGA 124

Qy   968 TGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATTCAAAGCTTGTGTTGTGCGGCCAGAA 1027
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 TGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATTCAAAGCTTGTGTTGTGCGGCCAGAA 184

Qy 1028 AGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTAAAATTGACTGGAA 1087
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 AGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTAAAATTGACTGGAA 244

Qy 1088 CAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATGACACCTC 1147
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 CAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCTGACGATGACACCTC 304

Qy 1148 CAATTTTGATGAACCAGCAGAGAATTCGTGGGTTCATCCTCCTCCGTGCCAGCTCGAGCCC 1207
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 CAATTTTGATGAACCAGCAGAGAATTCGTGGGTTCATCCTCCTCCGTGCCAGCTCGAGCCC 364

Qy 1208 CTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTTTGTGGGGTCACTGGG 1267
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365 CTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTCGTGTGTCGTCGTCACTGGG 424

Qy 1268 GATTCTTGGGTAGATCTGAGTCTGTTGTGTCGGGTCTCGCAAGACTAGCTC 1327
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425 GATTCTTGGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTC 484

Qy 1328 CATGGAAA 1335
         ||||||||

Db   485 CATGGAAA 492

RESULT 4
BG808196
LOCUS   BG808196   600 bp   mRNA   linear   EST 20-DEC-2001
DEFINITION 2082-86 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
ACCESSION   BG808196
VERSION   BG808196.1   GI:17955172
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 600)
  AUTHORS   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
  TITLE   Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
  JOURNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
  MEDLINE   21671825
  PUBMED   11812828
COMMENT   Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES   Location/Qualifiers
     source   1..600
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="neural retina"
                     /dev_stage="embryonic day 14.5 post-fertilization"
                     /clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Query Match   29.6%;   Score 438.4;   DB 4;   Length 600;
Best Local Similarity 86.4%;   Pred. No. 9.7e-122;
Matches 484;   Conservative   0;   Mismatches   76;   Indels   0;   Gaps   0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCAACCGGG 60
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 TCAAGTATGGTGTGCGGAACCCGCCGGAACCCGGGAAACCACCATTGCAACAGCAGATGT 100

Qy   61 CCTCCAGGCTGAATCGTCGTCTTCCAGGGGAAACACCACCCTTATGACTGCAACAGCAGATGT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 CCTCCAGGCTAAATCTTCTTCTTCCAGGGGAAACACCGCCCTCTTCTTCGCCTCGCCTCGGCG 160

Qy   121 CTCCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTGTTCTCTTCCTTGAAGAATGCAGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 CTGCTCTTTCCCGGAAGGGGATGCTAGACGCCCTCTTGTTCGCCTCTTGAAGAGTGCAGCC 220

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AACCCGCCTGATGATGAAGATGAAGCACGTGAGCAGCTTTGTTCCAGAAGTATTCCGACACCA 280

Qy   241 TAGCTGAGTTACAGGAGCTCAGTGGTTGCAGTGGCAGTGGTGAAGTGGAAGACTTCAGAAGCCTTGTAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 TAGCCGAGTTGCGGGAGCTCGAGCAGTGGCAGTGGTGAAGTGGAAGACTTCGAAGCCTTGTGG 340

Qy   301 GTTGTGGTCACTTGCTGAAGTGCAGTGCAGTGGTGAAGTGGTGAAGAAAGCAACCACGGGACATCTATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 GCTGTGGTCACTTGCTGCTGAAGTGCAGTGGTGGTTTAGAGAGAAGAAGCGGACCGGGGGGACGTCTATG 400

Qy   361 CTATGAAAGTGATGAAGAAGAAAGGCTTAATGGCCCAGGAGGCTTCATTTTTTGAGG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 CCATGAAAATCATGAAGAATGAAGAAGAGGCTTTGCTGCCGCCAGGAACAGGTTTCATTTTTTCCGAGG 460

Qy   421 AAGAGGCGGAACATATTATCTGAAGCACAAGCCCGTGGATCCCCCAATTACAGTAGTATGCCT 480
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Query Match                 28.6%;    Score 423.8;  DB 4;   Length 427;
Best Local Similarity       99.5%;    Pred. No. 2.4e-117;
Matches 425;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy   132  CGAGAAGGGATTAGATGCCCTCTTCTTTGTTCTTCTTTGAAGAATGCAGTCAGCCTGCTCTG  191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CGAGAAGGGATTAGATGCCCTCTTTGTTCTTCTTTGAAGAATGCAGTCAGCCTGCTCTG   60

Qy   192  ATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTA  251
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Db    61  ATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTA  120

Qy   252  CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTGTGGTCAC  311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTGTGGTCAC  180

Qy   312  TTTGCTGAAGTGCAGGTGGTAAGAGAAGCAACCGGGACATCTATGCTATGAAAGTG  371
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGACATCTATGCTATGAAAGTG  240

Qy   372  ATGAAGAGAAGGCTTTATTCGGCCCAGGAGCAGGTTCATTTTTGAGGAAGAGCGGAAC  431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATGAAGAGAAGGCTTTATTCGGCCCAGGAGCAGGTTCATTTTTGAGGAAGAGCGGAAC  300

Qy   432  ATATTATCTCGAAGCACAAGCCGTGACAAGCCCCAATTACAGTATGCCTTTCAGGACAAA  491
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  ATATTATCTCGAAGTACAAGCCGTGATCCTCAATTACAGTATGCCTTTCAGGACAAA  360

Qy   492  AATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGTCACTTTTGAAT  551
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Db   361  AATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGTCACTTTTGAAT  420

Qy   552  AGATATG  558
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Db   421  AGATATG  427
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Db   461  AGGAGGAGGAACATATTATCTCGGAGCACGAGCTCCTTGGAATCCCCAGTTACAGTACGCCT  520
Qy   481  TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATAATCAGCCTGGAATAATCAGCCTGAGGGGACTTGCTGT  540
          |||||||||||||  ||||||  |||||||  ||||||||||||  ||||||||||||||||
Db   521  TTCAGGACAAAAATAACCTTTACCTGGTCATGGAATAATCAGCCTGAGGGGGATTTGCTGT  580
Qy   541  CACTTTTGAATAGATATGAG  560
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Db   581  CGCTTCTGACCAGATACGAG  600
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RESULT 5
BG944539
LOCUS   BG944539   427 bp   mRNA   linear   EST 15-JAN-2003
DEFINITION ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library)
            Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
ACCESSION   BG944539
VERSION   BG944539.1 GI:14343911
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 427)
AUTHORS   Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE   Gene expression in proliferating human erythroid cells
JOURNAL   Genomics 59 (2), 168-177 (1999)
MEDLINE   99339981
PUBMED   10409428
COMMENT   Contact: Jeffery L. Miller
            Laboratory of Chemical Biology
            National Institute of Diabetes and Digestive and Kidney Diseases
            Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
            20892, USA
            Tel: 301 402 2373
            Fax: 301 435 5148
            Email: jm7f@nih.gov
            DNA Sequencing and analyses by National Institutes of Health
            Intramural Sequencing Center (NISC).
            Plate: 51 row: f column: 11
            Seq primer: -21M13 forward primer (ABI).
FEATURES   Location/Qualifiers
     source   1..427
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ax51f11"
                     /sex="unknown"
                     /tissue_type="blood"
                     /cell_type="Erythroid Cells"
                     /cell_line="Primary Culture of Peripheral Blood
                     Mononuclear Cells"
                     /dev_stage="Progenitor; EPO responsive CD71++++"
                     /lab_host="SOLR"
                     /clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
                     library)"
                     /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
                     Site 2: EcoRI; 65,000 proliferating erythroid cells from
                     the buffy coat of a blood donation were obtained by flow
                     cytometric separation after a 5-day culture period in the
                     presence of erythropoietin. Total RNA was purified from
                     the sorted cell population using TRIzol reagent. RNA (0.3
                     ug) was converted into double stranded cDNA using
                     Clontech's CapFinder cDNA Library Construction Kit
                     (Clontech) according to the manufacturer's protocol and
                     cloned into EcoRI digested Lambda Zap II vector
                     (Stratagene). The phage library was amplified once prior
                     to in vivo excision in SOLR cells. Individual colonies
                     were grown, and the cDNA inserts were sequenced in high
                     throughput (NIH intramural sequencing center
                     http://www.nisc.nih.gov/)."
ORIGIN

RESULT 6
CR746792
LOCUS   CR746792   485 bp   mRNA   linear   EST 30-AUG-2004
DEFINITION CR746792 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGp998E239412 5', mRNA sequence.
            IMAGE:4149886
ACCESSION   CR746792
VERSION   CR746792.1 GI:51660027
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 485)
AUTHORS   Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
            Peters,M., Radelof,U. and Schneider,D.
TITLE   I.M.A.G.E. cDNA Clone Collection;
JOURNAL   Unpublished (2004)
COMMENT   Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; IMAGp998E239412.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES   Location/Qualifiers
     source   1..485
                     /organism="Homo sapiens"
                     /mol_type="mRNA"

Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.

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        /db_xref="taxon:9606"
        /clone="IMAGP998B239412 ; IMAGE:4149886"
        /tissue_type="glioblastoma with EGFR amplification"
        /lab_host="DH10B (T1 phage-resistant)"
        /clone_lib="NCI_CGAP_Brn64"
        /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 1.57 kb. Constructed by Life
        Technologies. Note: this is a NCI_CGAP Library."
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FEATURES   Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129/Sv x CD1"
                     /db_xref="taxon:10090"
                     /dev_stage="p.c. 14.5"
                     /lab_host="E. coli-DH12S (GIBCO)"
                     /clone_lib="Kaestner ngn3 wt"
                     /note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
                     Not I; Site_2: Sal I; The library was prepared by
                     Catherine S. Lee and has not been published. The pancreas
                     was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
                     2000). The cDNA's were prepared with an oligo containing a
                     NotI site, and SalI linkers were added to the ends. The
                     inserts were cut with NotI before being cloned into the
                     NotI-SalI sites in the vectors. This is one of two
                     libraries, ngn3 wt and ngn3 -/-. The wt library is in
                     pSPORT1, T7 promoter is 5'."

ORIGIN

Query Match   27.6%;   Score 409.4; DB 7;   Length 485;
Best Local Similarity   99.8%;   Pred. No. 6.3e-113;
Matches   410; Conservative   0; Mismatches   1;   Indels   0;   Gaps   0;

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Qy     1 TCAAATATGGAGCGCCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
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Db    75 TCAAATATGGAGCGCCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG  134

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  194

Qy   121 CTCCTCTTTCCGAGAAGGGGATATTAGATGCCCTCTTCGTCTCTTTGAAGAATGCAGTC  180
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Db   195 CTCCTCTTTCCGAGAAGGGGATATTAGATGCCCTCTTCGTCTCTTTGAAGAATGCAGTC  254

Qy   181 AGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA  240
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Db   255 AGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA  314

Qy   241 TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
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Db   315 TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  374

Qy   301 GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG  360
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Db   375 GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG  434

Qy   361 CTATGAAAGTGATGAAGAGAAGGCTTATTGGCCCAGGAGCAGGTTTCAT  411
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Db   435 CTATGAAAGTGATGAAGAGAAGGCTTATTGGCCCAGGAGCAGGTTTCAT  485
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RESULT 7
BQ417810
LOCUS   BQ417810   617 bp   mRNA   linear   EST 23-MAY-2002
DEFINITION 1k51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
            TR:O88937 O88937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
            ; mRNA sequence.
ACCESSION   BQ417810
VERSION   BQ417810.1   GI:21123011
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 617)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,A.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bliscain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE   Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
  COMMENT   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557

ORIGIN

Query Match   27.0%;   Score 400.4; DB 5;   Length 617;
Best Local Similarity   86.0%;   Pred. No. 3.9e-110;
Matches   443; Conservative   0; Mismatches   72; Indels   0; Gaps   0;

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Qy     1 TCAAATATGGAGCGCCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
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Db   103 TCAAGTATGTGTGCGAACCCGCCGGAGGCCAGTGCCTCCGGAGCCCAGTCCAGTCGGG  162

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
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Db   163 CCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCCATGACTCAACAGCAGATGT  222

Qy   121 CTCCTCTTTCCGAGAAGGGGATATTAGATGCCCTCTTCGTCTCTTTGAAGAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||
Db   223 CTGCTCTTTCCGGAAGGGATGCTAGACGTGAGCGTGAGCAGTC  282

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   283 AACCCGCCCGTGATGAAGATGAAGCACGTGAGCAGCTTTGTCCAGAGTATTCCGACACCA  342

Qy   241 TAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
         |||||||||||||||||||||||||||||||||||||||||||
Db   343 TAGCCGAGTTGCGGGAGCTGCAGGTCGCAGGAGACTTCGAAGACTTCGAAGCCTGTGG  402

Qy   301 GTTGTGGTCACTTGCTGAGTGCAGGTGCAGGTGTAAGAGAAGCAACCGGGACATCTATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   403 GCTGTGGTCACTTCGCTGAGTGCGAGTGGNTAGCAGAGNTAGCAGAAGGCGACCGGGNACAGCGTCTATG  462

Qy   361 CTATGAAAGTGATGAAGAGAAGGCTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG  420
         |||||||||||||||||||||||||
Db   463 CCATGAAAATCATGAAGAGAAGAGAGCCTTGCTGGCCCAGGAACAGGTTTCATTTTTCGAGG  522

Qy   421 AAGAGCGGACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
         |||||||||||||||||||||||||||||||
Db   523 AGGAGGAACATATTATCTCGGAGCACGACGTCCTTGGATCCCCCAGTACACGTACACGCCT  582

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAA  515
         ||||||||||||||||||||||||||||||||||||
Db   583 TTCAGGACAAAAATAACCTTTACCTGGTCATGGAA  617
```

RESULT 8
CN682405
LOCUS   CN682405   481 bp   mRNA   linear   EST 17-MAY-2004

```
DEFINITION  E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
            density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04
            5', mRNA sequence.
ACCESSION   CN682405
VERSION     CN682405.1  GI:47448856
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 481)
AUTHORS     Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlesinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE       Transcriptome analysis of mouse stem cells and early embryos
JOURNAL     PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: E0164 row: B column: 04
            Seq primer: M13 Reverse
            High quality sequence stop: 481
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..481
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129sv/EvTac"
                     /db_xref="niaEST:E0164B04-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:E0164B04 IMAGE:30782511"
                     /sex="Male"
                     /tissue_type="Embryonic Stem Cell"
                     /cell_line="129.3 ES cells"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
                     h, low density) cDNA library (Long)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
                     cells were plated at density 3x103/cm2, on gelatin-coated
                     plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
                     medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
                     0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
                     beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
                     streptomycin. Double-stranded cDNAs were synthesized with
                     an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCCTTTTTTTTTTTTTTT-3'] from
                     2ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.8 kb. The library was
                     constructed by Yulan Piao."
ORIGIN
```

```
Query Match             25.7%;  Score 380;  DB 7;  Length 481;
Best Local Similarity   88.0%;  Pred. No. 5.9e-104;
Matches  426;  Conservative   0;  Mismatches  55;  Indels   3;  Gaps   1;

Qy  281 CGAAGTCAGAAGTCTTGTAGGTTGTGTCACTTTGCTGAAGTGCAGTGGTTAGAGAGAA 340
        |||||||| ||| ||||| |||||||||||| |||||||||||||||||||||||||||
Db    1 CGAAGTCGAAGCCTTGTGGCGTGTGTCACTTCGCTGAAGTGCAGTGGTTAGAGAGAA 60

Qy  341 AGCAACCGGGGACATCTATGCTATGAAGTGATGAAGAAGAAGAGGCTTTATTGCGCCCAGGA 400
        |||||||| |||||||||| ||||||||| |||||||||||||||||||| ||| ||||||
Db   61 GGGCGACCGGGACGTCTATGCCATGAAGAAATCATGAGAAGAAGAGGCTTTGCTGGCCCAGGA 120

Qy  401 GCAGGTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGAT 460
        |||||||||||||||||||| ||||||||| ||||||| |||||||||| ||||||
Db  121 ACAGGTTCATTTTCGAGGAGGAGGAACATATTATCTCGGAGCACGCGAGCAGTCCTTGGAT 180

Qy  461 CCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATTCTGTCATGGAATATCA 520
        ||||| ||| ||||||| ||||||| |||||| ||||| ||| |||||||||||||||||
Db  181 CCCCCAGTTACAGTACGACCCTTTCAGGACAAAAATAACCTTTACCTGGTCATGGAATATCA 240

Qy  521 GCCTGGAGGGGACTTGCTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCT 580
        ||||||||| ||||||||||||| ||||||| ||| |||| ||||||| ||| ||| ||  |
Db  241 GCCTGGAGGGGGATTTGCTGCTGTCGTCGTCCTTCGAACAGATACGAGGACCAATTAGATGAGAGCAT 300

Qy  581 GATACAGTTTTACCTAGCTGAGCTGATTTTGCGTGTTCACAGCGTTCATCTGATGGGATA 640
        || ||||||| ||||| ||||||| ||||| |||||| ||||||||||| |||||||||||
Db  301 GATCCAGTTTTACCTTGCTGAGCTGATTTTGCGTGTTCCACAGCGTGCCACCGATGGGATA 360

Qy  641 CGTGCATCGAGACATCAAGCCTGAGAACCTTCGTGACCGCACAGGACACATCAAGCT 700
        ||||||||||| ||||||||| ||||||||| ||||||||| ||| |||||||||||
Db  361 TGTGCATCGAGACATCAAGCCCGAGACATCCTCATCGACCGACGACGGGACACATCAAGCT 420

Qy  701 GGTGGATTTGGATCCGCCGCAAAATGAATTCAAACAACAAGATGGTGAAATGCCAAACTCCC 760
        |||||||||||||| ||| |||| ||||| ||| |||||||| ||  |||||||||||||
Db  421 GGTGGATTTGGATCAGCCGCCTAAGATGAATTCAAATAA---GGTGGATGCCAAACTCCC 477

Qy  761 GATT 764
        ||||
Db  478 CATT 481
```

```
RESULT 9
CN678533
LOCUS       CN678533               479 bp    mRNA        linear   EST 17-MAY-2004
DEFINITION  E0112C12-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
            density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12
            IMAGE:30777539 5', mRNA sequence.
ACCESSION   CN678533
VERSION     CN678533.1  GI:47444984
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 479)
AUTHORS     Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlesinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE       Transcriptome analysis of mouse stem cells and early embryos
JOURNAL     PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: E0112 row: C column: 12
            Seq primer: M13 Reverse
            High quality sequence stop: 479
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Db       361 TGTGCATCGAGACATCAAGCCGAGAACATCCTCATCGACCGGACGGGACCATCAAGCT 420
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Qy       701 GGTGGATTTTGGATCGCCGCCGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC 760
             ||||||||||||||||||| ||     || |||||   ||||||| |||||||||||||||
Db       421 GGTGGATTTTGGATCAGCCCGCTAAGATGAATTCAAATAA---GGTGTGATGCCAAACTCCC 477

Qy       761 GA 762
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Db       478 CA 479
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RESULT 10
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BF562826
LOCUS       BF562826                                    490 bp    mRNA      linear   EST 12-DEC-2000
DEFINITION  UI-R-BJOp-aip-b-06-0-UI.r1 UI-R-BJOp Rattus norvegicus cDNA clone
            UI-R-BJOp-aip-b-06-0-UI 5', mRNA sequence.
ACCESSION   BF562826
VERSION     BF562826.1  GI:11672556
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 490)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road    4156   MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1797673
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
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                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BJOp-aip-b-06-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-BJOp"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJOp
                     library is a subtracted library derived from the UI-R-AA1,
                     UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AE1, UI-R-AF1, and
                     UI-R-AG1 libraries. These libraries represent tissues from
                     rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
                     at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
                     canal at 15 dpc, and ventricle at 13 dpc. The tag is a
                     string of 5-6 nucleotides present between the Not I site
                     and the oligo-dT track. The library was constructed as
                     described by Bonaldo, Lennon and Soares,  Genome Research
                     6: 791-806, 1996."
ORIGIN
```

```
Query Match         22.8%;  Score 337;  DB 2;  Length 490;
Best Local Similarity 85.3%;  Pred. No. 7.9e-91;
Matches 376;  Conservative 0;  Mismatches 65;  Indels 0;  Gaps  0;

Qy         1 TCAAATATGGAGCGCCGGAATCCTTTGGATGCGGTGGTGCTGCTGAACCCATTGCCAACCGGG 60
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```
FEATURES        POLYA=No.
     source          Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/EvTac"
                     /db_xref="niaEST:E0112C12-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:E0112C12 IMAGE:30777539"
                     /sex="Male"
                     /tissue_type="Embryonic Stem Cell"
                     /cell_line="129.3 ES cells"
                     /clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
                     h, low density) cDNA library (Long)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
                     cells were plated at density 3x103/cm2, on gelatin-coated
                     plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
                     medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
                     0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
                     beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
                     streptomycin. Double-stranded cDNAs were synthesized with
                     an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTTTTT-3'] from
                     2ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.8 kb. The library was
                     constructed by Yulan Piao."
ORIGIN
```

```
Query Match         25.5%;  Score 378;  DB 7;  Length 479;
Best Local Similarity 88.0%;  Pred. No. 2.4e-103;
Matches 424;  Conservative 0;  Mismatches 55;  Indels 3;  Gaps  1;

Qy       281 CGAAGTCAGAAGTCTTGTAGGTGTGGTCACTTTGCTGAAGTGCAGGTGGTTAAGAGAGAA 340
             |||||| |||| ||| |||||||||||||||||||||||||||||||||||| |||||||
Db         1 CGAAGTTCGAAGCCTTGTGGGCGTGGTCACTTCGCTGAAGTGCAGGTGGTTAGAGAGAGA 60

Qy       341 AGCAACCGGGACAATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGA 400
             ||||| ||||| || |||| ||||||||||||||||||||||||| |||||||||||||||
Db        61 GGCGACCGGGACGTCTATCCCATGAAAATCATGAAGAAGAAGAAGGCTTTGCTGGCCCAGGA 120

Qy       401 GCAGGTTCATTTTGACGGAAGAGCGGAACATATTATCCTGAAGCACAACGCCGTGGAT 460
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Db       121 ACAGGTTCATTTTCGAGGAGGAGGAACATATTATCCTGAAGCACCAGCGTCCTTGGAT 180

Qy       461 CCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCA 520
             ||||| |||||||||||| ||||| |||||||||||||||||||||||||||||||||
Db       181 CCCCCAGTTACAGTACGCGCCTTTCAGGACAAAAATAACCTTTACCTGGTCATGGAATATCA 240

Qy       521 GCCTGGAGGGGACTTGCTCGTCACTTTGAATAGATATGAGGACCAGTTAGAGATAAAACCT 580
             |||||||||||| |||||| |||||||||||||||||||||||||||||||||||||||||
Db       241 GCCTGGAGGGGATTTGCTCGTCGCTTCTGAACAGATACGACGAGGACCAATTAGAGTGAGCAT 300

Qy       581 GATACAGTTTACCTAGCTGAGCTGATTTTGGCGTTCTTCACAGCCGTTCATCTGATGGGATA 640
             |||| ||||| |||| ||||||||||||||| ||| ||||||||||||||||||||||||||
Db       301 GATCCAGTTTTACCTTGCTGAGCTGATTTTGGCGTTCTTCCACAGCGTGCACCAGATGGGATA 360

Qy       641 CGTGCATCGAGACATCAAGCCGAGAACATTCTCGTTGACCGCACGAGGACACATCAAGCT 700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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                    Library constructed by Life Technologies. Investigators
                    providing samples: Lothar Hennighausen/Priscilla Furth,
                    NIH Reference for transgenic model: Li et al., Cell Growth
                    and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match    22.3%;  Score 329.8;  DB 4;  Length 821;
Best Local Similarity 84.2%;  Pred. No. 1.5e-88;
Matches  454;  Conservative    0;  Mismatches   77;  Indels    8;  Gaps    7;

Qy      1 TCAAATATGGAGGCGGAACCTTCGATGCTGGTGCTGCTGGAACCCATTGCCAACCGGGG   60
          ||||| |||||| | ||||||  || |||| |||| | ||| | |||||||||||  ||||
Db    117 TCAAGTATGGTGTGCGGAACCCGCCGGAGGCCAGTGCCTCCGAGCCCAGTCGAGTCGGGG  176

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||| ||||| ||||||||||||||||||| ||  | ||||||||||||||||||
Db    177 CCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATGACTCAACAGCAGATGT  236

Qy    121 CTCCTCTTCCCGAGAGGGATATTAGATAGTGCCTCCTTGTTCTCTTTGAAGAATGCAGTC  180
          || |||||| |||| ||||| | ||| | ||||||||  |||||||| |||||||| ||||
Db    237 CTGCTCTTTCCCGGGAAGGGATGCTAGACGCCTCCTTCGCTCTCTTGGAAGAGTGCAGCC  296

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA   240
          | || ||| |||||||||| |||||||||||||||||  | ||| |||||||||||||||
Db    297 AACCCGCCCTGATGAAGATGAAGCACGTGAGCACGTGAGCAGCTTAGTCCAGAGTATTCCGACACCA   356

Qy    241 TAG-CTGAGTTACAGAGCGTCCAGCCTTCGCGCAAAGGACACGTGAA-GTCAGAAGTCTTGT  298
          ||| |||||||| | |||| |||||||  | | |||| |||   || | || |||| ||||
Db    357 TAGCCCGAGTTGCGGAGCTGCGGCCGTCGCAGCGTCGGAGACTTCGGAGGAAGTTCGAAGCCTTGT  416

Qy    299 AGGTTGGTCACTTTGCTGAAGTGCTGAAGTGCAGGTGTAA-GAGAGAAAGCAACCGGGACACATCT  357
          |||||||| |||| | ||||||||||||||| |||||||| |||||||||| || |||| || ||
Db    417 GGGCTGGTCACTTCGCTGAAGTGCTGAAGTGCAGGTGGTGTTACGAGGTGGTGTTACGAGGAAGAGGCGACCGGGACGTCT  476

Qy    358 ATGCTATGAAAGTGATGA-AGAAGAAGGCTTATTGGCCCAGGAGCCAGGTTTCATTTTT   416
          |||| ||||||  ||||| ||| ||||||| |||||| |  ||| |||||||||||||||
Db    477 ATGCCATGAAAATCATGACAGAGAAGAGAGAGGCTTATTTGCTCGCCGCGAACAGGTTTCATTTTTC  536

Qy    417 GAGGAGAGCCGAA-CATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTA   475
          |||||||||| || ||||||| ||| ||||||||| ||||||||| |  |||| |||||
Db    537 GAGGAGAGGAGGAACCATATTATCTCGGAGCACGAGTCCTGGATCCACCAGTTACAGTA  596

Qy    476 TGCCTTTCAGGAC-AAAAATCACCTTTATCTGGTCATGG--AATATCAGCCTGGAGGGG  531
          ||| |||||||   |||||||  |||| |||||||||||  ||||||||||| ||||||
Db    597 CGCCTTTCAGGACCACCAAAAATAAACTTTACCTGGTCATGCAATGGACCACTATCAGCCTGGAGGGG  655
```

RESULT 11

BI654262
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LOCUS       BI654262       821 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603280370F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5310496 5',
            mRNA sequence.
ACCESSION   BI654262
VERSION     BI654262.1   GI:1556498
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 821)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1786 row: 1 column: 17
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
     source          1..821
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NMRI"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5310496"
                     /tissue_type="tumor; gross tissue"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam4"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
```

```
Db     50 TCAAGTATGGAGGTGCGGAACCCGTCCGAGGCCAGTGCCCCCGAGCCCATTGCCAGTCGGGG  109
          ||||| |||||| | ||||||  || |||| ||||  || | |||||||||||   ||||
Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||| ||||| |||||||||||||||||| || ||  | ||||||||||||||||||
Db    110 CCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATGACTCAACAGCAGATGT  169

Qy    121 CTCCTCTTCCCGAGAGGGATATTAGATAGTGCCTCCTTGTTCTCTTTGAAGAATGCAGTC  180
          || |||||| |||| ||||| | ||| | ||||||||  |||||||| |||||||| ||||
Db    170 CTGCTCTTTCCCGGGAAGGGGTGTTAGATGCCCTCTTCGTTCTCTTTGTTGAAGAGTGCAGTC  229

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
          | || ||| |||||||||| |||||||||||||||   | ||| |||||||||||||||
Db    230 AGCCTGCCCTGATGAAGATAAAGCACGTGAGCAGCTTCGTCGTCCGGAAGTATTCTGACACGA  289

Qy    241 TAGCTGAGTTACAGGAGCGTCCAGCCTTCGCGCAAAGGACTTCAGAGTCTTGTAG  300
          || |||||||| | |||| |||||||  | | |||| ||||| ||||||  |||
Db    290 TAGCCGAGTTACGCGGGGACGTCGGTCGGTCAGTGTGCGAAGTGCGAAGTGCTTGTGG  349

Qy    301 GTTGTGGTCACTTGCTGAAGTGCTGCAGTGGTCAGGTGTAAGAGAGAAAGCAACCGGGACATCTATG  360
          |||||||| |||  |||||| | | ||  | | |||||||||||||  ||| || |||| || ||
Db    350 GCTGCGGTCACTTCGCCGCGAAGTGCAGGTGTGCAGTGTGGGATGTCTACG  409

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCCAGGTTTCATTTTTGAGG  420
          ||||||||  |||||||||||||||| |||||| |  ||| ||||||||||||||||||
Db    410 CCATGAAGATCATGAAGAAGAAGGCGGCTTTGCGGGGCCCAGGAGCCAGGTTTCATTTTTCGAGG  469

Qy    421 AAGAGCCGAACATATTATCTC  441
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Db    470 AGGAGAGGAACATATTATCCC  490
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RESULT 12

CG501399
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LOCUS       CG501399       449 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST45249 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45249,
            mRNA sequence.
ACCESSION   CG501399
VERSION     CG501399.1   GI:37275067
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 449)
AUTHORS     Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
```

(Left column)

```
                4000 Research Forest Drive, The Woodlands, TX 77381, USA
                Email: materials@lexgen.com
                Gene trap sequence tag generated by 3' RACE from mouse ES cells as
                described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
  Class: Gene Trap.
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                /mol_type="mRNA"
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                /clone="OST45249"
                /cell_type="embryonic stem cell"
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ORIGIN

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Best Local Similarity  91.8%;  Pred. No. 8.6e-88;
Matches  345;  Conservative  0;  Mismatches  31;  Indels  0;  Gaps  0;

Qy  1102  CTCCCCCCCTTCGTTCCCACCCTCCAGTCCGACGATGACACCTCCAATTTTGATGAAC 1161
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Db     6  CTCCTCCCCCTTCGTCCCCACCCTCCAGTCTGACGATGACACCTCCAATTTTGATGAAC 65

Qy  1162  CAGAGAAGAATTCGTGGGTTTCATCCTCCGTGCCAGTGAGCCCCTCAGGCTTCTCGG 1221
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    66  CAGAGAAGAATTCGTGGGTTTCATCCTCCGTGTGCCAGTGAGCCCCTCGGGCTTCTCAG 125

Qy  1222  GTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGAT 1281
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Db   126  GCGAGAGCTGCCGTTTGTGGGGTCGGGGTATCTGGGGTATCTTGGTAGAT 185

Qy  1282  CTGAGTCTGTGTGTGTCGGGGTCGGACTCCCCTGCCCAAGGTTAGCTCCATGAAAAGAAAC 1341
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Db   186  CTGAGTCTGTGTCGTGTCGGGGTCGGACTCCCCTGCCCAAGGTTAGCTCCATGNAAAGAAAC 245

Qy  1342  TTCTCATCAAAAGCAAAGAGCTACAAGACTCCAGGACAGTGTCACAAGGTATTTATTT 1401
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   246  TTCTCATCAAAAGCAAAGAGCTCCAGGACTTCCAGGACAGTGTCACAAGGTATCTATCT 305

Qy  1402  CCGCAGCCGGCCTCCTTCCTTGCTCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCG 1461
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   306  CCACAGCCGGCCTCACGTCCTTGCTCCAGGATCCTCCAGTCAATATATGCCGAGGGATGTG 365

Qy  1462  CCCGGGGGCCGCTGCTG 1477
          |||||||||||| |||||
Db   366  CCGGGGGCCACTGCTG 381
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LOCUS         CG501400        450 bp    mRNA       linear     GSS 01-OCT-2003
DEFINITION    OST45250 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45250,
              mRNA sequence.
ACCESSION     CG501400
VERSION       CG501400.1  GI:37275069
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 450)
AUTHORS       Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
              Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
              Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
              Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
              Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-z.,
              Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
              Zhu,Q., Person,C. and Sands,A.T.
TITLE         Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
              screen to identify potential targets for therapeutic intervention
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT       Contact: Zambrowicz BP
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(Right column)

```
                OmniBank
                Lexicon Genetics Incorporated
                4000 Research Forest Drive, The Woodlands, TX 77381, USA
                Email: materials@lexgen.com
                Gene trap sequence tag generated by 3' RACE from mouse ES cells as
                described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
  Class: Gene Trap.
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                /cell_type="embryonic stem cell"
                /clone_lib="Mus musculus 129Sv/Ev"
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Query Match      21.9%;   Score 325;  DB 9;  Length 450;
Best Local Similarity  91.7%;  Pred. No. 3.5e-87;
Matches  343;  Conservative  0;  Mismatches  31;  Indels  0;  Gaps  0;

Qy  1108  CCCCCTTCGTTCCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGA 1167
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Db     2  CCCCCTTCGTCCCCACCCTCAAGTCTGACGATGACACCTCCAATTTTGATGAACCAGAGA 61

Qy  1168  AGAATTCGTGGGTTTCATCCTCCGTGCCAGTGAGCCCCTCAGGCTTCTCGGGTGAAG 1227
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    62  AGAATTCGTGGGTTTCATCCTCCGTGTGCCAGTGAGCCCCTCGGGCTTCTCAGGCGAAG 121

Qy  1228  AACTGCCGTTTGTGGGGTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGT 1287
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   122  AGCTGCCGTTTGTGGGGATTTTCGTACAGCAAGGCACTGGGGTATCTTGGTAGATCTGAGT 181

Qy  1288  CTGTTGTGTCGGGTCGGACTCCCCTGCCCAAGACTAGCTCCATGGAAAAGAAACTTCTCA 1347
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   182  CTGTCGTGTCGGAGTCCGACTCCCCTGCCCAAGGTTAGCTCCATGAAAAGAAACTTCTCA 241

Qy  1348  TCAAAAGCAAAGAGCTACAAGACTCTCAGGACAGTGTCACAAGGTATTATTCCGCAG 1407
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Db   242  TCAAAAGCAAAGAGCTCCAGGACTCCAGGACAGTGTCACAAGGTATCATCTCCACAG 301

Qy  1408  CCGGCCTCCTTCCTTGCTCCAGGATCCTCCCGTATATGCCAAGGGATCCGCCCGGG 1467
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Db   302  CCGGCCTCCCGTCCTTGCTCCAGGATCCTCCAGTCAATATATGCCGAGGGATCCGCCCGGG 361

Qy  1468  GCCGCTGCTGGCTC 1481
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Db   362  GCCACTGCTTGANC 375
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ACCESSION     CG652891
VERSION       CG652891.1  GI:37476740
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 512)
AUTHORS       Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
              Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
              Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
              Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
              Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-z.,
              Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
              Zhu,Q., Person,C. and Sands,A.T.
TITLE         Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
              screen to identify potential targets for therapeutic intervention
```

JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT   Contact: Zambrowicz BP
          OmniBank
          Lexicon Genetics Incorporated
          4000 Research Forest Drive, The Woodlands, TX 77381, USA
          Email: materials@lexgen.com
          Gene trap sequence tag generated by 3' RACE from mouse ES cells as
          described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
          Class: Gene Trap.
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Best Local Similarity 92.0%;   Pred. No. 4.4e-85;
Matches 346; Conservative 0; Mismatches 29; Indels   1; Gaps   1;

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Qy 1102 CTCCTCCCCCTTGTTCCACCCTCCAAGTCGACGATGACACCTCCAATTTTGATGAAC 1161
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Db    8 CTCCTCCCCCTTCG-TCCCCNCCTCCAAGTCTGACGATGACACCTCCAATTTTGATGAAC 66

Qy 1162 CAGAGAAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGCTGAGCCCCTCCAGGCTTCTCGG 1221
        |||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||| |
Db   67 CAGAGAAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGCTGAGCCCCTCCGGGCTTCTCAG 126

Qy 1222 GTGAAGAACTGCCGTTTGTCGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGAT 1281
        | |||||| ||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db  127 GCGAAGAGCTGCCGTTTGTCGGGGTTTTCGTACAGCAAGGCACTGGGGTATCTTGGTAGAT 186

Qy 1282 CTGAGTCTGTTGTCGTGCGGGTCGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAAGAAAC 1341
        |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  187 CTGAGTCTGTTGTCGTGCGGGTCGTCTGGACTCCCCTGCCAAGGTTAGCTCCATGGAAAGAAAC 246

Qy 1342 TTCTCATCAAAAGCAAAGAGAGCTCCAGGACTACAAGACTTCAGGACAAGTGTCACAAGGTATTTATT 1401
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        || ||||||| |||| |||| |||||||||||||||||| | |||||| |||||| |
Db  307 CCACAGCCGGCCTCCGTCCGTCCTTGCTCCAGGATCCTCCAGTCAATATATGCCGAGGGATCTG 366

Qy 1462 CCCGGGGCCGCTGCTG 1477
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Db  367 CCCGGGGCCCACTGCTG 382
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DEFINITION IL2-UT0073-170900-167-H01 UT0073 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF380737
VERSION   BF380737.1 GI:11369862
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 340)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags

  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2-UT0073-
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          High quality sequence stop: 339.
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                   /note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
                   Site 2: SmaI; A mini-library was made by cloning products
                   derived from ORESTES PCR (U.S. Letters Patent application
                   No. 196,716 - Ludwig Institute for Cancer Research)
                   profiles into the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
ORIGIN

Query Match   21.2%;   Score 314.2;   DB 2;   Length 340;
Best Local Similarity 97.6%;   Pred. No. 6.2e-84;
Matches 319; Conservative 0; Mismatches   8; Indels   0; Gaps   0;

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Qy 1101 TCTCCTCCCCCCTTGGTCCACCCTCCAAGTCCGACGATGACACCTCCAATTTTGATGAA 1160
        ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
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Qy 1161 CCAGAGAAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGCTGAGCCCTCCAGGCTTCTCG 1220
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Db   89 TCTGAGTCTGTTGTCGTGCGGGTCGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAGAAGAAA 30

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Db   29 CTTCTCATCAAAAGCAAAGAGCCCCAA 3
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1481	100.0	1481	8	ACA61394	Aca61394 cDNA enco
2	1481	100.0	1515	10	AAD59938	Aad59938 Human kin
3	1481	100.0	1515	12	ADO40591	Ado40591 Human kin
4	1477.8	99.8	1765	10	ABZ68726	Abz68726 Nucleotid
5	1476.2	99.7	2066	6	AAD26454	Aad26454 Nucleotid
6	1471.8	99.4	1485	10	ABZ68725	Abz68725 Nucleotid
7	1388.2	93.7	5877	8	ADA05643	Ada05643 Human kin
8	1388.2	93.7	6156	6	ABQ78871	Abq78871 Human kin
9	1388.2	93.7	6165	6	AAL55217	Aal55217 Human CRI
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11	1388.2	93.7	6165	9	AAL55214	Aal55214 Human CRI
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14	1385	93.5	1870	12	ADN62808	Adn62808 Human NOV
15	1381.8	93.3	6162	10	ADF60993	Adf60993 ORF of pa
16	1381.8	93.3	6574	6	AAD39191	Aad39191 Human MDP
17	1381.8	93.3	6574	10	ADF60992	Adf60992 Pain asso
18	1381.8	93.3	6574	13	ADQ89099	Adq89099 Human uro
19	1372	92.6	6159	4	AAS06701	Aas06701 Polynucle
20	1372	92.6	8656	12	ADJ96544	Adj96544 Human cit
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26	1365.8	92.2	6201	12	ADN62818	ADN62818 Human NOV
27	1143.6	77.2	2380	10	ABZ68776	ABZ68776 Nucleotid
28	947.2	64.0	2162	8	ABX71191	ABX71191 Novel hum
29	945.4	63.8	957	11	ADN62729	ADN62729 Human cit
30	925	62.5	1048	5	AAS79753	AAS79753 DNA encod
31	744.8	50.3	1133	10	ADJ79946	ADJ79946 Human kin
32 c	578.8	39.1	2896	5	ABV30132	ABV30132 Human pro
33 c	441.8	29.8	446	5	ABV15823	ABV15823 Human pro
34 c	434.4	29.3	485	5	ABV45624	ABV45624 Human pro
35	247.2	16.7	3835	8	ABT33346	ABT33346 NOVX DNA
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37	246.8	16.7	1530	6	AAD38845	AAD38845 Human Kin
38	246.8	16.7	4698	12	ADP47966	ADP47966 Human MRC
39	246.8	16.7	4707	12	ADF95101	ADF95101 Human ser
40	246.8	16.7	4944	12	ADF95099	ADF95099 Human ser
41	246.8	16.7	5373	6	AAD30567	AAD30567 Human kin
42	246.8	16.7	5373	12	ADQ15093	ADQ15093 Human can
43	246.8	16.7	5438	12	ADJ96545	ADJ96545 Human dys
44	246.8	16.7	5619	12	ADI40903	ADI40903 Human kin
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ALIGNMENTS

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ID   ACA61394 standard; cDNA; 1515 BP.
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AC   ACA61394;
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DT   11-AUG-2003  (first entry)
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DE   cDNA encoding novel human kinase.
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KW   Human; ss; gene; gene therapy; kinase; antisense.
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PD   30-JAN-2003.
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PF   11-SEP-2002; 2002US-00238709.
XX
PR   13-MAR-2001; 2001US-00804471.
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PA   (APPL-) APPLERA CORP.
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PI   Webster M, Yan C, Di Francesco V, Beasley EM;
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DR   WPI; 2003-438978/41.
DR   P-PSDB; ABU10126.
XX
PT   New human kinase peptides useful as models or targets for the development
PT   of therapeutic agents that modulate kinase activity, for eliciting immune
PT   response, and in identifying compounds that modulate kinase activity or
PT   expression.
XX
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PS
XX
CC   Claim 4; Fig 1; 207pp; English.
CC   The invention relates to a novel isolated human kinase. The kinase
CC   peptides and nucleic acids are useful as models for the development of
CC   human therapeutic targets, in the identification of therapeutic proteins,
CC   and serve as targets for the development of human therapeutic agents that
CC   modulate kinase activity in cells and tissues that express the kinase.
CC   The proteins can be used to raise or to elicit another immune response,
CC   as a reagent in assays designed to determine the levels of the protein in
CC   biological fluids, as markers for tissue in which the corresponding
CC   protein is preferentially expressed, in the identification of modulators
CC   of the peptides and in pharmacogenomic analysis. The nucleic acids are
CC   useful as hybridisation probes, in constructing vectors, host cells or
CC   transgenic animals expressing all or a part of the nucleic acid, for
CC   monitoring the effectiveness of modulating compounds on the expression or
CC   activity of the transporter gene in clinical trials or in treatment
CC   regimen, in gene therapy and as antisense constructs to control
CC   transporter gene expression in cells, tissue and organisms. The present
CC   sequence represents cDNA encoding a novel human kinase
XX
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1481;   DB 8;   Length 1515;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1481;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 TCAAATATGGAGCGCCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17 TCAAATATGGAGCGCCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 76

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 136

Qy  121 CTCCTCTTTCCCGAGAAGGGGATATTAGATGCGCCCTCTTTGTTCTCTTTGAAGAATGCA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  137 CTCCTCTTTCCCGAGAAGGGGATATTAGATGCGCCCTCTTTGTTCTCTTTGAAGAATGCA 196

Qy  181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  197 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 256

Qy  241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  257 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 316

Qy  301 GTTGTGTCACTTGCTGAAGTGCAGGTGCAGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  317 GTTGTGTCACTTGCTGAAGTGCAGGTGCAGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 376

Qy  361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  377 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 436

Qy  421 AAGAGCGGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  481 TTCAGGACAAAAATCACCCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
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Db  497 TTCAGGACAAAAATCACCCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 556

Qy  541 CACTTTTGATAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
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Db  557 CACTTTTGATAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 616

Qy  601 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
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Db  617 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy  661 CTGAGAACATTCTCGTTGACCGACCACAGGACACACATCAAGCTGGTGATTTGGATCTGCCG 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  677 CTGAGAACATTCTCGTTGACCGACCACAGGACACACATCAAGCTGGTGATTTGGATCTGCCG 736

Qy  721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796

Qy  781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACTCACGGCCTGGACT 840
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Db  797 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACTCACGGCCTGGACT 856

Qy  841 GTGACTGGTGGTCAGTGGGCGTGATTGGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  857 GTGACTGGTGGTCAGTGGGCGTGATTGGCCTATGAGATGATTATGGGAGATCCCCCTTCG 916

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  917 CAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 976

Qy  961 TTCCAGATGACCCCAAAGTGACGCAGTGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  977 TTCCAGATGACCCCAAAGTGACGCAGTGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1036

Qy 1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCCATCTAAAATTG 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1037 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCCATCTAAAATTG 1096

Qy 1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTTCAAGTCCGACGATG 1140
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Db 1097 ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTTCAAGTCCGACGATG 1156

Qy 1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCGTCCTCCGTGCCAGC 1200
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Db 1157 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCGTCCTCCGTGCCAGC 1216

Qy 1201 TGAGCCCCTCAGGCTTCTCGGGTGAGAACTGCCGTTGTGGGGTTTGTGCGGGTCTGAGTC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1217 TGAGCCCCTCAGGCTTCTCGGGTGAGAACTGCCGTTGTGGGGTTTGTGCGGGTCTGAGTC 1276

Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTTGTCGTGTCGGGTCTGGACTCCCTGCCAAGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1277 CACTGGGGATTCTTGGTAGATCTGAGTCGTTGTCGTGTCGGGTCTGGACTCCCTGCCAAGA 1336

Qy 1321 CTAGCTCCATGGAAAAGAAACTTCATCAAAAGCAAAGAGAGCTACAAGACTCTCAGGACA 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1337 CTAGCTCCATGGAAAAGAAACTTCATCAAAAGCAAAGAGAGCTACAAGACTCTCAGGACA 1396

Qy 1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGGGCCTCCTTCCTTGCTCCGAGATCCTCCGT 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1397 AGTGTCACAAGGTATTTATTTCCGCAGCCGGGCCTCCTTCCTTGCTCCGAGATCCTCCGT 1456

Qy 1441 CCGTATATGCCAAGGATCCGCCCGGGCCCGCTGCTGGCTC 1481
         ||||||||||||||||||||||||||||||||||||||||
Db 1457 CCGTATATGCCAAGGATCCGCCCGGGCCCGCTGCTGGCTC 1497
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RESULT 2
AAD59938
ID   AAD59938 standard; cDNA; 1515 BP.
XX
AC   AAD59938;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Human; kinase protein; diagnostic; therapeutic; immune response;
KW   pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   5'UTR   1..6
FT   /*tag= a

```
FT   CDS          7..1500
FT                /tag= b
FT                /product= "Human kinase protein"
FT   3'UTR        1501..1515
FT                /tag= c
XX
PN   US2002132322-A1.
XX
PD   19-SEP-2002.
XX
PF   13-MAR-2001; 2001US-00804471.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (WEBS/)  WEBSTER M.
PA   (YANC/)  YAN C.
PA   (DFRA/)  DI FRANCESCO V.
PA   (BEAS/)  BEASLEY E M.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI: 2003-687480/65.
DR   P-PSDB; AAE39504.
XX
PT   New isolated human kinase proteins, useful as models for developing human
PT   therapeutic targets, or for treating a disorder associated with an
PT   absence of, inappropriate or unwanted expression of the protein, e.g.
PT   cancer.
XX
PS   Claim 4; Fig 1; 0pp; English.
XX
CC   The present invention relates to human kinase proteins and nucleic acids
CC   encoding them all of which are useful in the development of human
CC   therapeutics and diagnostic composition and methods. The invention is
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents. The invention is also useful in
CC   drug screening assays, in assays to determine the biological activity of
CC   the protein, to raise antibodies and to elicit another immune response.
CC   The antibodies are useful in pharmacogenomic analysis, for inhibiting
CC   protein function and for tissue typing. The transgenic animals are useful
CC   for studying the function of kinase protein, identifying and evaluating
CC   modulators of kinase protein activity. The invention is also used in gene
CC   therapy. The present sequence is the human kinase cDNA. The human kinase
CC   gene is located on chromosome 12
XX
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1481;  DB 10;  Length 1515;
Best Local Similarity   100.0%;
Matches 1481;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCATTGCCAACCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCATTGCCAACCGGG 76

Qy         61 CCTCCAGGCTGAATCTGTTCTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CCTCCAGGCTGAATCTGTTCTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 136

Qy        121 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC 196

Qy        181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 256

Qy        241 TAGCTGAGTTACAGGAGCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TAGCTGAGTTACAGGAGCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 316

Qy        301 GTTGTGGTCACTTTGCTGAGTGCAGTGGTAAGAGAGAAGCAACCGGGGACATCTATG 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTTGTGGTCACTTTGCTGAGTGCAGTGGTAAGAGAGAAGCAACCGGGGACATCTATG 376

Qy        361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCAGGTTTCATTTTTTGAGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCAGGTTTCATTTTTTGAGG 436

Qy        421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 496

Qy        481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 556

Qy        541 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 616

Qy        601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy        661 CTGAGACACATTCTCGTTGACCGCACAGGACACATCAAGCTGTGTGGATTTTGGATCTGCCG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CTGAGACACATTCTCGTTGACCGCACAGGACACATCAAGCTGTGTGGATTTTGGATCTGCCG 736

Qy        721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796

Qy        781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATCGAAAAGGCACCTACGGCCTGGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATCGAAAAGCACCTACGGCCTGGACT 856

Qy        841 GTGACTGGTGTCAGTGGCGCTGAATGCCTATGGAGATGATTAATGGGAGATCCCCCTCG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 GTGACTGGTGTCAGTGGCGCTGAATGCCTATGGAGATGATTAATGGGAGATCCCCCTCG 916

Qy        901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 976

Qy        961 TTCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATCCAAAGCTTCAAAGCTTGTTGTGCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATCCAAAGCTTCAAAGCTTGTTGTGCG 1036

Qy       1021 GCCAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGCTGCTGCCATCCTTTCTTCCTCTAAAATTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GCCAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGCTGCTGCCATCCTTTCTTCCTCTAAAATTG 1096

Qy       1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCGTGGTTTCATCCTCTCCGTGCCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCGTGGTTTCATCCTCTCCGTGCCAGC 1156

Qy       1141 ACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTGTGGGGTTTCATCGTTGTTGTACAGCAAGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 ACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCGTTGTTGTACAGCAAGG 1216

Qy       1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTGTGGGGTCTGAGAA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTGTGGGGTCTGAGAA 1276

Qy       1261 CACTGGGGATTCTTGGTAGATCGAGTCGTGTGTCGGGTCGGGTCTGGGTCTCGAGACTCCCCTGCCAAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 CACTGGGGATTCTTGGTAGATCGAGTCGTGTGTCGGGTCGGGTCTGGGTCTCGAGACTCCCCTGCCAAGA 1336

Qy       1321 CTAGCTCCATGGAAAAGAAACTTCATCAAAAGCAAAGACTACAAAGACTCTCAGGACA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 CTAGCTCCATGGAAAAGAAACTTCATCAAAAGCAAAGACTACAAAGACTCTCAGGACA 1396

Qy       1381 AGTGTCACAAGGTATTATTTCCCGACGCCGCCTCCTTGCTCACGGATCCTCCCCGT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    17  TCAAAATGGAGGCCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG      76
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  CCTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCACCCTTATGACTCAACAGCAGATGT   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    77  CCTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCACCCTTATGACTCAACAGCAGATGT   136

Qy   121  CTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTCTTGTTCTTCTTGAAGAATGCAGTC     180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   137  CTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTCTTGTTCTTCTTGAAGAATGCAGTC     196

Qy   181  AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA      240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   197  AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA      256

Qy   241  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG    300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   257  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG    316

Qy   301  GTTGTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG     360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   317  GTTGTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG     376

Qy   361  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTCATTTTTTGAGG     420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   377  CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTCATTTTTTGAGG     436

Qy   421  AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT      480
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Db   437  AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGATCCCCAATTACAGTATGCCT      496

Qy   481  TTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT    540
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Db   497  TTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT    556

Qy   541  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG    600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   557  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG    616

Qy   601  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC    660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   617  AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC    676

Qy   661  CTGAGACATTCTCGTTGACCGGCACAGGACACATCAAGCTGCTGTGGATTTTGGATCTGCCG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   677  CTGAGACAATTCTCGTTGACCGGCACAGGACACATCAAGCTGCTGTGGATTTTGGATCTGCCG  736

Qy   721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA    780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   737  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA    796

Qy   781  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT     840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   797  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT     856

Qy   841  GTGACTGGTGGTCAGTGGGCCGGGCGATTGCCTATGAGCATGATGATTATGGGAGATCCCCTCG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   857  GTGACTGGTGGTCAGTGGGCCGGGCGATTGCCTATGAGCATGATGATTATGGGAGATCCCCTTCG  916

Qy   901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT    960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   917  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT    976

Qy   961  TTCCAGATGACCCCAAAGTGAGCGAGCAGTGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   977  TTCCAGATGACCCCAAAGTGAGCGAGCAGTGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1036

Qy  1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTGCTCCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1037  GCCAGAAAGAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTGCTCCTAAAATTG 1096

Qy  1081  ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG   1140
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Db  1097  ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG   1156
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Db  1397  AGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTCCTTGCTCCAGGATCCTCCCGT    1456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441  CCGTATATGCCAAGGGGATCCGCCCGGGGGCCGCTGCTGGCTC                   1481
          ||||||||||||||||||||||||||||||||||||||||||
Db  1457  CCGTATATGCCAAGGGGATCCGCCCGGGGGCCGCTGCTGGCTC                   1497
```

RESULT 3
AD040591
ID   AD040591 standard; cDNA; 1515 BP.
XX
AC   AD040591;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Kinase; rho/rac-interacting citron kinase; drug screening;
KW   kinase related disorder; human; chromosome 12; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   5'UTR   1..6
FT   /tag= a
FT   CDS   7..1500
FT   /tag= b
FT   /product= "Human kinase protein"
FT   3'UTR   1501..1515
FT   /tag= c
XX
PN   US2004091993-A1.
XX
PD   13-MAY-2004.
XX
PF   02-DEC-2003; 2003US-00724594.
XX
PR   13-MAR-2001; 2001US-00804471.
PR   11-SEP-2002; 2002US-00238709.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2004-374957/35.
DR   P-PSDB; AD040592.
XX
PT   New isolated human kinase proteins and nucleic acids, useful for
PT   developing human therapeutic targets, identifying therapeutic proteins or
PT   serve as targets for the development of human therapeutic agents that
PT   modulate kinase activity.
XX
PS   Claim 4; SEQ ID NO 1; 207pp; English.
XX
CC   The present invention provides a kinase polypeptide and its encoding
CC   polynucleotide. The polypeptide and polynucleotide of the invention are
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents that modulate kinase activity in
CC   cells and tissues that express the kinase. The invention is also useful
CC   for biological assays related to kinases, in drug screening assays, for
CC   treating disorders characterized by an absence of inappropriate and
CC   unwanted expression of the protein. The present sequence is human kinase
CC   cDNA. The human kinase gene is located on chromosome 12.
XX
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match   100.0%; Score 1481; DB 12; Length 1515;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1  TCAAAATGGAGGCCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG      60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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XX
CC   The present sequence encodes a human citron rho/rac-interacting kinase-
CC   short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
CC   associated with the polypeptide dysfunction. The expression vector or the
CC   reagent is useful in the preparation of a medicament for modulating the
CC   activity of a human citron rho/rac-interacting kinase-short kinase in a
CC   disease, such as obesity or chronic obstructive pulmonary disease. These
CC   may also be used for treating obesity/ overweight-associated
CC   comorbidties, such as hypertension, diabetes, coronary artery disease,
CC   hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC   apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced
CC   fertility, and depression
XX
SQ   Sequence 1765 BP; 428 A; 430 C; 444 G; 463 T; 0 U; 0 Other;

Query Match
Best Local Similarity   99.8%;   Score 1477.8;   DB 10;   Length 1765;
                        99.9%;   Pred. 0;
Matches 1479;   Conservative   0;   Mismatches   2;   Indels   2;   Gaps   0;

Qy   1 TCAAAATATGGAGCGCGGAATCCTTTGATGCGTGCTGCTGCGAACCCATTGCCAACCCGGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   11 TCAAAATATGGAGCGCGGAATCCTTTGATGCGTGCTGCTGCGAACCCATTGCCAGCCCGGG   70

Qy   61 CCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 CCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCGTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCGTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy   241 TAGCTGAGTTACAGGAGCTCAGTGTGCAGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCAGTGTGCAGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG 310

Qy   301 GTTGTTGGTCACTTTGCTGAAGTGCAGTGGTGAGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTTGGTCACTTTGCTGAAGTGCAGTGGTGAGTGGTAAGAGAGAAAGCAACCGGGGACATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGCAGGTTCATTTTTTGAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACAGCAGGTTCATTTTTTGAGG 430

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCTTTATCTGCATGGAATATCAGCCTGAGGGGACTTGCTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGCATGGAATATCAGCCTGAGGGGACTTGCTGT 550

Qy   541 CACTTTTGAATAGATGATGAGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGATGATGAGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy   601 AGCTGATTTTGGCTGTTCACAGCGTCATCTGATGGGATACGTGCATCTGAGACATCAAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTTGGCTGTTCACAGCGTCATCTGATGGGATACGTGCATCTGAGACATCAAGC 670

Qy   661 CTGAGAACATTCGTGACCTGCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCGTGACCTGCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTGGACACCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTGGACACCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGACGGGATGAAAAGGCACCTACGGCCTGGACT 840

RESULT 4
AB268726
ID   AB268726 standard; DNA; 1765 BP.
XX
AC   AB268726;
XX
DT   16-MAY-2003 (first entry)
XX
DE   Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1494
FT   /tag= a
FT   /product= "citron rho/rac-interacting kinase-short
FT   kinase"
XX
PN   WO2003004629-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
PR   25-APR-2002; 2002US-0375015P.
XX
PA   (FARB) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   P-PSDB; ABP97687.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 18; 145pp; English.

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216

Qy   1201 TGAGCCCTCAGGCTTCTCGGTGAGAACTGCCGTTGTGGGGTTTTCGTACAGCAAGG 1260
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCAGGCTTCTCGGTGAGAACTGCCGTTGTGGGGTTTGTACAGCAAGG 1276

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCCCCTGCCAAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGAAAGAAAACTTCTCATCAAAGACAAAGAGCTACAAGACTCTCAGGACA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGAAAGAAAACTTCTCATCAAAGACAAAGAGCTACAAGACTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTATTTCCGCAGCCGCCTTCCTTCCGTTCCTCCGGATCCTCCCGT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397 AGTGTCACAAGGTATTATTTCCGCAGCCGCCTTCCTTCCGTTCCTCCGGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGATCCGCCCGGGGGCCGCTGCCGGCTC 1481
          ||||||||||||||||||||||||||||||||||||||||||
Db   1457 CCGTATATGCCAAGGGATCCGCCCGGGGGCCGCTGCCGGCTC 1497

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Db         ||||||||||||||||
       791 TGGCTCCTGAAGTGCTGACTGGGCGTGATGAACGGGATGGAGATGATTTATGGAGATCCCCTTCG 850
Qy     841 GTGACTGTGGTGGTGGGCGTGATTGCCTATGAGATGATTTATGGAGATCCCCTTCG 900
           ||||||||||||||||
Db     851 GTGACTGTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGAGATCCCCTTCG 910
Qy     901 CAGAGGGAACCTCTGCCAGACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
           ||||||||||||||||
Db     911 CAGAGGGAACCTCTGCCAGACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 970
Qy     961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCGATTCAAAGCTTGTGTGCG 1020
           ||||||||||||||||
Db     971 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCGATTCAAAGCTTGTGTGCG 1030
Qy    1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCGCCATCCTTCTTCTTCTAAAATTG 1080
           ||||||||||||||||
Db    1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCGCCATCCTTCTTCTTCTAAAATTG 1090
Qy    1081 ACTGGAACAACATTCGTAACTTCCTCCCCCTTGTTCCCACCCTCAAGTTCCGACGATG 1140
           ||||||||||||||||
Db    1091 ACTGGAACAACATTCGTAACTTCCTCCCCCTTGTTCCCACCCTCAAGTTCGACGATG 1150
Qy    1141 ACACCTTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
           ||||||||||||||||
Db    1151 ACACCTTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210
Qy    1201 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGGGATTTCGTACAGACAAGG 1260
           ||||||||||||||||
Db    1211 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGGGATTTCGTACAGACAAGG 1270
Qy    1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
           ||||||||||||||||
Db    1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1330
Qy    1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGACTACAAGAGCTACAAGAGACTCTCAGGACA 1380
           ||||||||||||||||
Db    1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGACTACAAGAGCTACAAGAGACTCTCAGGACA 1390
Qy    1381 AGTGTCACAAGGTATTTATTTCCGCACCGGCCTCCTCCTTGCCTCCAGGATCCTCCCGT 1440
           ||||||||||||||||
Db    1391 AGTGTCACAAGGTATTTATTTCCGCACCGGCCGCCTCCTTGCCTCCAGGATCCTCCCCGT 1450
Qy    1441 CCGTATATGCCAAGGGGATCCGGCCCGGGGCCCGCTGCTGGCTC 1481
           ||||||||||||||||
Db    1451 CCGTATATGCCAAGGGGATCCGGCCCGGGGCCGCTGCTGGCTC 1491
```

RESULT 5
AAD26454
ID   AAD26454 standard; cDNA; 2066 BP.
XX
AC   AAD26454;
XX
DT   26-MAR-2002 (first entry)
XX
DE   Human kinase PKIN-7 cDNA.
XX
KW   Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;
KW   Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   14..1507
FT   /*tag= a
FT   /product= "Human PKIN-7 protein"
XX
PN   WO20196547-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX
PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
PI   Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
PI   Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
PI   Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI   Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI   Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX
DR   WPI; 2002-090207/12.
DR   P-PSDB; AAB16261.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.
XX
PS   Claim 5; Page 180-181; 197pp; English.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-7 cDNA
XX
SQ   Sequence 2066 BP; 515 A; 497 C; 516 G; 538 T; 0 U; 0 Other;

Query Match   99.7%; Score 1476.2; DB 6; Length 2066;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1478; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGTGCTGGTGCGTGTCGGTGAACCCATTGCGAACCCATTGCCAACCGGG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGTGCTGGTGCGTGTCGGTGAACCCATTGCCAACCGGG   83
Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCTTTATGACTCAACAGCAGATGT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 143
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Qy    121  CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144  CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC  203

Qy    181  AGCCTGCTCTGATGAAGATAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204  AGCCTGCTCTGATGAAGATAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  263

Qy    241  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG  323

Qy    301  GTTGTGGTCACTTGCTGAAGTGCAGGTGTAAGAGAGAAGCAACCGGGACATCTATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324  GTTGTGGTCACTTGCTGAAGTGCAGGTGTAAGAGAGAAGCAACCGGGACATCTATG  383

Qy    361  CTATGAAAGTGATGAAGACATATTATCTCGAAGGACAAGCCCGTGGATCCCCAATTACAGTATGCCT  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384  CTATGAAAGTGATGAAGACATATTATCTCGAAGGACAAGCCCGTGGATCCCCAATTACAGTATGCCT  443

Qy    421  AAGAGCGGAACATATTATCTCGAAGGACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444  AAGAGCGGAACATATTATCTCGAAGCACAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  503

Qy    481  TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    504  TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  563

Qy    541  CACTTTTGAATAGATAGATGAGGACCAGTTAGTAGAGTGAAAACCTGATACAGTTTTACCTAGCTG  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    564  CACTTTTGAATAGATAGATGAGGACCAGTTAGTAGAGTGAAAACCTGATACAGTTTTACCTAGCTG  623

Qy    601  AGCTGATTTTGGCTGTGTTCACAGCGGTTCATCTGATGGATACGTGCATCGAGACATCAAGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    624  AGCTGATTTTGGCTGTGTTCACAGCGGTTCATCTGATGGATACGTGCATCGAGACATCAAGC  683

Qy    661  CTGAGAACATTCTCGTTGACCGGCACCAGGACACATCAAGCTGGTGTGGATTTGGATCTGCCG  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    684  CTGAGAACATTCTCGTTGACCGGCACCAGGACACATCAAGCTGGTGTGGATTTGGATCTGCCG  743

Qy    721  CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744  CGAAAATGAATTCAAACAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  803

Qy    781  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCGTGGACT  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCGTGGACT  863

Qy    841  GTGACTGGTGTGCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864  GTGACTGGTGTGCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  923

Qy    901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT  983

Qy    961  TTCCAGATGACCCCAAAGTGAGACTGAGCAGTGACACTTCTCAAAAGCTTGTGTGTGCG  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984  TTCCAGATGACCCCAAAGTGAGACTGAGCAGTGACACTTCTCAAAAGCTTGTGTGTGCG  1043

Qy   1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTCTTCTTCTCTAAAATTG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTCTTCTTCTCTAAAATTG  1103

Qy   1081  ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104  ACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1163

Qy   1141  ACACCTCCAATTTTGATGAACCAGGAAGAGAATTCGTGGGGTTCATCCTCCGTGCCGCAGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164  ACACCTCCAATTTTGATGAACCAGGAAGAGAATTCGTGGGGTTCATCCTCCGTGCCGCAGC  1223

Qy   1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGTGGGGTTTTGTGTACAGCAAGG  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGTGGGGTTTTGTGTACAGCAAGG  1283

Qy   1261  CACTGGGGATTCTTGGTAGATCTGAGTCGTGTTCGTGTCGGGGTCTGGACTCCCTGCCAAGA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284  CACTGGGGATTCTTGGTAGATCTGAGTCGTGTTCGTGTCGGGGTCTGGACTCCCCTGCCAAGA  1343

Qy   1321  CTAGCTCCATGAAAAAGAACTTCTCATCAAAGCAAAAGAGTACAGAGACTTCAGGACA  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344  CTAGCTCCATGAAAAAGAACTTCTCATCAAAGCAAAAGAGTACAAGAGACTTCAGGACA  1403

Qy   1381  AGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTCCTTCCTTCCAGGATCCTCCCGTT  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404  AGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTCCTTCCTTCCAGGATCCTCCCCGT  1463

Qy   1441  CCGTATATGCCAAGGGATCCGCCCGGGCCCGGCCTGCTGGCTC  1481
           |||||||||||||||||||||||||||||||||||||||||||
Db   1464  CCGTATATGCCAAGGGATCCGCCCGGGCCGCCTGCTGGCTC  1504
```

RESULT 6

```
ABZ68725
ID   ABZ68725    standard; DNA; 1485 BP.
XX
AC   ABZ68725;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..1485
FT                  /*tag= a
FT                  /partial
FT                  /product= "citron rho/rac-interacting kinase-short
FT                  kinase"
XX
PN   WO200304629-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
PR   25-APR-2002; 2002US-0375015P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   P-PSDB; ABP97681.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 1; 145pp; English.
XX
CC   The present sequence encodes a human citron rho/rac-interacting kinase-
CC   short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
CC   associated with the polypeptide dysfunction. The expression vector or the
```

```
CC   reagent is useful in the preparation of a medicament for modulating the
CC   activity of a human citron rho/rac-interacting kinase-short kinase in a
CC   disease, such as obesity or chronic obstructive pulmonary disease. These
CC   may also be used for treating obesity/ overweight-associated
CC   comorbidities, such as hypertension, diabetes, coronary artery disease,
CC   hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC   apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced
CC   fertility, and depression
XX
SQ   Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;

Query Match             99.4%;  Score 1471.8;  DB 10;  Length 1485;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1473;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG   60
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||
Db     11 TCAAATATGGACGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG   70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy    121 CTCCTCTTCCCGAGAGGGATATTAGTAGATGCCCTCTTGTCTCTTTGAAGAAATGCAGTC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTCCCGAGAGGGATATTAGTAGATGCCCTCTTGTCTCTTTGAAGAAATGCAGTC  190

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAGTATTCCGACACCA   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCGGGAGTATTCCGACACCA   250

Qy    241 TAGCTGAGTTACAGGAGACTTCGGCAAGGACTTCGGCAAGACTCAGAAGTCTTGTAG   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TAGCTGAGTTACAGGAGACTTCGGCAAGGACTTCGGCAAGACTCAGAAGTCTTGTAG   310

Qy    301 GTTGTGTGGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAGAGAACCAACCGGG   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGTGGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAGAGAACCAACCGGG   370

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCTTTCATTTTTTGAGG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGGCTTTCATTTTTTGAGG   430

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  550

Qy    541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  610

Qy    601 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  670

Qy    661 CTGAGGAACATTCTCGTTGACCGACCAGGACACACAAGCTGGTGGATTTTGGATCTGCCG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGGAACATTCTCGTTGACCGACCAGGACACACAAGCTGGTGGATTTTGGATCTGCCG  730

Qy    721 CGAAAATGAATTCAAACAAGAGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 CGAAAATGAATTCAAACAAGAGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACA  790

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT  850

Qy    841 GTGACTGGTGGTCAGTGGCGCTGAGTTGCCTATGAGATGAGATGATTTATGGGAGATCCCCCTTCG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GTGACTGGTGGTCAGTGGCCGTGAGTTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  910

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  970

Qy    961 TTCCAGATGACCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 TTCCAGATGACCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCGCCATCCTTTCTTCTCTAAAATTG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCGCCATCCTTTCTTCTCTAAAATTG 1090

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCACCCTTCAAGTCCGACGATG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCACCCTTCAAGTCCGACGATG 1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTGTGGGTTTTGTACAGCAAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTGTGGGTTTTGTACAGCAAGG 1270

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGGTGTGTCTGGGGTCTGGACTCCCCTGCCAAGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGGTGTGTCTGGGGTCTGCGGACTCCCCTGCCAAGA 1330

Qy   1321 CTAGCTCCATGAAAGAAACTTCTCATCAAAAGCAAAGACTTCAGACACTCTCAGGACA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 CTAGCTCCATGAAAGAAACTTCTCATCAAAAGCAAAGACAAAGACTTCAGACACTCTCAGGACA 1390

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCGTCCTTCCTGCTCCTGCGTCCTCCTTCCCGT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1391 AGTGTCACAAGGTATTTATTTCCGCAGCCGTCCTTCCTGCTCCTGCGTCCTCCTTCCCGT 1450

Qy   1441 CCGTATATGCCAAGGATCCGGGGGCCCGTGC 1475
          |||||||||||||||||||||||||||||||
Db   1451 CCGTATATGCCAAGGATCCGGGGGCCCGTGC 1485


RESULT 7
ADA05643
ID   ADA05643  standard; cDNA; 1870 BP.
XX
AC   ADA05643;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human NOV1b encoding cDNA SEQ ID NO:3.
XX
KW   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW   immunomodulator; cytostatic; nootropic; neuroprotective;
KW   antiparkinsonian; antilipaemic; gene therapy; human disease;
KW   metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2..1870
FT                   /tag= a
FT                   /product= "NOV1b"
XX
PN   WO2003029424-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031373.
XX
```

CC   and antilipaemic activities, and can be used in gene therapy. The
CC   polypeptide is useful in manufacturing a medicament for treating a
CC   syndrome associated with a human disease. The polypeptide or the nucleic
CC   acid molecule may be used to diagnose, treat or prevent metabolic
CC   disorders such as diabetes or obesity, infections, cachexia, cancer,
CC   neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC   disease, immune disorders, haematopoietic disorders and various
CC   dyslipidaemias. The nucleic acids can also be used as hybridisation
CC   probes, in chromosome mapping, tissue typing, preventive medicine and
CC   pharmacogenomics. The present sequence encodes a human NOVX protein from
CC   the present invention.
XX
SQ   Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

Query Match   93.7%; Score 1388.2; DB 8; Length 1870;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1390;   Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 83

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATGACTCAACAGCAGATGT 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATGACTCAACAGCAGATGT 143

Qy   121 CTCCTCTTCCCGAGAGAGGATATTAGATAGATGCCCTCTTCTTTGTTCTCTTTGAAGAATGCAGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 CTCCTCTTCCCGAGAGAGGATATTAGATAGATGCCCTCTTCTTTGTTCTCTTTGAAGAATGCAGTC 203

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 263

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 323

Qy   301 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAGAAGCAACCGGGGACATCTATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAGAAGCAACCGGGGACATCTATG 383

Qy   361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCATTTTTGAGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCATTTTTGAGG 443

Qy   421 AAGAGCGGACATATATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 AAGAGCGGACATATATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT 503

Qy   481 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 563

Qy   541 CACTTTGAATAGATATGAGGACCAGTAGATGAAACCTGATACAGTTTACCTAGCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 CACTTTGAATAGATATGAGGACCAGTAGATGAAACCTGATACAGTTTACCTAGCTG 623

Qy   601 AGCTGATTTTGGCTGTTCATCTGATGGGATAGTGCATGGAGACATCAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 AGCTGATTTTGGCTGTTCATCTGATGGGATAGTGCATGGAGACATCAAGC 683

Qy   661 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGCGTGGATTTTGGATCTGCCG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 CTGAGAACATTCGTTGACCGCACAGGACACATCAAGCTGCGTGGATTTTGGATCTGCCG 743

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   744 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA 803

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT 863

PR   02-OCT-2001;   2001US-0326483P.
PR   05-OCT-2001;   2001US-0327435P.
PR   05-OCT-2001;   2001US-0327449P.
PR   09-OCT-2001;   2001US-0327917P.
PR   09-OCT-2001;   2001US-0328029P.
PR   09-OCT-2001;   2001US-0328044P.
PR   09-OCT-2001;   2001US-0328056P.
PR   12-OCT-2001;   2001US-0328849P.
PR   15-OCT-2001;   2001US-0329414P.
PR   17-OCT-2001;   2001US-0330142P.
PR   18-OCT-2001;   2001US-0330309P.
PR   22-OCT-2001;   2001US-0341058P.
PR   24-OCT-2001;   2001US-0339266P.
PR   24-OCT-2001;   2001US-0343629P.
PR   29-OCT-2001;   2001US-0349575P.
PR   01-NOV-2001;   2001US-0346357P.
PR   17-APR-2002;   2002US-0373260P.
PR   19-APR-2002;   2002US-0373815P.
PR   19-APR-2002;   2002US-0373817P.
PR   19-APR-2002;   2002US-0373826P.
PR   19-APR-2002;   2002US-0373884P.
PR   22-APR-2002;   2002US-0374977P.
PR   16-MAY-2002;   2002US-0381037P.
PR   16-MAY-2002;   2002US-0381038P.
PR   16-MAY-2002;   2002US-0381042P.
PR   17-MAY-2002;   2002US-0381642P.
PR   28-MAY-2002;   2002US-0386556P.
PR   29-MAY-2002;   2002US-0383831P.
PR   25-JUN-2002;   2002US-0391335P.
PR   01-OCT-2002;   2002US-00262511
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI   Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI   Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI   Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI   Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR   WPI; 2003-381626/36.
DR   P-PSDB; ADA05644.
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT   preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT   cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 20; Page 100; 586pp; English.
XX
CC   The present invention describes NOVX proteins, where X can be 1 to 55
CC   (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC   described above and a carrier; (2) a kit comprising, in one or more
CC   containers, the composition described above; (3) an isolated nucleic acid
CC   molecule which encodes a NOVX protein of the invention; (4) a vector
CC   comprising the nucleic acid molecule described above; (5) a cell
CC   comprising the above vector; (6) an antibody that immunospecifically
CC   binds to the polypeptide described above; (7) methods for determining the
CC   presence or amount of the above polypeptide or nucleic acid molecule in a
CC   sample; (8) methods for determining the presence of or predisposition to
CC   a disease associated with altered levels of expression of the above
CC   polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC   method of identifying an agent that binds to the polypeptide described
CC   above; (10) a method for identifying a potential therapeutic agent for
CC   use in treating a pathology that is related to an aberrant expression or
CC   aberrant physiological interactions of the polypeptide; (11) a method of
CC   screening for a modulator of activity or of latency or predisposition to
CC   a pathology associated with the polypeptide; (12) a method for modulating
CC   the activity of the polypeptide described above; (13) methods of treating
CC   or preventing a pathology associated with the above polypeptide in a
CC   mammal; and (14) a method for producing the above polypeptide. NOVX
CC   sequences have antidiabetic, anorectic, antibacterial, virucide,
CC   immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian

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PI   Yu X, Miranda M, Friddle CJ;
XX
DR   WPI; 2002-599796/64.
DR   P-PSDB; ABB81928.
XX
PT   Novel polynucleotide encoding human proteins that are structurally
PT   similar to animal kinases, useful for drug screening, diagnosis, in gene
PT   therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT   applications.
XX
PS   Disclosure; Page 44-45; 50pp; English.
XX
CC   The invention relates to a novel human protein that shares structural
CC   similarity with animal kinases, including serine-threonine kinases,
CC   particularly Citron rho-interacting kinases. The proteins of the
CC   invention have nootropic and cytostatic activity. The polynucleotides may
CC   have a use in gene therapy. The encoded novel polypeptides are useful for
CC   generating antibodies, as reagents in diagnostic assays, for identifying
CC   other cellular gene products related to NHP and as reagents in assays for
CC   screening for compounds that are useful in the treatment of mental,
CC   biological or medical disorders and diseases including cancer. The
CC   sequence encodes a novel human kinase of the invention
XX
SQ   Sequence 5877 BP; 1680 A; 1433 C; 1583 G; 1181 T; 0 U; 0 Other;

Query Match            93.7%;  Score 1388.2;  DB 6;  Length 5877;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 1390;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    .1 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCGAACCACCGGG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCGAACCACCGGG   70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCACCCTTATGACTCAACAGCAGATGT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCACCCTTATGACTCAACAGCAGATGT  130

Qy   121 CTCCTCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTGTCTCTTTGAACAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   131 CTCCTCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTGTCTCTTTGAAGAATGCAGTC  190

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAGTATTCCGACACCA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAGTATTCCGACACCA  250

Qy   241 TAGCTGAGTTACAGGAGCTCAAGCTTCGGCGAAGACTTCGAAGTCAGAAGTCTTGTAG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCGAAGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy   301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG  370

Qy   361 CTATGAAAGTGATGATGAAGAAGAAGGCTTATTGGCCAGGAGGACAAGCAGGTTTTTGAGG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGATGAAGAAGAAGGCTTATTGGCCAGGAGGACAAGCAGGTTTTTGAGG  430

Qy   421 AAGAGCGGAACATATTATCTCGAAGGACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATTATCTCGAAGGACAACAAGCCCGTGGATCCCCAATTACAGTATGCCT  490

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGTCATGGAATATCAGCTGTGCTGT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGTCATGGAATATCAGCTGTGCTGT  550

Qy   541 CACTTTTGAATAGATATGAGGAGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATAGATATGAGGAGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG  610

Qy   601 AGCTGGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  670
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Qy   841 GTGACTGGTGGTCAGTGGGCGTGATGTGCCATGAGATGATTTATGGAGATCCCCCTTCG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   864 GTGACTGGTGGTCAGTGGGCGTGATGTGCCATGAGATGATTTATGGAGATCCCCCTTCG  923

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT  983

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTCTTGATCTGATTCAAAGCTTGTGTGCG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   984 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTCTTGATCTGATTCAAAGCTTGTGTGCG 1043

Qy  1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTCTTCCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1044 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTCTTCCTAAAATTG 1103

Qy  1081 ACTGGAACAACATTGTAACTCTCTCCCCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1104 ACTGGAACAACATTGTAACTCTCTCCCCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG 1163

Qy  1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1164 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1223

Qy  1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGGGGTTTCGTACAGCAAGG 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTTGTGGGGTTTCGTACAGCAAGG 1283

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTTGTGTGTCGGGTCTCGACTCCCCTGCCAAGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1284 CACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTTGTGTGTCGGGTCTCGACTCCCCTGCCAAGA 1343

Qy  1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGAGCTACAAGAGACTTCTCAGGACA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1344 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGAGCTACAAGAGACTTCTCAGGACA 1403

Qy  1381 AGTGTCACAAGGT 1393
         ||||||||||| |
Db  1404 AGTGTCACAAGAT 1416
```

```
RESULT 8
ABQ78871
ID   ABQ78871 standard; cDNA; 5877 BP.
XX
AC   ABQ78871;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human kinase cDNA #2.
XX
KW   Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
KW   Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..5877
FT                  /*tag= a
FT                  /product= "Kinase"
XX
PN   WO200259325-A2.
XX
PD   01-AUG-2002.
XX
PF   20-DEC-2001; 2001WO-US050497.
XX
PR   27-DEC-2000; 2000US-0258335P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
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XX
PN WO2003004523-A1.
XX
PD 16-JAN-2003.
XX
PF 28-JUN-2002; 2002WO-EP007156.
XX
PR 02-JUL-2001; 2001US-0301841P.
PR 11-DEC-2001; 2001US-0338651P.
PR 25-APR-2002; 2002US-0375014P.
XX
PA (FARB) BAYER AG.
XX
PI Zhu Z;
XX
DR WPI; 2003-221576/21.
XX
PT New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT polynucleotide, useful in preventing, ameliorating or treating diseases
PT associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT Alzheimer's disease.
XX
PS Disclosure; Page 217-222; 237pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a human
CC citron rho/rac-interacting kinase polypeptide. The isolated
CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC specification. The human citron rho/rac-interacting kinase (CRIK)
CC polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC treating diseases associated with human CRIK dysfunction such as obesity
CC and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC cancer including endometrial, breast, prostate and colon cancer),
CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC disease), chronic obstructive pulmonary disease, or diabetes. These can
CC also be used to treat pain associated with the disorders. The human CRIK
CC polypeptide is also useful in diagnostic assays or in genetic testing.
CC The expression vector or the reagent is useful in preparing a medicament
CC for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC central nervous system disorder, or chronic obstructive pulmonary
CC disease. The fusion protein is useful for generating antibodies against a
CC CRIK polypeptide and for use in various assay systems. The methods are
CC useful in producing and detecting the polynucleotide and polypeptide and
CC in screening for agents that modulate the activity of the human CRIK
CC polypeptide. This polynucleotide sequence represents a DNA sequence
CC relating to the human CRIK protein of the invention
XX
SQ Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

Query Match   93.7%;   Score 1388.2;   DB 9;   Length 6156;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1390;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy     1 TCAAATATGGAGCGCGGAATCCTTGAATGCTGGTGCTGCGAACCCATTGCCAACCCGGG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    11 TCAAATATGGAGCGCGGAATCCTTGAATGCTGGTGCTGCGAACCCATTGCCAGCCCGGG   70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCACCCTTTATGACTCAACAGCAGATGT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCACCCTTTATGACTCAACAGCAGATGT  130

Qy   121 CTCCTCCTTCCCGAGAGGGATATTAGAATGCCCTTCGTTGTTCTCTTTGAAGAATGCAGTC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCCTTCCCGAGAGGGATATTAGAATGCCCTTCGTTGTTCTCTTTGAAGAATGCAGTC  190

Qy   181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  250

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG  310
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Qy   661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGATTTTGGATCTGCCG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGATTTTGGATCTGCCG  730

Qy   721 CGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA  790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT  850

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATCATTATGATTTCCAGCGGTTTTGAAAT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATCATTATGATTTCCAGCGGTTTTGAAAT  970

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGACAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTGCG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGACCCCAAAGTGAGCAGTGACAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTGCG 1030

Qy  1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTCTCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTCTCTAAAATTG 1090

Qy  1081 ACTGAACAACATTCGTAACTCTCTCCCCCCTTCGTTCCACCCTCAGTCCGACGATG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091 ACTGAACAACATTCGTAACTCTCTCCCCCCTTCGTTCCACCCTCAGTCCGACGATG 1150

Qy  1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCCCGTGCCAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCCCGTGCCAGC 1210

Qy  1201 TGAGCCCCTCCAGGCTTCTCCGGGTGAAGAACTGCCGTTGTGGGGTTTCTCTACAGCAAGG 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211 TGAGCCCCTCCAGGCTTCTCCGGGTGAAGAACTGCCGTTGTGGGGTTTCTCTACAGCAAGG 1270

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCCCCTGCCAAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCCCCTGCCAAGA 1330

Qy  1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGACTCTCAGGACA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGACTCTCAGGACA 1390

Qy  1381 AGTGTCACAAGGT 1393
         |||||||||||
Db  1391 AGTGTCACAAGAT 1403
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RESULT 9
AAL55217
ID AAL55217 standard; DNA; 6156 BP.
XX
AC AAL55217;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human CRIK related DNA sequence, SEQ ID No 8.
XX
KW Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW central nervous system disorder; chronic obstructive pulmonary disease;
KW diabetes; pain; ds.
XX
OS Homo sapiens.

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Db    11 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCGCGGG 70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCTTTCCGAGAAGGGATATTAGATGCCCTTCTTTGTTCTCTTTGAAGAATGCAGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTTCCGAGAAGGGATATTAGATGCCCTTCTTTGTTCTCTTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTTGTCCGGAAGTATTCCGACACCA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTTGTCCGGAAGTATTCCGACACCA 250

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy   301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTGTAAGAGAGAAGCACCGGGACAATCTATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTGTAAGAGAGAAGCACCGGGACAATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 430

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy   541 CACTTTGAATAGATAGAGGACCAGTTAGTGATGAAAACCTGATACAGTTTTACCTAGCTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTGAATAGATAGAGGACCAGTTAGTGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy   601 AGCTGATTTGGCTGTTCACAGCGGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTGGCTGTTCACAGCGGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy   661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATCTGCCG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATCTGCCG 730

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGACTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGACTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 850

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCCATGAGATGATTTATGGGAGATCCCCCTTCG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCGTGATTGCCCATGAGATGATTTATGGGAGATCCCCCTTCG 910

Qy   901 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTCCAGCCGGTTTTTGAAAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTCCAGCCGGTTTTTGAAAT 970

Qy   961 TTCCAGATGACCCCAAAGTGACGAGCAGTGACTTTCTTGATTCTGATTCAAAGCTTGTTGTGCG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGACCCCAAAGTGACGAGCAGTGACTTTCTTGATTCTGATTCAAAGCTTGTTGTGCG 1030

Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCCTAAAATTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCCTAAAATTG 1090

Qy  1081 ACTCGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091 ACTCGGAACAACATTCGTAACTCTCCTCCCCCCTCGTTCCCACCCTCAAGTCCGACGATG 1150

Qy  1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy  1201 TGAGCCCCTGCAGGCTTCTCGGGTGGAGAACTGCCGGTTTGTGGGGTTTGTACAGCAAGG 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211 TGAGCCCCTGCAGGCTTCTCGGGTGGAGAACTGCCGGTTTGTGGGGTTTGTACAGCAAGG 1270

Qy  1261 CACTGGGGATTCTTGGTAGATCGAGTCGAGTGTGTCGGGTCGACTCCCTGCCAAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1271 CACTGGGGATTCTTGGTAGATCGAGTCGAGTGTGTCGGGTCGACTCCCTGCCAAGA 1330

Qy  1321 CTAGCTTCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAAGACTTCAGGACA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1331 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAAGACTTCAGGACA 1390

Qy  1381 AGTGTCACAAGT 1393
         ||||||||||||
Db  1391 AGTGTCACAAGAT 1403
```

RESULT 11
AAL55214
ID   AAL55214 standard; DNA; 6165 BP.
XX
AC   AAL55214;
XX
DT   01-MAY-2003 (first entry)
XX
DE   Human CRIK encoding DNA sequence, SEQ ID No 1.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cyostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   diabetes; pain; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..6165
FT   /*tag= a
FT   /product= "Human CRIK protein"
XX
PN   WO2003004523-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0338651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
DR   P-PSDB; AAO26959.
XX
PT   New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Example 1; Fig 1; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human

CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho/rac-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This polynucleotide sequence represents a DNA sequence
CC   encoding a human CRIK protein of the invention
XX
SQ   Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

Query Match   93.7%;   Score 1388.2; DB 9;   Length 6165;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1390;   Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 TCAAATATGGAGCGGCGGAATCCTTGGATGCTGCTGTGCTGCTGAACCCATTGCCAACCGGG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11 TCAAATATGGAGCGGCGGAATCCTTGGATGCTGCTGTGCTGCTGAACCCATTGCCAGCCGGG 70

Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCTTCCCGAGAAGGAGATATTAGATGCCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCTTCCCGAGAAGGAGATATTAGATGCCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCTGATGAAGATTAAGCACGTGAACAACTTGTCCGGAAGTATTCCGACACCA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCTGATGAAGATTAAGCACGTGAACAACTTGTCCGGAAGTATTCCGACACCA 250

Qy   241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy   301 GTTGTGGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAAGAGAGGCTTTATTGGCCCAGGAGCGAGCAGTTTCATTTTTTGAGG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGAGGCTTTATTGGCCCAGGAGCGAGCAGTTTCATTTTTTGAGG 430

Qy   421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGAATCCCCAATTACAGTATGCCT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGAATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT 550

Qy   541 CACTTTTGAATGAATGAGGACCAGTTAGATGAAAACCTTGATACAGTTTACCTAGCTG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTTGAATGAATGAGGACCAGTTAGATGAAAACCTTGATACAGTTTACCTAGCTG 610

Qy   601 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy   661 CTGAGACAATTCGTTGACCGCCACAGGACACATCAAGCTGCTGGGATTTGGATCTGCCG 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGACAATTCGTTGACCGCCACAGGACACATCAAGCTGCTGGGATTTGGATCTGCCG 730

Qy   721 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTCGGGACCCCAGATTACA 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTCGGGACCCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGATGGAAAAGGCACCTACGGCCTGGACT 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGATGGAAAAGGCACCTACGGCCTGGACT 850

Qy   841 GTGACTGGTGGTCAGTGGCGTGATTGCCTATGAGATGATTTATGGGAGATGTCCCCTTCG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGCGGTTTTGAAAT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTTGAAAT 970

Qy   961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCGTGATCTGATTCGATTCAAAGCTTGTTGTGCG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCGATTCAAAGCTTGTTGTGCG 1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTTCTAAAATTG 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTTCTAAAATTG 1090

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGCCCGACGATG 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCTCGACGATG 1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGCGGGTTTTGTGGGGTTTTGTGCGGGT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGCGGGTTTTGTGGGGTTTTGTACAGCAAGG 1270

Qy   1261 CACTGGGGATTCTTGTAGATCTGAGTCTGTGTTGTCGGGTCTGAGACTCCCCTGCCAAGA 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271 CACTGGGGATTCTTGTAGATCTGAGTCTGTGTTGTCGGGTCTGAGACTCCCCTGCCAAGA 1330

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCATCAAAGAAGAGCTACAAAGACTCTCAGGACA 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 CTAGCTCCATGGAAAAGAAACTTCATCAAAGAAGAGCTACAAAGACTCTCAGGACA 1390

Qy   1381 AGTGTCACAAGT 1393
              ||||||||||||
Db   1391 AGTGTCACAAGAT 1403

RESULT 12
AAD38864
ID   AAD38864 standard; cDNA; 6298 BP.
XX
AC   AAD38864;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Human kinase (PKIN) -21 cDNA.
XX
KW   Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
KW   acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW   asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW   development; hepatitis; cardiovascular; hypertension; drug screening;
KW   myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW   fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW   hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-HIV;
KW   neuroprotective; hepatoprotective; hypotensive; cardiant; nephrotropic;
KW   hyperlipidaemia; enzyme; gene; ss.
XX

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             55..6219
FT                   /tag= a
FT                   /product= "Human kinase (PKIN)-21"
XX
PN   WO200233099-A2.
XX
PD   25-APR-2002.
XX
PF   20-OCT-2001; 2001WO-US047728.
XX
PR   20-OCT-2000; 2000US-0242410P.
PR   27-OCT-2000; 2000US-0244068P.
PR   03-NOV-2000; 2000US-0245708P.
PR   09-NOV-2000; 2000US-0247672P.
PR   16-NOV-2000; 2000US-0249565P.
PR   22-NOV-2000; 2000US-0252730P.
PR   01-DEC-2000; 2000US-0250807P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;
PI   Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
PI   Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
PI   Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
PI   Thangavelu K, Khan FA, Ison CH;
XX
DR   WPI; 2002-454603/48.
DR   P-PSDB; AAE24150.
XX
PT   New human kinase polypeptide, for diagnosing, preventing and treating
PT   cancer, immune system disorders, growth and development disorders,
PT   cardiovascular disorders and lipid disorders.
XX
PS   Claim 5; Page 207-209; 210pp; English.
XX
CC   The invention relates human kinases (PKIN) and their corresponding
CC   nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC   treating and preventing cancer, an immune system disorder (e.g., acquired
CC   immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
CC   atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC   growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC   cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC   Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC   Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC   hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC   compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC   condition or a disease associated with the expression of PKIN in a
CC   biological sample. A composition comprising PKIN or an agonist or
CC   antagonist of PKIN is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional PKIN.
CC   PKIN is useful in a number of drug screening techniques and to analyse
CC   the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC   knockin humanised animals or transgenic animals to model human diseases,
CC   and in somatic or germline gene therapy. The present sequence is human
CC   PKIN cDNA
XX
SQ   Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;
```

Query Match   93.7%;   Score 1388.2;   DB 6;   Length 6298;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1390;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy      1 TCAAATATGAGCGCGGGAATCCTTTGGATGCTGGATGCTGCTGAACCCATTGCCAACCGGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 TCAAATATGAGCGCGGGAATCCTTTGGATGCTGGATGCTGCTGAACCCATTGCCAACCGGG  124

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  184
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Qy    121 CTCCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTGTCTCTTGTCTCTTGAGAAATGCAGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 CTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTGTCTCTTGTCTCTTGAGAAATGCAGTC  244

Qy    181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA  304

Qy    241 TAGCTGAGTTACAGGAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 TAGCTGAGTTACAGGAGCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG  364

Qy    301 GTTGTGGTCACTTTGCTGAGGTGCAGGTGGTAAGGAGAGAAAGCAACCGGGACATCTATG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GTTGTGGTCACTTTGCTGAGGTGCAGGTGGTAAGGAGAGAAAGCAACCGGGACATCTATG  424

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGGACGCAGGTTTCATTTTTTGAGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 CTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGGACGCAGGTTTCATTTTTTGAGG  484

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT  544

Qy    481 TTCAGGACAAAAATCACCTTTATCTTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 TTCAGGACAAAAATCACCTTTATCTTGGTCATGGAATATCAGCCTGAGGGGACTTGCTGT  604

Qy    541 CACTTTTGAATAGATATGAGGACCAGTAGATGAAGATGAAAACCTGATACAGTTTACCTAGCTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 CACTTTTGAATAGATATGAGGACCAGTAGATGAAGATGAAAACCTGATACAGTTTACCTAGCTG  664

Qy    601 AGCTGATTTTGGCTGTCACAGCGTTCATCTGATGGGATAGTGCATCGAGACATCAAGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 AGCTGATTTTGGCTGTCACAGCGTTCATCTGATGGGATAGTGCATCGAGACATCAAGC  724

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGGATTTTGGATCTGCCG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGGATTTTGGATCTGCCG  784

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  844

Qy    781 TGGCTCCTGAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGCTCCTGAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGACT  904

Qy    841 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTATGGGAGATCCCCCTTCG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 GTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTATGGGAGATCCCCCTTCG  964

Qy    901 CAGAGGGAACCTCTGCCAGAACCTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CAGAGGGAACCTCTGCCAGAACCTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 1024

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTGATTCAAAGCTTGTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTGATTCAAAGCTTGTGTGCG 1084

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCGCCATCCTTTCTTCTTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCGCCATCCTTTCTTCTTCTAAAATTG 1144

Qy   1081 ACTGAACAACATTCGTAACTCTCCTCCCCCCCCTTCGTTCCACCCTCGTTCCACCCTCAAGTCCGACGATG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 ACTGAACAACATTCGTAACTCTCCTCCCCCCCCTTCGTTCCACCCTCGTTCCACCCTCAAGTCCGACGATG 1204

Qy   1141 ACACCTCCAATTTGATGACCAGAGAAGAGATTCGTGGGTTTCATCCTCCTCCGTGCCAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 ACACCTCCAATTTGATGACCAGAGAAGAGATTCGTGGGTTTCATCCTCCTCCGTGCCAGC 1264

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTGTGTACAGCAAGG 1260
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Db         ||||||||||||||||||||||||||||||
      1265 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAGAAGG 1324
Qy    1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    1325 CACTGGGGATTCTTGGTAGATCTGAGTCGTCGTGTCGGGTCTGGACTCCCCTGCCAAGA 1384
Qy    1321 CTAGTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
           ||||||||||||||||||||||||||||||||||||||||||||
Db    1385 CTAGTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1444
Qy    1381 AGTGTCACAAGT 1393
           ||||||||||||
Db    1445 AGTGTCACAAGAT 1457
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RESULT 13

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AAL55215
ID   AAL55215 standard; DNA; 8603 BP.
XX
AC   AAL55215;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Human CRIK related DNA sequence, SEQ ID No 4.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   diabetes; pain; ds.
XX
OS   Homo sapiens.
XX
PN   WO200304523-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0336651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
XX
PT   New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Disclosure; Fig 4; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human
CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho/rac-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
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CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This polynucleotide sequence represents a DNA sequence
CC   relating to the human CRIK protein of the invention
XX
SQ   Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other;
```

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Query Match             93.7%;  Score 1388.2;  DB 9;  Length 8603;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1390;  Mismatches     0;  Conservative    0;  Indels    3;  Gaps     0;
```

```
Qy     1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCAACCAACCGGG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCAACCAACCGGG 70

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy   121 CTCCTCCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CTCCTCCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 190

Qy   181 AGCCTGCTCGTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGCCTGCTCGTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy   241 TAGCTGAGTTACAGGAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251 TAGCTGAGTTACAGGAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy   301 GTTGTGTGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGGACATCTATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GTTGTGTGTCACTTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGGACATCTATG 370

Qy   361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCCAGGTTCATTTTTTGAGG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCCAGGTTCATTTTTTGAGG 430

Qy   421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTATGCCT 490

Qy   481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 550

Qy   541 CACTTTGAATGATATGAGGACCAGTAGGATGAAAACCTGATACAGTTTTACCTAGCTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 CACTTTGAATGATATGAGGACCAGTAGGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy   601 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy   661 CTGAGAACATTCGTTGACCGGCCACAGGACACATCAAGCTGGTGGGATTTTGGATCTGCCG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 CTGAGAACATTCGTTGACCGGCCACACGACACATCAAGCTGGTGGGATTTTGGATCTGCCG 730

Qy   721 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 850
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Qy    841  GTGACTGGTCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851  GTGACTGGTCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG  910

Qy    901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT    960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT    970

Qy    961  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTCAAAGCTTGTTGTGCG    1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTCAAAGCTTGTTGTGCG    1030

Qy   1021  GCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCCTTCTAAAATTG  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031  GCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCCTTCTAAAATTG  1090

Qy   1081  ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1091  ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAGTCTGACGATG  1150

Qy   1141  ACACCTCCAATTTGATGAACCAGACCAGAGAGAATTCGTGGGGTTCATCCTCTCCGTGCCAGC  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151  ACACCTCCAATTTGATGAACCAGACCAGAGAGAATTCGTGGGGTTCATCCTCTCCGTGCCAGC  1210

Qy   1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGG  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGG  1270

Qy   1261  CACTGGGGATTCTTCGTAGATCTGAGTCTCGTGTGTCGGGGTCTGACTCCCCTGCCAAGA  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271  CACTGGGGATTCTTCGTAGATCTGAGTCTCGTGTGTCGGGGTCTGACTCCCCTGCCAAGA  1330

Qy   1321  CTAGCTCCATGGAAAAGAAACTTCTCATCATCAAAAGCAAAGAGAGCTCACAAGAGACTCTCAGGACA  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331  CTAGCTCCATGGAAAAGAAACTTCTCATCATCAAAAGCAAAGAGAGCTCACAAGAGACTCTCAGGACA  1390

Qy   1381  AGTGTCACAAGGT  1393
           |||||||||||
Db   1391  AGTGTCACAAGAT  1403
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RESULT 14
ADN62808
ID   ADN62808 standard; DNA; 1870 BP.
XX
AC   ADN62808;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human NOV1b DNA.
XX
KW   ds; gene; human; NOVX; metabolic disorder; diabetes; obesity;
KW   infectious disease; anorexia; cancer; cancer-associated cachexia;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia;
KW   metabolic syndrome X; wasting disorder.
XX
OS   Homo sapiens.
XX
PN   US2004038223-A1.
XX
PD   26-FEB-2004.
XX
PF   01-OCT-2002; 2002US-00262511.
XX
PR   02-OCT-2001; 2001US-0326483P.        PR   15-OCT-2001; 2001US-0329414P.
PR   05-OCT-2001; 2001US-0327435P.        PR   17-OCT-2001; 2001US-0330142P.
PR   05-OCT-2001; 2001US-0327449P.        PR   18-OCT-2001; 2001US-0330309P.
PR   09-OCT-2001; 2001US-0327917P.        PR   22-OCT-2001; 2001US-0341058P.
PR   09-OCT-2001; 2001US-0328029P.        PR   24-OCT-2001; 2001US-0339266P.
PR   09-OCT-2001; 2001US-0328044P.        PR   24-OCT-2001; 2001US-0343629P.
PR   09-OCT-2001; 2001US-0328056P.        PR   29-OCT-2001; 2001US-0349575P.
PR   12-OCT-2001; 2001US-0328049P.        PR   01-NOV-2001; 2001US-0346357P.
                                          PR   17-APR-2002; 2002US-0373260P.
                                          PR   19-APR-2002; 2002US-0373815P.
                                          PR   19-APR-2002; 2002US-0373817P.
                                          PR   19-APR-2002; 2002US-0373826P.
                                          PR   19-APR-2002; 2002US-0373884P.
                                          PR   22-APR-2002; 2002US-0374977P.
                                          PR   16-MAY-2002; 2002US-0381037P.
                                          PR   16-MAY-2002; 2002US-0381038P.
                                          PR   16-MAY-2002; 2002US-0381042P.
                                          PR   17-MAY-2002; 2002US-0381642P.
                                          PR   28-MAY-2002; 2002US-0383656P.
                                          PR   29-MAY-2002; 2002US-0383831P.
                                          PR   25-JUN-2002; 2002US-0391135P.
XX
PA   (SMIT/)  SMITHSON G.
PA   (MILL/)  MILLET I.
PA   (PEYM/)  PEYMAN J A.
PA   (KEKU/)  KEKUDA R.
PA   (JUJJ/)  JU J.
PA   (LILL/)  LI L.
PA   (GUOX/)  GUO X.
PA   (PATT/)  PATTURAJAN M.
PA   (SPYT/)  SPYTEK K A.
PA   (EDIN/)  EDINGER S R.
PA   (ELLE/)  ELLERMAN K.
PA   (MALY/)  MALYANKAR U M.
PA   (ORTT/)  ORT T.
PA   (GORM/)  GORMAN L.
PA   (ZERH/)  ZERHUSEN B D.
PA   (ANDE/)  ANDERSON D W.
PA   (ZHON/)  ZHONG M.
PA   (CATT/)  CATTERTON E.
PA   (JIWW/)  JI W.
PA   (MILL/)  MILLER C E.
PA   (RAST/)  RASTELLI L.
PA   (STON/)  STONE D J.
PA   (PENA/)  PENA C E A.
PA   (SHEN/)  SHENOY S G.
PA   (SHIM/)  SHIMKETS R A.
PA   (ROTH/)  ROTHENBERG M E.
PA   (LEAC/)  LEACH M D.
PA   (AGEE/)  AGEE M L.
PA   (BERG/)  BERGHS C.
PA   (DIPI/)  DIPIPPO V A.
PA   (EISE/)  EISEN A.
PA   (GANG/)  GANGOLLI E A.
PA   (RIEG/)  RIEGER D K.
PA   (SPAD/)  SPADERNA S K.
XX
PI   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI   Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI   Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI   Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI   Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR   WPI; 2004-213931/20.
DR   P-PSDB; ADN62809.
XX
PT   Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT   diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS   Claim 20; SEQ ID NO 3; 395pp; English.
XX
CC   The invention relates to isolated NOVX polypeptides and polynucleotides.
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CC   NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC   treat a medical condition in human related to the aberrant expression and
CC   activity of NOVX polypeptides. For example, NOVX polypeptides and
CC   polynucleotides may be used to treat disorders associated with decreased
CC   expression or activity of NOVX by supplementing the patient our
CC   production or to rectify mutations. Conversely, antisense NA molecules
CC   may be administered to down regulate expression of NOVX polypeptides by
CC   binding with the cells own genes and preventing their expression. NOVX
CC   polynucleotides and complementary sequences may also be used as DNA
CC   Probes in diagnostic assays to detect and quantitate the presence of
CC   similar sequences in samples, and so which patients may be in need of
CC   restorative therapy. NOVX polypeptides may also be used as antigens in
CC   the production of antibodies and in assays to identify modulators
CC   (agonists and antagonists) of the expression and activity of NOVX. The
CC   anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC   used to modulate NOVX polynucleotide expression and activity of NOVX
CC   polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC   diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC   polypeptides and polynucleotides may be used in this way to prevent,
CC   diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC   disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC   disorders, Alzheimer's Disease, Parkinson's Disease, immune disorder,
CC   haematopoietic disorders, and the various dyslipidaemias, metabolic
CC   disturbances associated with obesity, the metabolic syndrome X and
CC   wasting disorders associated with chronic diseases and various cancers.
CC   They may also be used as antibacterial agents. The present sequence
CC   represents DNA encoding a human NOVX protein.
XX
SQ   Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

Query Match    93.5%;   Score 1385;   DB 12;   Length 1870;
Best Local Similarity   99.6%;   Pred. No. 0;
Matches 1388;   Conservative 0;   Mismatches 0;   Indels 5;   Gaps 0;

Qy      1 TCAAATATGGAGCGCGGAATCCTTTGATGTCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     24 TCAAATATGGAGCGCGGAATCCTTTGATGTCTGGTGCTGCTGAACCCATTGCCAGCCGGG 83

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 143

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCCTCTTGTTCTCTTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCCTCTTGTTCTCTTTGAAGAATGCAGTC 203

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACCACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACCACCA 263

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCCAAAGGACTTCGGAGTCCGAGAAGTCTTGTAG 300
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 TGACTGAGTTACAGGAGCTCCAGCCTTCGGCCAAAGGACTTCGGAGTCCGAGAAGTCTTGTAG 323

Qy    301 GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAACCGGGGACAATCTATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 GTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAACCGGGGACAATCTATG 383

Qy    361 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 443

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGAATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGAATCCCCAATTACAGTATGCCT 503

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    504 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 563

Qy    541 CACTTTTGAATAGATAGAGGACCAGTTAGATGAAAACCTAGAAAACCTGATCACAGTTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    564 CACTTTTGAATAGATAGAGGACCAGTTAGATGAAAACCTAGAAAACCTGATCACAGTTTTACCTAGCTG 623

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACTGCATCGAGACATCAAGC 660
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    624 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 683

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    684 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 743

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 803

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTACGGCCTGACT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTACGGCCTGACT 863

Qy    841 GTGACTGGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 GTGACTGGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 923

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGATGAATTTCCAGCGGTTTTGAAAT 960
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 983

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 TTCCAGATGACCCCAAAGTGAGCAGTGACAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1043

Qy   1021 GCCAGAAGAGAGAGACTGAAGTTGAGGTCTTGCTGCCATCCTTTCTTCCTCAAAATTG 1080
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   1044 GCCAGAAGAGAGAGACTGAAGTTGAGGTCTTGCTGCGCCATCCTTTCTTCCTCAAAATTG 1103

Qy   1081 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1104 ACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCACCCTCAAGTCTGACGATG 1163

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCCCGTGCCAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCCCGTGCCAGC 1223

Qy   1201 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGTGGGTTTGTTACAGCAAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 TGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGTGGGTTTTTCGTTACAGCAAGG 1283

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCGTGCCCAAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCGTGCCCAAGA 1343

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGTCACAAGAGACTCTCAGGACA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGTCACAAGAGACTCTCAGGACA 1403

Qy   1381 AGTGTCACAAGGT 1393
          |||||||||||
Db   1404 AGTGTCACAAGAT 1416
```

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RESULT 15
ADF60993
ID   ADF60993 standard; cDNA; 6162 BP.
XX
AC   ADF60993;
XX
DT   12-FEB-2004 (first entry)
XX
DE   ORF of pain associated human gene, 2207.
XX
KW   Pain modulation; pain disorder; painful disorder; potassium channel;
KW   kinase expression; inflammatory pain; chronic pain; neuropathic pain;
KW   causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;
KW   analgesic; antiinflammatory; gene; ss.
XX
```

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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..6162
FT                   /tag= a
FT                   /product= "2207 polypeptide"
XX
PN   US2003153525-A1.
XX
PD   14-AUG-2003.
XX
PF   19-DEC-2002; 2002US-00325430.
XX
PR   19-DEC-2001; 2001US-0341953P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Silos-Santiago I, Rosenfeld JB;
XX
DR   WPI; 2003-897732/82.
DR   P-PSDB; ADF60994.
XX
PT   Identifying a compound capable of treating a pain disorder comprises
PT   assaying the ability of the compound to modulate specific, e.g., kinases
PT   or potassium channel, nucleic acid expression or polypeptide activities.
XX
PS   Disclosure; SEQ ID NO 11; 80pp; English.
XX
CC   The present invention relates to a method for identifying a compound
CC   capable of modulating pain or painful disorders. The method comprises
CC   assaying the ability of the compound to modulate specific nucleic acid
CC   expression/activity e.g. potassium channel, or kinase
CC   expression/activity. The method and compounds are useful for treating
CC   pain or painful disorders e.g. inflammatory pain, chronic pain,
CC   neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache
CC   pain and tissue pain. The present sequence encodes a human protein
CC   associated with pain.
XX
SQ   Sequence 6162 BP; 1746 A; 1528 C; 1680 G; 1208 T; 0 U; 0 Other;

Query Match             93.3%;  Score 1381.8;  DB 10;  Length 6162;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1386;  Conservative  0;  Mismatches  0;  Indels  7;  Gaps  0;

Qy      1 TCAAATATGAGCGCGGAATCGTTTGGATGCTGGTGCTGGTGCTGACCCATTGCCAACCGGG 60
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |||||
Db     11 TCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGGTGCTGACCCATTGCCAGCCGGG 70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy    121 CTCCTCTTTCCCAGGAAGGGGGATATTAGATGCCCCTCTTTGTCTCTTTGAAGAATGCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTTCCCAGGAAGGGGGATATTAGATGCCCCTCTTTGTCTCTTTGAAGAATGCAGTC 190

Qy    181 AGCCTGCTCTGATGAAGATGAAGATTAAGCACGTGAAGACGTGGTAAGAGAAAGCAACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 AGCCTGCTCTGATGAAGATGAAGATTAAGCACGTGAAGACGTGGTAAGAGAAAGCAACACCA 250

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy    301 GTTGTGTGGTCACTTTGCTGATGAAGTGCAGGTGCAGGTGTAAGAGAAAGCAACCGGGACA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGTGGTCACTTTGCTGATGAAGTGCAGGTGCAGGTGTAAGAGAAAGCAACCGGGACA 370

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGAGCACAAGCACAGTTTCATTTTTTGAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGAGCACAAGCACAGTTTCATTTTTTGAGG 430

Qy    421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 540
          ||||||||||||||||||| ||  |||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 550

Qy    541 CACTTTGAATAGATAGTGAGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTGAATAGATAGTGAGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy    601 AGTCGATTTGGCTGTCTCACAGCGTTCATCTGATGGGATAGCTGCATCGAGACATCAAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGTCGATTTGGCTGTCTCACAGCGTTCATCTGATGGGATAGCTGCATCGAGACATCAAGC 670

Qy    661 CTGAGAACATTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTGGATCTGCCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACATTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGATCTGCCG 730

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy    781 TGGCTTCCTGAAGTGCTGACTGGTGATGAACGGGATGCGAAAAGGCCACTACGGCCTGACT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 TGGCTTCCTGAAGTGCTGACTGGTGATGAACGGGATGCGAAAAGGCCACTACGGCCTGACT 850

Qy    841 GTGACTGGTGGTCAGTGGGCGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCTTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GTGACTGGTGGTCAGTGGGCGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCTTCG 910

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCAGCGGTTTTGAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATAACATTATGAATTTCCAGCGCGTTTTGAAAT 970

Qy    961 TTCCGATGACCCCAAAGTGAGCAGCAGTGACGTTTCTTGATCTGATTCGATTCAAAGGTGTTGTGCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 TTCCAGATGACCCCAAAGTGAGCAGCAGTGACGTTTCTTGATCTGATTCGATTCAAAGTTGTGTGCG 1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCTCCCATCCTTTCTTCCTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGTTGCTGCCATCCTTTCTTCCTCTAAAATTG 1090

Qy   1081 ACTGAACAACATTCGTAACTCTCCCCCCTTCGTTCCACCCTCAAGTCCGACGATG 1140
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Qy   1141 ACACCTCCAATTTTGATGAACCAGCAGAAGAATTCGTCGGTTTCATCCTCTTCCGTGCCAGC 1200
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Db   1151 ACACCTCCAATTTTGATGAACCAGCAGAAGAATTCGTCGGTTTCATCCTCTTCCGTGCCAGC 1210

Qy   1201 TGAGCCCCTCAGGCTTCTCCGGGTGAAGAACTGCCGGTTTGTGGGGTTTGTGGGGTTTGTTGTACAGCAAGG 1260
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Qy   1261 CACTGGGATTCTTGGTAGATCTGAGTCTGATGTCTGTTGTGTGCGGGTCTGACTCCCCTGCCAAGA 1320
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Qy   1321 CTAGCTCCATGGAAAAGAAAACTTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 CTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAAACTTCTCATCAAGAGCTACAAGACTCTCAGGACA 1390

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Search completed: March 19, 2005, 08:21:32
Job time : 752.892 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        March 19, 2005, 06:53:57 ; Search time 6311.06 Seconds
                                          (without alignments)
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Title:         US-10-724-594-1_COPY_17_1497
Perfect score: 1481
Sequence:      1 tcaaatatggagcgcggaat.........cccggggccgctgctggctc 1481

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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          1: gb_ba:*
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          6: gb_pat:*
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         11: gb_sts:*
         12: gb_sy:*
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         14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1481	100.0	1515	6	AR253937	AR253937 Sequence
2	1481	100.0	1515	6	AR453415	AR453415 Sequence
3	1477.8	99.8	1765	6	AX671044	AX671044 Sequence
4	1476.2	99.7	2066	6	AX642956	AX642956 Sequence
5	1471.8	99.4	1485	6	AX671037	AX671037 Sequence
6	1388.2	93.7	5877	6	AR534559	AR534559 Sequence
7	1388.2	93.7	5877	6	AX574427	AX574427 Sequence
8	1388.2	93.7	6156	6	AX671112	AX671112 Sequence
9	1388.2	93.7	6165	6	AR534558	AR534558 Sequence
10	1388.2	93.7	6165	6	AX574425	AX574425 Sequence
11	1388.2	93.7	6165	6	AX671105	AX671105 Sequence
12	1388.2	93.7	6298	6	AX504254	AX504254 Sequence
13	1388.2	93.7	8576	9	AY257469	AY257469 Homo sapi
14	1388.2	93.7	8603	6	AX671108	AX671108 Sequence
15	1383.8	93.4	1799	9	AY209000	AY209000 Homo sapi
16	1381.8	93.3	6159	6	AX429514	AX429514 Sequence
17	1381.8	93.3	6574	6	AX429512	AX429512 Sequence
18	1372	92.6	6159	6	AX166510	AX166510 Sequence
19	1365.8	92.2	6189	6	AX503780	AX503780 Sequence
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21	1143.6	77.2	2380	6	AX671042	AX671042 Sequence
22	1143.6	77.2	2380	10	AF086823	AF086823 Mus muscu
23	1075.6	72.6	6954	10	AF086824	AF086824 Mus muscu
24	1067.6	72.1	1386	10	AF070065	AF070065 Rattus no
25	947.2	64.0	2162	6	AR542171	AR542171 Sequence
26	744.8	50.3	1133	6	AR411948	AR411948 Sequence
27	744.8	50.3	1133	6	AR475453	AR475453 Sequence
28	578.8	39.1	2896	6	CQ498283	CQ498283 Sequence
29	445.2	30.1	5920	6	CQ723254	CQ723254 Sequence
30	441.8	29.8	446	6	CQ483947	CQ483947 Sequence
31	434.4	29.3	485	6	CQ513776	CQ513776 Sequence
32	288.8	19.5	2284	9	AK123136	AK123136 Homo sapi
33	271.8	18.4	3356	6	CQ722706	CQ722706 Sequence
34	257.2	17.4	4967	10	AF070066	AF070066 Mus muscu
35	247.2	16.7	3835	6	AX817259	AX817259 Sequence
36	247.2	16.7	3985	6	AX817261	AX817261 Sequence
37	246.8	16.7	1530	6	AX504235	AX504235 Sequence
38	246.8	16.7	4680	9	AY648038	AY648038 Homo sapi
39	246.8	16.7	4707	6	AX952383	AX952383 Sequence
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41	246.8	16.7	5373	6	AX746189	AX746189 Sequence
42	240	16.2	6335	6	AX827351	AX827351 Sequence
43	240	16.2	6335	10	AF021935	AF021935 Rattus no
44	236.8	16.0	4917	6	CQ878498	CQ878498 Sequence
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ALIGNMENTS

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AR253937
LOCUS       AR253937                1515 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6479269.
ACCESSION   AR253937
VERSION     AR253937.1  GI:27302420
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1515)
  AUTHORS   Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6479269-A 1 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..1515
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                     /mol_type="genomic DNA"

ORIGIN

Query Match             100.0%;  Score 1481;  DB 6;  Length 1515;
Best Local Similarity   100.0%;
Matches 1481;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 76

Qy         61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Db         77 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 136

Qy        121 CTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTCTTTGAAGAATGCAGTC 180
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Db        137 CTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTCTTTGAAGAATGCAGTC 196

Qy        181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240
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Db        197 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 256

Qy        241 TAGTCGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
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Db   1337 CTAGCTTCCATGCAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1396
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Qy   1381 AGTGTCACCAAGGTATTATTCCGCAGCCGCGGCCTCCTTCCTTCCTTGCTCCAGGATCCTCCCGT 1440
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Db   1397 AGTGTCACCAAGGTATTATTCCGCAGCCGCGGCCTCCTTCCTTCCTTGCTCCAGGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGATCCGCCCGGGCCGCGCCTGCTGCTC 1481
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RESULT 2
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LOCUS       AR453415                1515 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6680188.
ACCESSION   AR453415
VERSION     AR453415.1  GI:42686143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1515)
  AUTHORS   Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6680188-A 1 20-JAN-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Best Local Similarity   100.0%;
Matches 1481;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 TCAAAATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
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Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTATGACTCAACAGCAGATGT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTATGACTCAACAGCAGATGT 136

Qy    121 CTCCTCCTTTCCCGAGAAGGATATTAGAGATGTGCCCTTCTTGTTCTTCTTTGAAGAATGCAGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 CTCCTCCTTTCCCGAGAAGGATATTAGAGATGTGCCCTTCTTGTTCTTCTTTGAAGAATGCAGTC 196

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 256

Qy    241 TAGCTGAGTTACAGGAGCTTCGGCAAAGAACTTCGAAGTCGAGAGTCTTGTAG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 TAGCTGAGTTACAGGAGCTTCGGCAAAGAACTTCGAAGTCGAGAGTCTTGTAG 316

Qy    301 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGACAACCGGGACATCTATG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGACAACCGGGACATCTATG 376

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGACAGGTTCATTTTTGAGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGACAGGTTCATTTTTGAGG 436

Qy    421 AAGAGCCGGAACATATTATCTCGAAGACAAGCCCGTGGATCCCAATTACAGTATGCCT 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 AAGAGCCGGAACATATTATCTCGAAGACAAGCCCGTGGATCCCAATTACAGTATGCCT 496

Qy    481 TTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 TTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGAGGGGACTTGCTGT 556

Qy    541 CACTTTTGAATAGATATGAGGACCAGTAGAGATGAAAACCTGATGAAAACTCTCACTAGCTG 600
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Db    257 TAGCTGAGTTACAGGAGCTTCGGCAAAGAACTTCGAAGTCGAGAGTCTTGTAG 316
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Qy    301 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGACAACCGGGACATCTATG 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 GTTGTGGTCACTTGCTGAAGTGCAGGTGGTAAGACAACCGGGACATCTATG 376

Qy    361 CTATGAAAGTGATGAAGAAGAGGCTTATTGGCCCAGGACAGGTTCATTTTTGAGG 420
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Qy    421 AAGAGCCGGAACATATTATCTCGAAGACAAGCCCGTGGATCCCAATTACAGTATGCCT 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    481 TTCAGGACAAAAATCACCTTTATCTGTGAATATCAGCCTGAGGGGACTTGCTGT 540
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Qy    541 CACTTTTGAATAGATAGATGAGGACCAGTTTACCTAGCTG 600
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Db    557 CACTTTTGAATAGATAGATGAGGACCAGTTTACCTAGCTG 616

Qy    601 AGCTGATTTTGGCTGTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    661 CTGAGACATTCTCGTTGACCGCACAGGACACATCAAGCTCGTGGATCTGCCG 720
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Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796

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Db    797 TGGCTCCTGAAGTGCTGACTGCTGATGATGAACGGGATGGAAAAGGCCACCTACGGCCTGGACT 856

Qy    841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
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Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATACATTTCCAGCGCGGTTTTTGAAAT 960
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Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTTTCTTCAAAGCTTGTTGTGTGCCG 1020
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Qy   1141 ACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Qy   1321 CTAGCTTCCATGCAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
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REFERENCE    1
AUTHORS      Zhu,Z.
TITLE        Regulation of human citron rho/rac-interacting kinase-short kinase
JOURNAL      Patent: WO 03004629-A 8 16-JAN-2003;
             Bayer Aktiengesellschaft (DE)
FEATURES     Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Query Match          99.8%;   Score 1477.8;   DB 6;   Length 1765;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 1479;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db     11 TCAAATATGGAGCGCCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCCGGG 70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Qy    181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
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Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
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Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCCAGATTACA 780
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Db    557 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTG 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
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Db    617 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676

Qy    661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATCTGGTGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATCTGGTGATCTGCCG 736

Qy    721 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCAAGCTTTGGGACCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCAAGCTTTGGGACCCCAGATTACA 796

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAAGGCACCTACGGCCTGGACT 840
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Db    797 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGGAAAAGGCACCTACGGCCTGGACT 856

Qy    841 GTGACTGGTGGTCAGTGGGCGGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 GTGACTGGTGGTCAGTGGGCGGATTGCCTATGAGATGATTTATGGGAGATCCCCCCTTCG 916

Qy    901 CAGAGGGAACCTCTGCCAGAACCTCAATAACATATGAATTCCAGCGGTTTTTGAAAT 960
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Db    917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 976

Qy    961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1020
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Db    977 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG 1036

Qy   1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTG 1096

Qy   1081 ACTGGAACAACATTCGTAACCTCTCCCCCCTTCGTTCTCCACCCTCAAGTCCGACGATG 1140
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Db   1097 ACTGGAACAACATTCGTAACCTCTCCCCCCTTCGTTCTCCACCCTCAAGTCCGACGATG 1156

Qy   1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Db   1157 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTGTACAGCAAGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTGTACACGCAAGG 1276

Qy   1261 CACTTGGGGATTCTTCGGTAGATCTGAGTCGTGTTGTGCGGTCTCGAGTCCCCTGCCAAGA 1320
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Db   1277 CACTTGGGGATTCTTCGGTAGATCTGAGTCGTGTTGTGCGGTCTCGAGTCCCCTGCCAAGA 1336

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGAGCTACAAGAGCTCTCAGGACA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAGAGCTACAAGAGCTCTCAGGACA 1396

Qy   1381 AGTGTCACAAGGTATTTATTTCCGCAGCCCGGCCTCCTTGCTCCAGGATCCTCCCGT 1440
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Db   1397 AGTGTCACAAGGTATTTATTTCCGCAGCCCGGCCTCCTTGCTCCAGGATCCTCCCGT 1456

Qy   1441 CCGTATATGCCAAGGGGATCCGCCCGGGGCCGCTGCTGGCTC 1481
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Db   1457 CCGTATATGCCAAGGGGATCCGCCCGGGGCCGCTGCTGGCTC 1497
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RESULT 3
AX671044

LOCUS       AX671044                1765 bp    DNA        linear      PAT 27-MAR-2003
DEFINITION  Sequence 8 from Patent WO03004629.
ACCESSION   AX671044
VERSION     AX671044.1    GI:29329510
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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/note="Incyte ID No: 3951059CB1"

ORIGIN

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Query Match    99.7%;  Score 1476.2;  DB 6;  Length 2066;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1478;  Conservative 0;  Mismatches 0;  Indels 3;  Gaps 0;
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Qy     1 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    24 TCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATTGCCAGCCGGG 83

Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT 143

Qy   121 CTCCTCTTCCCGAGAAGGGATATTAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 CTCCTCTTCCCGAGAAGGGATATTAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 203

Qy   181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTCTTGTAG 240
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Db   204 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTCTTGTAG 263

Qy   241 TAGCTGAGTTACAGGAGCTCGAAGTCGGGGACATCTATG 300
           |||||||||||||||||||||||||||||||||||||||
Db   264 TAGCTGAGTTACAGGAGCTCGAAGTCGGGGACATCTATG 323

Qy   301 GTTGTGTCACTTGCTGCAGGTGCAGGTGGTAAGACTCAACCGGGACATCTATG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 GTTGTGTCACTTGCTGCAGGTGCAGGTGGTAAGACTCAACCGGGACATCTATG 383

Qy   361 CTATGAAAGTGATGAAGAAGGCTTATTGGCCAGGAGCACAAGCAGGTTCATTTTTGAGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 CTATGAAAGTGATGAAGAAGGCTTATTGGCCAGGAGCACAAGCAGGTTCATTTTTGAGG 443

Qy   421 AAGAGCGGAACACATATCTGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 480
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Db   444 AAGAGCGGAACACATATCTGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 503

Qy   481 TTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 540
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Db   504 TTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCTGGAGGGGACTTGCTGT 563

Qy   541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAGAACCTGATAACAGTTTTACCTAGCTG 600
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Db   564 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAGAACCTGATAACAGTTTTACCTAGCTG 623

Qy   601 AGCTGATTTGCTGTTCACAGCGTTCATCGATGGGATACGTGCATCGAGACATCAAGC 660
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Db   624 AGCTGATTTGCTGTTCACAGCGTTCATCGATGGGATACGTGCATCGAGACATCAAGC 683

Qy   661 CTGAGACATTCGTGACCGGCACAGAGACACATCAAGCTGGTGGATTTGGATCTGCCG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   684 CTGAGACATTCGTGACCGGCACAGAGACACATCAAGCTGGTGGATTTGGATCTGCCG 743

Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACA 780
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Db   744 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACA 803

Qy   781 TGGCTCCGAAGTGCTGACTGCTGACTGCTGATGAACGGGATGGAAAAGGCCACTACGGCTGGACT 840
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Db   804 TGGCTCCGAAGTGCTGACTGCTGACTGCTGATGAACGGGATGGAAAAGGCCACTACGCCTGGACT 863

Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTCG 900
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Db   864 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTCG 923

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Db   924 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 983

Qy   961 TTCCGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGCTTGTGTGTGCCG 1020
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Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 910

Qy   901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
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Qy   961 TTCCGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTTGTGCG 1020
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Db   971 TTCCGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTGTTGTGCG 1030

Qy  1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1080
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Db  1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTAAAATTG 1090

Qy  1081 ACTGGAACAACATTCGTAACCTCCTCCCCCCCTTGTCCCACCCTTCAAGTCCGACGATG 1140
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Db  1091 ACTGGAACAACATTCGTAACCTCCTCCCCCCCTTGTCCCACCCTTCAAGTCCGACGATG 1150

Qy  1141 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Db  1151 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy  1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1260
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Db  1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTCGTACAGCAAGG 1270

Qy  1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTCGTTGTGTGTCGGGTCTGGACTCCCCAAGA 1320
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Qy  1321 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
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Db  1331 CTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1390

Qy  1381 AGTGTCACAAGGTATTATTTCCGCAGCCGGCCGCCGCCCTCCTTCCTTGCTCCAGGATCCTCCCGT 1440
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Db  1391 AGTGTCACAAGGTATTATTTCCGCAGCCGGCCGCCGCCCTCCTTCCTTGCTCCAGGATCCTCCCGT 1450

Qy  1441 CCGTATATGCCAAGGATCCGCCCCGGGGCCGTGGGCTC 1481
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RESULT 4

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AX642956
LOCUS       AX642956              2066 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 33 from Patent WO01096547.
ACCESSION   AX642956
VERSION     AX642956.1  GI:28550096
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
            Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
            Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
            Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
            Hafalia.A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
            Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,
            Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
  TITLE     Humain kinases
  JOURNAL   Patent: WO 01096547-A 33 20-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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Db   1044 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTTCTCTAAAATTG 1103

Qy   1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAGTCCGACGATG 1140
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Qy   1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Qy   1381 AGTGTCACAAGGTATTATTTCCCGAGCCGGCCTCCTTCCTGCCTCCAGGATCCTCCCGT 1440
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Qy   1441 CCGTATATGCCAAGGGATCCGCCCCGGGGGCCGCTGCGGCTC 1481
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Db   1464 CCGTATATGCCAAGGGATCCGCCCCGGGGGCCGCTGCGGCTC 1504
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RESULT 5
AX671037
LOCUS   AX671037   1485 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION Sequence 1 from Patent WO03004629.
ACCESSION   AX671037
VERSION   AX671037.1 GI:29329507
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE   Regulation of human citron rho/rac-interacting kinase-short kinase
  JOURNAL   Patent: WO 03004629-A 1 16-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

Query Match   99.4%; Score 1471.8; DB 6; Length 1485;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1473; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Db     11 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCGTGCTGCAACCCATTGCCAACCCGGG 70

Qy     61 CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Db     71 CCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 190
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Qy 481 TTCAGGACAAAATCACCTTTATCTGGTCATGCGAATATCAGCTGGAGGGGACTTGCTGT 540
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Db 491 TTCAGGACAAAATCACCTTTATCTGGTCATGCGAATATCAGCTGGAGGGGACTTGCTGT 550

Qy 541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAGTTAAAACCTGATACAGTTTACCTAGCTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAGTTAAAACCTGATACAGTTTACCTAGCTG 610

Qy 601 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGAGACATCAGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 611 AGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGAGACATCAGC 670

Qy 661 CTGAGAACATTCTCGTTGACCGCACAGACACTCGGTGGATTTTGGATCTGCCG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 671 CTGAGAACATTCTCGTTGACCGCACAGACACTCGGTGGATTTTGGATCTGCCG 730

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Qy 781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCCTGGACT 840
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Qy 901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGGTTTTGAAAT 960
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Qy 961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATTCGATCGACTTCAAAGCTTGTTGTGCG 1020
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Db 971 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATTCGATCGACTTCAAAGCTTGTTGTGCG 1030

Qy 1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTTGAAGGTCTTCTTCTGTGCTGCCATCCTTTCTTCTCTAAAATTG 1080
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Db 1031 GCCAGAAAGAGAGACTGAAGTTGAAGGTTGAAGGTCTTCTTCTGTGCTGCCATCCTTTCTTCTCTAAAATTG 1090

Qy 1081 ACTGGAACAACATTCGTAACTCTCTCCGCCCCTTCGTTCCCACCCTTCGTTCCCACGTCCGACGATG 1140
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Db 1091 ACTGGAACAACATTCGTAACTCTCTCCGCCCCTTCGTTCCCACCCTTCGTTCCCACGTCCGACGATG 1150

Qy 1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCTCGTTGTCTGTGTCTGGGTCTCCCTGCCCAAGA 1320
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Qy 1381 AGTGTCACAAGT 1393
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RESULT 7
AX574427
LOCUS   AX574427   5877 bp   DNA   linear   PAT 07-JAN-2003
DEFINITION Sequence 3 from Patent WO02059325.
ACCESSION   AX574427
VERSION   AX574427.1 GI:27551752
KEYWORDS
SOURCE   Homo sapiens (human)

Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTCCCTGCCCAAGA 1320
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Db 1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTCCCTGCCCAAGA 1330

Qy 1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGAGAGAAACTTCTCAGGACA 1380
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Db 1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGAGAGAAACTTCTCAGGACA 1390

Qy 1381 AGTGTCACAAGTATTATTTCTTCCGAGCGGCCTCCTTGCTCCTTGCTCCTTCCGGAGGATCCTCCGT 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1391 AGTGTCACAAGTATTATTTCTTCCGAGCGGCCTCCTTGCTCCTTGCTCCTTCCGGAGGATCCTCCGT 1450

Qy 1441 CCGTATATGCCAAGGATCCGCGCCCGGGCGCCGCTGC 1475
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Db 1451 CCGTATATGCCAAGGATCCGCGCCCGGGCGCCGCTGC 1485

RESULT 6
AR534559
LOCUS   AR534559   5877 bp   DNA   linear   PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6734009.
ACCESSION   AR534559
VERSION   AR534559.1 GI:53924886
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 5877)
  AUTHORS   Yu.X.S., Miranda.M. and Friddle,C.J.
  TITLE   Human kinases and polynucleotides encoding the same
  JOURNAL   Patent: US 6734009-A 3 11-MAY-2004;
FEATURES   Location/Qualifiers
     source   1..5877
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   93.7%; Score 1388.2; DB 6; Length 5877;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1390; Conservative   0; Mismatches   0; Indels   3; Gaps   0;

Qy   1 TCAAAATATGGAGCGCGGAATCCTTTGGATGCGTGGTGCTGCTGAAACCATTGCCAACCGGG 60
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Qy   61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Qy 121 CTCCTCTTTCCCGAGAAGGGATTAGATATGAGTCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 180
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Db 131 CTCCTCTTTCCCGAGAAGGGATTAGATATGAGTCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 190

Qy 181 AGCCTGCTCGATGAAGATTAAGCACGTGCAACTTGTCCGGAAGTTCCGACCACCA 240
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Db 191 AGCCTGCTCGATGAAGATTAAGCACGTGCAACTTGTCCGGAAGTTCCGACCACCA 250

Qy 241 TAGCTGAGTTACAGAGGACTTCGGCAAAGGACTTCGAAGTCTTGTAG 300
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Db 251 TAGCTGAGTTACAGAGGACTTCGGCAAAGGACTTCGAAGTCTTGTAG 310

Qy 301 GTTGTGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGGAGAAACACCGGGACATCTATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 311 GTTGTGTCACTTGCTGAAGTGCAGGTGCAGGTGGTAAGGAGAAACACCGGGACATCTATG 370

Qy 361 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 420
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Db 371 CTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 430

Qy 421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Db 431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

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ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Yu,X., Miranda,M. and Friddle,C.J.
TITLE      Human kinases and polynucleotides encoding the same
JOURNAL    Patent: WO 02059325-A 3 01-AUG-2002;
           Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
   source  1..5877
           /organism="Homo sapiens"
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           /db_xref="taxon:9606"
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Query Match         93.7%;    Score 1388.2;   DB 6;   Length 5877;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1390;  Conservative  0;   Mismatches  3;   Indels  0;   Gaps   0;

Qy      1 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTCGTCGTCGGACCCATTGCCAACCGGG 60
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Db     11 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTCGTCGTCGGACCCATTGCCAGCCGGG 70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 130

Qy    121 CTCCTCCTTTCCCGAGAAGGGGATAATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 180
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Db    131 CTCCTCCTTTCCCGAGAAGGGGATAATTAGATGCCCTCTTGTTCTCTTTGAAGAATGCAGTC 190

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Db    191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy    241 TAGCTGAGTTACAGGAGCTTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG 300
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Db    251 TAGCTGAGTTACAGGAGCTTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAGTCTTGTAG 310

Qy    301 GTTGTGGTCACTTTGCTCAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 360
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Db    311 GTTGTGGTCACTTTGCTCAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 370

Qy    361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 420
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Db    371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTTGAGG 430

Qy    421 AAGAGCGGAACATATATCTCGAGCAACAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Db    431 AAGAGCGGAACATATATCTCGAGCAACAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
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Db    491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy    541 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATCACAGTTTACCTAGCTG 600
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Db    551 CACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATCACAGTTTACCTAGCTG 610

Qy    601 AGCTGATTTTGGCGTGTTCACAGCGTTCATCTGATGGGATACGTGCATGCAGACATCAAGC 660
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Db    611 AGCTGATTTTGGCGTGTTCACAGCGTTCATCTGATGGGATACGTGCATGGCATCAGACATCAAGC 670

Qy    661 GGAGAACATTCTCGTTGACCGGACCACAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACATTCTCGTTGACCGGACCACAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAAACTCCCGATTGGGACCCCAGATTACA 790

Qy    781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCGCTGGACT
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Db    791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTACGGCGCTGGACT 850

Qy    841 GTGACTGGTGGTGTCAGTGGCGTGGCCGTGATTGCCTATGAGATGATTTATGGGAGATGACCCCCTTCG 900
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Db    851 GTGACTGGTGGTGTCAGTGGCGTGGCCGTGATTGCCTATGAGATGATTTATGGGAGATGACCCCCTTCG 910

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATACACATTATGAATTCCAGCGGTTTTGAAAT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGAGGGAACCTCTGCCAGAACCTTCAATACACATTATGAATTCCAGCGGTTTTGAAAT 970

Qy    961 TTCCAGATGAGACCCCAAAGTGAGCAGTCGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1020
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Db    971 TTCCAGATGAGACCCCAAAGTGAGCAGTCGACTTTCTTGATCGATTCAAAGCTTGTTGTGCG 1030

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTAAATTG 1080
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Db   1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTCTTCTTCTAAATTG 1090

Qy   1081 ACTGGAACACACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTTCGTTCCCCAAGTCCGACGATG 1140
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Db   1091 ACTGGAACACACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTTCGTTCCCCAAGTCTGACGATG 1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Db   1151 ACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACGTGCCGGTTTGTGCGGTTTGTGTGGGGTTTCGTACAGCAAGG 1260
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Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACGTGCCGGTTTGTGCGGTTTGTGTGGGGTTTCGTACAGCAAGG 1270

Qy   1261 CACTCGGGGATTCTTGTAGATCTGAGTCTGAGTGCGGGTCTGGACTCCCTGCCAAGA 1320
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Db   1271 CACTCGGGGATTCTTGTAGATCTGAGTCTGAGTGCGGGTCTGGACTCCCTGCCAAGA 1330

Qy   1321 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAGACTTCAGAGACA 1380
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Db   1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAGACTTCAGAGACA 1390

Qy   1381 AGTGTCACAAGGT 1393
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Db   1391 AGTGTCACAAGAT 1403
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RESULT 8
AX671112
LOCUS       AX671112                6156 bp    DNA        linear    PAT 27-MAR-2003
DEFINITION  Sequence 8 from Patent WO03004523.
ACCESSION   AX671112
VERSION     AX671112.1   GI:29329572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE     Regulation of human citron rho/rac-interacting kinase
  JOURNAL   Patent: WO 03004523-A 8 16-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES    Location/Qualifiers
   source   1..6156
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ORIGIN

Query Match         93.7%;    Score 1388.2;   DB 6;   Length 6156;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1390;  Conservative  0;   Mismatches  3;   Indels  0;   Gaps   0;

Qy      1 TCAAATATGGAGCGCGGGAATCCTTTGGATGCTGGTCGTCGTCGGAACCCATTGCCAACCGGG 60
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Qy 1141 ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCTCCGTGCCAGC 1200
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Qy 1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTCGTACAGCAGG 1260
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Qy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCTGCCAAGA 1320
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Db 1271 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCTGCCAAGA 1330

Qy 1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAGACAAAGAGTACAAAGACTTCAGACA 1380
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Db 1331 CTAGCTCCATGGAAAGAAACTTCTCATCAAAGACAAAGAGTACAAAGACTTCAGACA 1390

Qy 1381 AGTGTCACAGGT 1393
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Db 1391 AGTGTCACAGAT 1403

RESULT 9
AR534558
LOCUS AR534558   6165 bp DNA   linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6734009.
ACCESSION AR534558
VERSION AR534558.1 GI:53924885
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
     Unclassified.
REFERENCE 1 (bases 1 to 6165)
AUTHORS Yu,X.S., Miranda,M. and Friddle,C.J.
TITLE   Human kinases and polynucleotides encoding the same
JOURNAL Patent: US 6734009-A 1 11-MAY-2004;
FEATURES Location/Qualifiers
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source   /mol_type="genomic DNA"

ORIGIN

Query Match 93.7%; Score 1388.2; DB 6; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 CCTCCAGGCTGAATTCTGTTCTTCCAGGGGAAACACCCTTTATGACTCAACAGCAGATGT 120
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Db 71 CCTCCAGGCTGAATTCTGTTCTTCCAGGGGAAACACCCTTTATGACTCAACAGCAGATGT 130

Qy 121 CTCCTCCTTCCCGAGAGGGATATTAGATGCCTATGGAGATCCCCTTCG 180
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Db 131 CTCCTCCTTCCCGAGAGGGATATTAGATGCCTATGGAGATCCCCTTCG 190

Qy 181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Db 191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy 241 TAGCTGAGTTACAGGACTTCGAAGTCGGGGACACCTATG 300
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Qy 301 GTTGTGTCACTTGCTGAAGTGCAGGTGTGTAAGAGCAACCGGGGACATCCATG 360
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Db 311 GTTGTGTCACTTGCTGAAGTGCAGGTGTGTAAGAGCAACCGGGGACATCCATG 370

Qy 361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTGAGG 420
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Db 371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTGAGG 430

Qy 61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Qy 121 CTCCTCTTCCCGAGAGGGATATTAGATGCCTATGGAGAGATGATTAGCAGTC 180
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Qy 181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Db 191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy 241 TAGCTGAGTTACAGGACTTCGAAGTCGGGGACACCTATG 300
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Db 251 TAGCTGAGTTACAGGACTTCGAAGTCGGGGACATCCATG 310

Qy 301 GTTGTGTCACTTGCTGAAGTGCAGGTGTGTAAGAGCAACCGGGGACATCCATG 360
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Db 311 GTTGTGTCACTTGCTGAAGTGCAGGTGTGTAAGAGCAACCGGGGACATCCATG 370

Qy 361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTGAGG 420
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Db 371 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGTTTCATTTTTGAGG 430

Qy 421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Db 431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 490

Qy 481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
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Db 491 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 550

Qy 541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
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Db 551 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy 601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
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Db 611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670

Qy 661 CTGAGACAATTCTCGTTGACCGCACGGGACACAGGACACATCAAGCTGGTCGGAATTTTGGATCCTGCCG 720
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Db 671 CTGAGACAATTCTCGTTGACCGCACGGGACACAGGACACATCAAGCTGGTGGTGATTTTGGATCCTGCCG 730

Qy 721 CGAAAATGAATTCAAACAACAGAGATGTGAATGCCAAACTCCCATTGGGACCCCAGATTACA 780
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Db 731 CGAAAATGAATTCAAACAACAGAGATGTGAATGCCAAACTCCCATTGGGACCCCAGATTACA 790

Qy 781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 840
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Db 791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTACGGCCTGGACT 850

Qy 841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGAGATGATTAGCAGTC 900
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Db 851 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGAGATGATTAGCAGTC 910

Qy 901 CAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTGAAAT 960
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Qy 961 TTCCAGATGACCCCAAAGTGAGCAGTTGGACTCTTGATCTGATTCTTCTTGTGTGCG 1020
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Db 971 TTCCAGATGACCCCAAAGTGAGCAGTTGGACTCTTGATCTGATTCTTCTTGTGTGCG 1030

Qy 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGAAGGTCCTGCCATCCTTTCTTCTTCTAAAATTG 1080
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Db 1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGAAGGTCCTGCCATCCTTTCTTCTTCTAAAATTG 1090

Qy 1081 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTTCGTTCCCACCCTTCGTTCCCAAGTCCGACGATG 1140
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Db 1091 ACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTTCGTTCCCAAGTCCGACGATG 1150

ACCESSION   AX574425
VERSION   AX574425.1   GI:27551751
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yu.X., Miranda,M. and Friddle,C.J.
  TITLE   Human kinases and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059325-A 1 01-AUG-2002;
             Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   93.7%; Score 1388.2; DB 6; Length 6165;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1390;   Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy      1 TCAAATATGGAGCGCGAACTCCTTGGATGCGTGGTGCTGCTGAACCCATTGCCAACCGGG   60
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Db     11 TCAAATATGGAGCGCGGAACTCCTTGGATGCGTGGTGCTGCTGAACCCATTGCCAGCCGGG   70

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  130

Qy    121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTCTCTTTGAAGAATGCAGTC  190

Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAACTTGTCCGACACCA  240
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Db    191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAACTTGTCCGACACCA  250

Qy    241 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAAGTCAGAAGTCTTGTAG  300
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Db    251 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAAGTCAGAAGTCTTGTAG  310

Qy    301 GTTGTGGTCACTTTGCTGAAGTGCAGTGCAGTGCAGGTGGTAAGAGAAAGCAACCGGGACATCTATG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTTGTGGTCACTTTGCTGAAGTGCAGTGCAGTGCAGGTGGTAAGAGAAAGCAACCGGGACATCTATG  370

Qy    361 CTATGAAAGTGATGAGAAGAAGAGGCTTTATTGGCCAGCAGGTTTCATTTTTGAGG  420
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Db    371 CTATGAAAGTGATGAGAAGAAGAGGCTTTATTGGCCAGCAGGTTTCATTTTTGAGG  430

Qy    421 AAGAGCGGAACATATTATCTGGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 AAGAGCGGAACATATTATCTGGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT  490

Qy    481 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATAGAGGACCAGTTAGACAGTTTTACCTAGCTG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 TTCAGGACAAAAATCACCTTTATCTGTCATGGAATAGAGGACCAGTTAGACAGTTTTACCTAGCTG  550

Qy    541 CACTTTTGAATAGATATGAGGACTACAGAGTGCATCGAGACATCAAGC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CACTTTTGAATAGATATGAGGACTACAGAGTGCATCGAGACATCAAGC  610

Qy    601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC  670

Qy    661 CTGAGAACATTCTCGTTGACCGGACACATCAAGCTCGGTGTGGATTTTGGATCTGCCG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 CTGAGAACATTCTCGTTGACCGGACACATCAAGCTCGGTGTGGATTTTGGATCTGCCG  730

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
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Db    731  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGACCCCAGATTACA  790

Qy      1  TCAAAATGGAGCGCCGGAATCCTTTCGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG    60
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Db     11  TCAAAATGGAGCGCCGGAATCCTTTCGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG    70

Qy     61  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCACCCTTATGACTCAACAGCAGATGT   120
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Db     71  CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCACCCTTATGACTCAACAGCAGATGT   130

Qy    121  CTCCTCTTCCCGAGAGGGATATTATGATGCCCTCTTGTTCTCTTGAAGAATGCAGTC   180
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Db    131  CTCCTCTTCCCGAGAGAGGGATATTAGAATGCCCTCTTGTTCTCTTGAAGAATGCAGTC   190

Qy    181  AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA   240
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Db    191  AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA   250

Qy    241  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGTCGAAAGTCTTGTAG   300
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Db    251  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGTCGAAAGTCTTGTAG   310

Qy    301  GTTGTGTCACTTGCTGAAGTGCAGTGAGAAAGCAACCGGGGACAACATCTATG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311  GTTGTGTCACTTGCTGAAGTGCAGTGAGAAAGCAACCGGGGACAACATCTATG   370

Qy    361  CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTTGAGG   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371  CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTTGAGG   430

Qy    421  AAGAGCGGAACATATATTCGAAGCACCCGTGGATCCCAATTACAGTAGATGCCT   480
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Db    431  AAGAGCGGAACATATATTCGAAGCACCCGTGGATCCCAATTACAGTAGATGCCT   490

Qy    481  TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT   540
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Db    491  TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT   550

Qy    541  CACTTTTGAATAGATAGAGGACCAGTTAGATGAAACCTGATACAGTTTTACCTAGCTG   600
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Db    551  CACTTTTGAATAGATAGAGGACCAGTTAGATGAAACCTGATACAGTTTTACCTAGCTG   610

Qy    601  AGCTGATTTTGGCTGTTCAGCGGTTCACAGAGCGTTCATCTGATGGGATACGTGCATCAAGC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611  AGCTGATTTTGGCTGTTCAGCGGTTCACAGAGCGTTCATCTGATGGGATACGTGCATCAAGC   670

Qy    661  CTGAGAACATTCGTTGACCGTTGACCGACACATCAAGCTGGTGATTTTGGATCTGCCG   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671  CTGAGAACATTCGTTGACCGTTGACCGACACATCAAGCTGGTGATTTTGGATCTGCCG   730

Qy    721  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGACCCCAGATTACA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731  CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGACCCCAGATTACA   790

Qy    781  TGGCTCCTGAAGTGCTGACTGATGAACAAGAGGCACTCACGGCCTGGACT   840
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    791  TGGCTCCTGAAGTGCTGACTGATGAACAAGAGGCACTCACGGCCTGGACT   850

Qy    841  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCTTCG   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCTTCG   910

Qy    901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCACGCGGTTTTGAAAT   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGGTTTTGAAAT   970

Qy    961  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGCTGTTGTTGTGCG  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971  TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGCTGTTGTTGTGCG  1030

Qy   1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCGCCATCCTTTCTTCTCCTAAAATTG  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCGCCATCCTTTCTTCTCCTAAAATTG  1090

Qy   1081  ACTGGAACAACATTCGTAACTCTCTCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091  ACTGGAACAACATTCGTAACTCTCTCCCCCTTCGTTCCCACCCTCAAGTCGACGATG  1150

Qy   1141  ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCCTCGTCCCAGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151  ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCCTCGTCCCAGC  1210

Qy   1201  TGAGCCCCTACAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTTCGTACAGCAAGG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211  TGAGCCCCTACAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTTCGTACAGCAAGG  1270

Qy   1261  CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGGTCTGACTCCCCTGCCAAGA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271  CACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGGTCTGACTCCCCTGCCAAGA  1330

Qy   1321  CTAGCTCCATGGAAAAGAAAGAAACTTCTCATCAAAGAAGAGAGTACAAGAGCTCTCAGGACA  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331  CTAGCTCCATGGAAAAGAAAGAAACTTCTCATCAAAGAAGAGAGTACAAGAGCTCTCAGGACA  1390

Qy   1381  AGTGTCACAAGGT  1393
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Db   1391  AGTGTCACAAGAT  1403
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RESULT 11
AX671105

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LOCUS       AX671105           6165 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1 from Patent WO03004523.
ACCESSION   AX671105
VERSION     AX671105.1  GI:29329569
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE     Regulation of human citron rho/rac-interacting kinase
  JOURNAL   Patent: WO 03004523-A 1 16-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..6165
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match 93.7%; Score 1388.2; DB 6; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAGGACTTCGAAGTCTTGTAG 300
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Db    305 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAGGACTTCGAAGTCTTGTAG 364

Qy    301 GTTGTGGTCACTTGCTGAAGTGCAGTGGTAAGAGAAAGCAACCGGGACATCTATG 360
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    365 GTTGTGGTCACTTGCTGAAGTGCAGTGGTGAAGAGAAAGCAACCGGGACATCTATG 424

Qy    361 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCAGGAGGAGCAGGTTTCATTTTTTGAGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 CTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCAGGAGGAGCAGGTTTCATTTTTTGAGG 484

Qy    421 AAGAGCGGACACATATTATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Db    485 AAGAGCGGACACATATTATCTGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT 544

Qy    481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCGGCTGGGGGGACTTGCTGT 540
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Db    545 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCGGCTGGGGGGACTTGCTGT 604

Qy    541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 664

Qy    601 AGCTGATTTTGCGTGTTCATCTGCGTTCATCTGAGATACGTGCATCGAGACATCAAGC 660
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Db    665 AGCTGATTTTGCGTGTTCATCTGCGTTCATCTGAGATACGTGCATCGAGACATCAAGC 724

Qy    661 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
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Db    725 CTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 784

Qy    721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
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Db    785 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 844

Qy    781 TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGGATGCGAAAAGCCACTCACGGCCTGGACT 840
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Db    845 TGGCTTCCTGAAGTGCTGACTGTGATGAACGGGGATGCGAAAAGCCACTCACGGCCTGGACT 904

Qy    841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 964

Qy    901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTCCAGCGGTTTTTGAAAT 960
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Db    965 CAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTCCAGCGGTTTTTGAAAT 1024

Qy    961 TTCCAGTGACCCCAAAGTGACTTTCTTGATTCAAAGCTTGTTGTGCG 1020
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Db   1025 TTCCAGTGACCCCAAAGTGACTTTCTTGATTCAAAGCTTGTTGTGCG 1084

Qy   1021 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCTTGCTGCCATCCTTTCTTCTCTAAAATTG 1080
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Db   1085 GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTCTTGCTGCCATCCTTTCTTCTCTAAAATTG 1144

Qy   1081 ACTGGAACAACATTCGTAACTCCTCCCCCCCCTTCGTTCCACCCTCCAAGTCCGACGATG 1140
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Db   1145 ACTGGAACAACATTCGTAACTCCTCCCCCCCCTTCGTTCCACCCTCCAAGTCCGACGATG 1204

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Db   1205 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1264

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTCGGGTTTTGTACAGCAAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTCGGGTTTTGTACAGCAAGG 1324

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTCCGGACTCCCTGCCAAGA 1320
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Db   1325 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTCCGGACTCCCTGCCAAGA 1384

Qy   1321 CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAGCAAAGAGCTACAAAGACTCTCAGGACA 1380
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Qy   1081 ACTGGAACAACATTCGTAACTCCTCCCCCCCCTTCGTTCCACCCTCCAAGTCCGACGATG 1140
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Db   1091 ACTGGAACAACATTCGTAACTCCTCCCCCCCCTTCGTTCCACCCTCCAAGTCCGACGATG 1150

Qy   1141 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200
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Db   1151 ACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy   1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTCGGGTTTTGTACAGCAAGG 1260
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Db   1211 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTCGGGTTTTGTACAGCAAGG 1270

Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTCCGGACTCCCTGCCAAGA 1320
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Db   1271 CACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTCCGGACTCCCTGCCAAGA 1330

Qy   1321 CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAGCAAAGAGCTACAAAGACTCTCAGGACA 1380
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Db   1331 CTAGCTCCATGGAAAAGAAGAAACTTCTCATCAAAGCAAAGAGCTACAAAGACTCTCAGGACA 1390

Qy   1381 AGTGTCACAAGGT 1393
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Db   1391 AGTGTCACAAGAT 1403
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RESULT 12
AX504254

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LOCUS       AX504254                6298 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 43 from Patent WO0233099.
ACCESSION   AX504254
VERSION     AX504254.1  GI:23386094
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gururajan,R., Baughn,M.R., Walia,N.K., Elliott,V.S., Xu,Y.,
            Arvizu,C., Yao,M.G., Ramkumar,J., Ding,L., Tang,Y.T., Hafalia,A.J.,
            Nguyen,D.B., Gandhi,A.R., Lu,Y., Yue,H., Burford,N., Bandman,O.,
            Tribouley,C.M., Lal,P.G., Recipon,S.A., Lu,D.A., Borowsky,M.L.,
            Thornton,M., Swarnaker,A., Thangavelu,K., Khan,F.A. and Ison,C.H.
  TITLE     Human kinases
  JOURNAL   Patent: WO 0233099-A 43 25-APR-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..6298
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7484498CB1"
ORIGIN
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Query Match     93.7%;  Score 1388.2;  DB 6;  Length 6298;
  Best Local Similarity   99.8%;
  Matches 1390;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    0;

Qy      1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGCTGCTGAACCCATTGCCAACCGGG 60
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Db      1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGCTGCTGAACCCATTGCCAGCCGGG 60

Qy     61 CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Db     65 CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 124

Qy    121 CTCCTTCTTCCCGAGAAGGAGATATTAGATCGCCCTCTTGTTCTTGAAGAATGCAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 CTCCTCCTTTCCCGAGAAGGAGATATTAGATGCCCTCTTGTTCTTGAAGAATGCAGTC 184

Qy    181 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 304
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Db   1385 CTAGCTCCATGCGAAAGAAACTTCTCATCAAAGACAAGAGACTACAAGAGACTCTCAGGACA 1444
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Qy   1381 AGTGTCACAAGT 1393
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Db   1445 AGTGTCACAAGAT 1457
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RESULT 13
AY257469
LOCUS   AY257469   8576 bp   mRNA   linear   PRI 23-APR-2003
DEFINITION Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete
            cds.
ACCESSION   AY257469
VERSION   AY257469.1 GI:30088969
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 8576)
AUTHORS   Huang,C.Q., Wu,S.L., Shan,Y.X., Liu,S. and Xiao,P.J.
TITLE   Direct Submission
JOURNAL   Submitted (18-MAR-2003) Department of Biochemistry and Molecular
            Biology, Basic Medicine, Suzhou University, Renming Road 48,
            Suzhou, Jiangsu 215007, China
FEATURES   Location/Qualifiers
     source   1..8576
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                     /chromosome="12"
                     /map="12q24.23"
     gene   1..8576
                     /gene="CIT"
                     /note="synonym: CRIK"
     CDS   54..6137
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                     /note="serine/threonine protein kinases"
                     /codon_start=1
                     /product="rho/rac-interacting citron kinase"
                     /protein_id="AAP13528.1"
                     /db_xref="GI:30088970"
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Top-right protein sequence (continuation):

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ORIGIN

Query Match   93.7%; Score 1388.2; DB 9; Length 8576;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

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Qy     1 TCAAATATGGAGGCGGAATCCTTTGGATGCTGGTGCTGCTGCAACCACCATTGCAACCGGG   60
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Qy    61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT  120
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Qy   241 TAGCTGAGTTACAGGAGCCTGCAGCCTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG  300
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Qy   301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAAGCAACCGGGGACATCATG  360
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Qy   421 AAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCT  480
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Qy   481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCACCACTCCGAGGGGACTTGCTGT  540
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Db   544 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT  603

Qy   541 CACTTTTGAATAGATAGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  600
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Db   604 CACTTTTGAATAGATAGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG  663

Qy   601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGATACGTGCATCGAGACATCAAGC  660
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Qy   721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCAGATTACA  780
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Qy   781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACTACGGCCTGACT  840
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Qy   841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG  900
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Db   904 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG  963

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Qy    961  TTCCAGATGACCCCAAAGTGAGCAGTGAGATTAAGCACGTGACTTCTTGATTCAAAGCTTGTGTGCG 1020
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Qy   1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGAGGTCTTCTTCTTCTCTCTAAAATTG 1080
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Db   1084  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGAGGTCTTCTTCTTCTCTCTAAAATTG 1143

Qy   1081  ACTGGAACACATTCGTAACTCTCTCCACCCTCGTTCCACCCTCAAGTCTGACGATG 1140
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Qy   1141  ACACCTCCAATTTTGATGAACCAGGAGAAGAATTCGTGGGGTTCATCCTCTCCGTGCCAGC 1200
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Db   1204  ACACCTCCAATTTTGATGAACCAGGAGAAGAATTCGTGGGGTTCATCCTCTCCGTGCCAGC 1263

Qy   1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTTCGTACAGCAAGG 1260
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Db   1264  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGGTTTTCGTACAGCAAGG 1323

Qy   1261  CACTGGGATTCTTGGTAGATCTGAGTCTGTGTGTGCGGGTCTGAGACTCCCCTGCCAAGA 1320
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Qy   1321  CTAGCTCCATGGAAAGAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1380
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DEFINITION Sequence 4 from Patent WO03004523.
ACCESSION   AX671108
VERSION   AX671108.1 GI:29329570
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE   Regulation of human citron rho/rac-interacting kinase
  JOURNAL   Patent: WO 03004523-A 4 16-JAN-2003;
            Bayer Aktiengesellschaft (DE)
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ORIGIN

Query Match   93.7%; Score 1388.2; DB 6; Length 8603;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1390; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy     61  CCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Qy    121  CTCCTCTTTCCCGAGAAGGGGATATTAGATGCGCCCTTCTTTGTTCTCTTTGAAGAATGCAGTC 180
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Db   131  CTCCTCTTTCCCGAGAAGGGGATATTAGATGCGCCCTTCTTTGTTCTCTTTGAAGAATGCAGTC 190
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Qy   181  AGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 240
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Db   191  AGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTGTCCGGAAGTATTCCGACACCA 250

Qy   241  TAGCTGAGTTACAGAGACTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 300
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Db   251  TAGCTGAGTTACAGAGACTTCGGCAAAGACTTCGAAGTCAGAAGTCTTGTAG 310

Qy   301  GTTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 360
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Db   311  GTTGTGTCACTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGGACATCTATG 370

Qy   361  CTATGAAAGTGATGAAGAGAGAGGCTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420
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Qy   421  AAGAGCGGAACATATTATCTTCGAAGCACAAGCCGTGATCCCCAATTACAGTATGCCT 480
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Db   551  CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 610

Qy   601  AGCTGATTTTGGCTGTTCATCCTGATGGGATACGTGCATCGAGACATCAAGC 660
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Qy   661  CTGAGAACATTCGTTGACCGCACAGGACACACATCAAGCTCAAGCTGGTGTGGATTTTGGATCTCGCG 720
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Db   671  CTGAGAACATTCGTTGACCGCACAGGACACACATCAAGCTCAAGCTGGTGTGGATTTTGGATCTCGCG 730

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Qy   781  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGCCACCTACGGCCTGGACT 840
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Db   791  TGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGCCACCTACGGCCTGGACT 850

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Db   851  GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 910

Qy   901  CAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTTCCAGCGGTTTTGAAAT 960
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Db   911  CAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTTCCAGCGGTTTTGAAAT 970

Qy   961  TTCCAGATGACCCCAAAGTGAGCAGTGAGATTAAGCACGTGACTTCTTGATTCAAAGCTTGTGTGCG 1020
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Qy  1021  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGAGGTCTTCTTCTTCTCTCTAAAATTG 1080
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Db  1031  GCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGAGGTCTTCTTCTTCTCTCTAAAATTG 1090

Qy  1081  ACTGGAACAACATTCGTAACTCTCTAACTCTCCCACCCTTCGTTCCACCCTTCGTTGGGTTCATCCTCTCCGACGATG 1140
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Db  1151  ACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210

Qy  1201  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTTTTCGTACAGCAAGG 1260
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Db  1211  TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTTTTCGTACAGCAAGG 1270
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Qy    181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAGTATTCCGACACCA 240
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Db    244 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAGTATTCCGACACCA 303

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Db    304 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCAAAGACTCTCAGGACA   363

Qy    301 GTTGTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACGGGACATCTATG 360
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Db    364 GTTGTGTGTCACTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACGGGACATCTATG 423

Qy    361 CTATGAAAGTGATGAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTGAGG 420
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Db    424 CTATGAAAGTGATGAGAAGAAGGCTTTATTGGCCAGGAGCAGGTTCATTTTTGAGG 483

Qy    421 AAGAGCGGAACATATATCTCGAAGACAAGCCCGTGGATCCCCAATTACAGTATGCCT 480
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Qy    481 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540
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Db    544 TTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 603

Qy    541 CACTTTTGAATAGATAGATGAGAACCAGTTAGATGAAGAACCTGATACAGTTTTACCTAGCTG 600
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Db    604 CACTTTTGAATAGATAGATGAGAACCAGTTAGATGAAGAACCTGATACAGTTTTACCTAGCTG 663

Qy    601 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGAATACTGATGCATCGAGACATCAAGC 660
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Db    664 AGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGAATACTGATGCATCGAGACATCAAGC 723

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Db   1084 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGAAGGTCTGTCCATCCTTCTTCTGCTGCG 1143

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Qy   1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCCCTGCCAAGA 1320
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RESULT 15
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DEFINITION   Homo sapiens citron Rho-interacting kinase short form mRNA,
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ACCESSION   AY209000
VERSION   AY209000.1 GI:37784566
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1799)
AUTHORS   Mao,Y., Xie,Y. and Wu,Q.
TITLE   Cloning and characterizing a novel human CRIK-SK gene
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1799)
AUTHORS   Mao,Y., Xie,Y. and Wu,Q.
TITLE   Direct Submission
JOURNAL   Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
               220 Handan Road, Shanghai 200433, P.R. China
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ORIGIN

Query Match   93.4%; Score 1383.4; DB 9; Length 1799;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1387; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

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Db     64 TCAAATATGAGCGCGGAATCCTTTGGTGATGCTGGTCGCGTGCTGACACCCATTGCCAACCGGG 123

Qy     61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120
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Job time : 6314.06 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      March 19, 2005, 11:54:37 ; Search time 828.8 Seconds
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Title:         US-10-724-594-1
Perfect score: 1515
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Scoring table: IDENTITY NUC
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Searched:      554816 seqs, 297661598 residues

Total number of hits satisfying chosen parameters:      11089632

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1515	100.0	1515	1515	14	US-10-238-709-1	Sequence 1, Appli
3	1515	100.0	1515	1515	17	US-10-724-594-1	Sequence 33, Appli
4	1510.2	99.7	2066	2066	17	US-10-311-034-33	Sequence 43, Appli
5	1404.2	92.7	6298	6298	17	US-10-415-011-43	Sequence 3, Appli
6	1398.2	92.3	1870	1870	17	US-10-262-511-3	Sequence 3, Appli
7	1398.2	92.3	5877	5877	13	US-10-028-946-3	Sequence 3, Appli
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9	1398.2	92.3	6165	6165	13	US-10-028-946-1	Sequence 1, Appli
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17	1375.8	90.8	6189	11	US-09-964-956-10		Sequence 10, Appl
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22	955.4	63.1	957	17	US-10-412-897-1		Sequence 1, Appli
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ALIGNMENTS

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;   Sequence 1, Application US/09804471A
;   Patent No. US20020132322A1
;   GENERAL INFORMATION:
;   APPLICANT: WEBSTER, Marion et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001164
;   CURRENT APPLICATION NUMBER: US/09/804,471A
;   CURRENT FILING DATE: 2001-03-13
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1515
;   TYPE: DNA
;   ORGANISM: Human
US-09-804-471A-1

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Matches 1515;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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; Publication No. US20030022340A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-10-238-709-1

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Qy   121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGACGGGATATTAGATGCCCTCTTTGTTCTC 180
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Qy   721 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
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Qy   841 ACCTACGGCCTGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 900
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Qy  1021 CAAAGCTTGTTGTGCGGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080
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Db  1141 CTCAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGAAGAATTCGTGGGTTTCA 1200

Qy  1201 TCCTCTCCCGTGCCAGCTGAGCCCCTGAGCCCTCAGGCTTCTCGGGGTGAAGAACTGCCGTTTGTGGGG 1260
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RESULT 3
US-10-724-594-1
; Sequence 1, Application US/10724594
; Publication No. US2004091993A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL00116ADIV II
;  CURRENT APPLICATION NUMBER: US/10/724,594
;  CURRENT FILING DATE:  2003-12-02
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1515
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-724-594-1

Query Match        100.0%;  Score 1515;  DB 17;  Length 1515;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1515;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy        1 GGGGAGGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCGGTGGTGCTGCTGAA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGGAGGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCGGTGGTGCTGCTGAA 60

Qy       61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATG 120

Qy      121 ACTCAACAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGTAGTGCCCTCTTTGTTCTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACTCAACAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGTAGTGCCCTCTTTGTTCTC 180

Qy      181 TTTGAAGAATGCAGTCAGCCTGCTCTGTGATGAAGATTAAGCACGTGAGCAACTTTGTCGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TTTGAAGAATGCAGTCAGCCTGCTCTGTGATGAAGATTAAGCACGTGAGCAACTTTGTCGG 240

Qy      241 AAGTATTCCGACACCATAGCTGAGTTACAGGACCTTCGGCAAAGGACTTCGAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AAGTATTCCGACACCATAGCTGAGTTACAGGACCTTCGGCAAAGGACTTCGAA 300

Qy      301 GTCAGAAGTCTTGTAGGTTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GTCAGAAGTCTTGTAGGTTGGTCACTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360

Qy      361 ACCGGGGACATCTATGCTGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGATCCCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCGGGGACATCTATGCTGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGATCCCC 420

Qy      421 GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCGCGTGGATCAGCCT 480
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Db      421 GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCGCGTGGATCAGCCT 480

Qy      481 CAATTACAGTAGTGCCTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CAATTACAGTAGTGCCTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540

Qy      541 GGAGGGGACTTGCTGTCTGTCCAGTAGTGAGTGATGAATGAAAACCTGATACGTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGAGGGGACTTGCTGTCTGTCCAGTAGTGAGTGATGAATGAAAACCTGATACGTG 600

Qy      601 CAGTTTTACCTAGCTGAGCTTGTGTTCACAGCGTTCATCTGATGGGGATACGTG 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CAGTTTTACCTAGCTGAGCTTGTGTTCACAGCGTTCATCTGATGGGGATACGTG 660

Qy      421 GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCGCGTGGATCCCC 480
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Db      421 GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCGCGTGGATCCCC 480

Qy      481 CAATTACAGTATGCCTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
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Db      481 CAATTACAGTATGCCTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540

Qy      541 GGAGGGGACTTGCTGTCTGTCCAGTAGTGAGTGATGAATGAAAACCTGATACGTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGAGGGGACTTGCTGTCTGTCCAGTAGTGAGTGATGAATGAAAACCTGATACGTG 600

Qy      601 CAGTTTTACCTAGCTGAGCTTGTGTTCACAGCGTTCATCTGATGGGGATACGTG 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CAGTTTTACCTAGCTGAGCTTGTGTTCACAGCGTTCATCTGATGGGGATACGTG 660

Qy      661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720

Qy      721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGCAGATGGTGAATGCCAAACTCCCGATT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGCAGATGGTGAATGCCAAACTCCCGATT 780

Qy      781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGC 840

Qy      841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 900

Qy      901 GGGAGATCCCCTTGCGAGAGGAACCTTGCCAGAACCTTCAATAACATTATGAATTC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GGGAGATCCCCTTGCGAGAGGAACCTTGCCAGAACCTTCAATAACATTATGAATTC 960

Qy      961 CAGCCGGTTTGAAATTTCCAGATGAGCAGTCAGTTCTTGATCTGATT 1020
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CAGCCGGTTTGAAATTTCCAGATGAGCAGTCAGTTCTTGATCTGATT 1020

Qy     1021 CAAAGCTTGTGTGTGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTGCTGCGTGCCATCCT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CAAAGCTTGTGTGTGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTGCTGCGTGCCATCCT 1080

Qy     1081 TTCTTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTCGTTCCCACC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TTCTTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTCGTTCCCACC 1140

Qy     1141 CTCAAGTCGACGATGACACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 CTCAAGTCGACGATGACACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA 1200

Qy     1201 TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGTTTGTGGGG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCGTTTGTGGGG 1260

Qy     1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGTAGATCTGAGTCTGTGTCTGGGGTCTG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGTAGATCTGAGTCTGTGTCTGGGGTCTG 1320

Qy     1321 GACTCCCTGCCAAGACTAGCTCATGGAAAAGAAACTTCTCATCAAAGCAAAGAGCTA 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GACTCCCTGCCAAGACTAGCTCATGGAAAAGAAACTTCTCATCAAAGCAAAGAGCTA 1380

Qy     1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGGCCCCTTCCTTGC 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGGCCCCTTCCTTGC 1440

Qy     1441 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCGCCCGGGCCGCCTGCTGGCCTCTGA 1500
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Db     1441 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCGCCCGGGCCGCCTGCTGGCCTCTGA 1500
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```
APPLICANT:  GANDHI, Ameena R.
APPLICANT:  TRIBOULEY, Catherine M.
APPLICANT:  CHAWLA, Narinder K.
APPLICANT:  YAO, Monique G.
APPLICANT:  LU, Dyung Aina M.
APPLICANT:  GREENWALD, Sara R.
APPLICANT:  RAMKUMAR, Jayalaxmi
APPLICANT:  GRIFFIN, Jennifer A.
APPLICANT:  KEARNEY, Liam
APPLICANT:  BURFORD, Neil
APPLICANT:  NGUYEN, Danniel B.
APPLICANT:  TANG, Y. Tom
APPLICANT:  BAUGHN, Mariah R.
APPLICANT:  HE, Ann
APPLICANT:  THORNTON, Michael
APPLICANT:  HAFALIA, April
APPLICANT:  ARVIZU, Chandra S.
APPLICANT:  GURURAJAN, Rajagopal
APPLICANT:  LO, Terence P.
APPLICANT:  KHAN, Farrah A.
APPLICANT:  RECIPON, Shirley A.
APPLICANT:  AZIMZAI, Yalda
APPLICANT:  POLICKY, Jennifer L.
APPLICANT:  DING, Li
APPLICANT:  GRETHER, Megan
APPLICANT:  ELLIOTT, Vicki S.
APPLICANT:  THANGAVELU, Kavitha
APPLICANT:  BATRA, Sajeev
APPLICANT:  ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 2066
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33

Query Match          99.7%;  Score 1510.2;  DB 17;  Length 2066;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1512;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     1 GGGGAGGATGTTGAAGTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCGTGCTGCTGAA    60
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Db     8 GGGGAGGATGTTGAAGTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCGTGCTGCTGAA    67

Qy    61 CCCATTGCCAACCGGGGCTCCAGGCTGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG   120
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Db    68 CCCATTGCCAGCCGGGGCTCCAGGCTGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG   127

Qy   121 ACTCAACAGCAGATGTCCTCCTTTCCCGAGAAGGATATTAAGATGCCCTCCTTTGTTCTC    180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 ACTCAACAGCAGATGTCCTCCTTTCCCGAGAAGGATATTAAGATGCCCTCCTTTGTTCTC    187

Qy   181 TTTGAAGAATGCAGTCAGCCTGCTGATGAAGAGAGCGCGGAATCCTTTGAGCACGTTGTCCGG   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 TTTGAAGAATGCAGTCAGCCTGCTGATGAAGAGAGCGCGGAATCCTTTGAGCACGTTGTCCGG   247

Qy   241 AAGTATTCCGACACCATAGTCGAGTTACAGGAGCTTCAGCCTTCGGCAAAGGACTTCGAA    300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 AAGTATTCCGACACCATAGTCGAGTTACAGGAGCTTCAGCCTTCGGCAAAGGACTTCGAA    307

Qy   301 GTCAGAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGTGAAGTGCAGTGGTGAAGAGAAAGCA   360
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Qy   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCGTGGTG   720
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Db   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCGTGGTG   720

Qy   721 GATTTGGATCTGCCGCGGAAATGAATTCAAACAAGATGGTGAAATGCCAAACTCCCGATT   780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GATTTGGATCTGCCGCGGAAATGAATTCAAACAAGATGGTGAAATGCCAAACTCCCGATT   780

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAAGGC   840
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Db   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAAGGC   840

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGGCGTGATGATTTAT   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGGCGTGATGATTTAT   900

Qy   901 GGGAGATCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGGAGATCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC   960

Qy   961 CAGCCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTCTTGATCTGATT  1020
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Db   961 CAGCCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTCTTGATCTGATT  1020

Qy  1021 CAAAGCTGTGTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CAAAGCTGTGTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1080

Qy  1081 TTCTTCTCTAAAATTGACTGAACAACATTGTAACTCTCCTCCCCCCTTCGTTCCACC  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTCTTCTCTAAAATTGACTGAACAACATTGTAACTCTCCTCCCCCCTTCGTTCCACC  1140

Qy  1141 CTCAAGTCCGACGATGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCA  1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CTCAAGTCCGACGATGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCA  1200

Qy  1201 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCCGGTGAAGAACTGCCGTTTGTGGGG  1260
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Db  1201 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCCGGTGAAGAACTGCCGTTTGTGGGG  1260

Qy  1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG  1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG  1320

Qy  1321 GACTCCCCTGCCAAGACTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA  1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GACTCCCCTGCCAAGACTAGCTCCATGGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA  1380

Qy  1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTGC  1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTGC  1440

Qy  1441 TCCAGGATCCTCCCGTCCCGTATATGCCAAGGGATCCCAAGGGGCCTGCTCTGA  1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 TCCAGGATCCTCCCGTCCCGTATATGCCAAGGGATCCCAAGGGGCCTGCTCTGA  1500

Qy  1501 GCCGGCCTGATCCGTA  1515
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Db  1501 GCCGGCCTGATCCGTA  1515

RESULT 4
US-10-311-034-33
; Sequence 33, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BOROWSKY, Mark L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Yan
```

```
Db  1388 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTCCGCAGCCGGCCGCCTCCTTCCTTGC 1447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441 TCCAGGATCCTCCCGTCCGTATATGCCGTATATGCCAAGGGATCCCGCGTCCGTCTCGCTCTGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1448 TCCAGGATCCTCCCGTCCGTATATGCCGTATATGCCAAGGGATCCCGCGGGCCGGGCCGTGCTCGCTCTGA 1507

Qy  1501 GCCGCCTGATCCGTA 1515
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Db  1508 GCCGCCTGATCCGTA 1522
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RESULT 5

US-10-415-011-43

; Sequence 43, Application US/1041501l
; Publication No. US20040053394A1
; GENERAL INFORMATION:
;   APPLICANT: INCYTE CORPORATION
;   APPLICANT: GURURAJAN, Rajagopal
;   APPLICANT: BAUGHN, Mariah R.
;   APPLICANT: CHAWLA, Narinder K.
;   APPLICANT: ELLIOTT, Vicki S.
;   APPLICANT: XU, Yuming
;   APPLICANT: ARVIZU, Chandra S.
;   APPLICANT: YAO, Monique G.
;   APPLICANT: RAMKUMAR, Jayalaxmi
;   APPLICANT: DING, Li
;   APPLICANT: TANG, Y. Tom
;   APPLICANT: HAFALIA, April J.A.
;   APPLICANT: NGUYEN, Danniel B.
;   APPLICANT: GANDHI, Ameena R.
;   APPLICANT: LU, Yan
;   APPLICANT: YUE, Henry
;   APPLICANT: BURFORD, Neil
;   APPLICANT: BANDMAN, Olga
;   APPLICANT: TRIBOULEY, Catherine M.
;   APPLICANT: LAL, Preeti G.
;   APPLICANT: RECIPON, Shirley A.
;   APPLICANT: LU, Dyung Aina M.
;   APPLICANT: BOROWSKY, Mark L.
;   APPLICANT: THORNTON, Michael B.
;   APPLICANT: SWARNAKER Anita
;   APPLICANT: THANGAVELU, Kavitha
;   APPLICANT: KHAN, Farrah A.
;   APPLICANT: ISON, Craig H.
;   TITLE OF INVENTION: HUMAN KINASES
;   FILE REFERENCE: PI-0262 USN
;   CURRENT APPLICATION NUMBER: US/10/415,011
;   CURRENT FILING DATE: 2003-04-18
;   PRIOR APPLICATION NUMBER: PCT/US01/47728
;   PRIOR FILING DATE: 2001-10-20
;   PRIOR APPLICATION NUMBER: US 60/242,410
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: US 60/244,068
;   PRIOR FILING DATE: 2000-10-27
;   PRIOR APPLICATION NUMBER: US 60/245,708
;   PRIOR FILING DATE: 2000-11-03
;   PRIOR APPLICATION NUMBER: US 60/247,672
;   PRIOR FILING DATE: 2000-11-09
;   PRIOR APPLICATION NUMBER: US 60/249,565
;   PRIOR FILING DATE: 2000-11-16
;   PRIOR APPLICATION NUMBER: US 60/252,730
;   PRIOR FILING DATE: 2000-11-22
;   PRIOR APPLICATION NUMBER: US 60/250,807
;   PRIOR FILING DATE: 2000-12-01
;   NUMBER OF SEQ ID NOS: 44
;   SOFTWARE: PERL Program
; SEQ ID NO 43
;   LENGTH: 6298
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1

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Db   308 GTCAGAAGTCTTGTAGTGTTGTGTCACTTTGCTGAAGTGCTGGTAAGAGAGAGAAAGCA 367
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Qy   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG 427

Qy   421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAGCCGTGGATCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAGCCGTGGATCCCC 487

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 547

Qy   541 GGAGGGGACTTGCTCGTGCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   548 GGAGGGGACTTGCTCGTGCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 607

Qy   601 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTGTTCACAGCCGTTCATCTGATGGGATACGTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTGTTCACAGCCGTTCATCTGATGGGATACGTG 667

Qy   661 CATCGAGACATCAAGCCTGAGACACATTCTCGTTGACCGGCCACAGGACACATCAAGCTGGTG 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   668 CATCGAGACATCAAGCCTGAGACACATTCTCGTTGACCGGCCACAGGACACATCAAGCTGGTG 727

Qy   721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   728 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATT 787

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   788 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGC 847

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   848 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 907

Qy   901 GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   908 GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 967

Qy   961 CAGCCGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   968 CAGCCGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1027

Qy  1021 CAAAGCTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1028 CAAAGCTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1087

Qy  1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1088 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1147

Qy  1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCA 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1148 CTCAAGTCTGACGATGACACCTCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTCA 1207

Qy  1201 TCCTCTCCGTGCCAGCTGAGCCCTTCAGGCTTCTCGGGTGAAGAACTGCGCGTTTGTGTGGGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1208 TCCTCTCCGTGCCAGCTGAGCCCTTCAGGCTTCTCGGGTGAAGAACTGCGCGTTTGTGTGGGG 1267

Qy  1261 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCGAGTCTGTGTGTCGGGTCTG 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1268 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCGAGTCTGTGTGTCGGGTCTG 1327

Qy  1321 GACTCCCCTGCCAAGACTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGAGCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1328 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTA 1387

Qy  1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTCCGCAGCCGGCCGCCTCCTTGC 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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US-10-415-011-43

Query Match   92.7%; Score 1404.2; DB 17; Length 6298;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     1  GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    49  GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA   108

Qy    61  CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109  CCCATTGCCAGCCGGGGCCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATG   168

Qy   121  ACTCAACAGCAGAGATGTCTCCCTCTTTCCCGAGAAGGGATAATTAGATGCCCTTTGTTCTC   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169  ACTCAACAGCAGAGATGTCTCCCTCTTTCCCGAGAAGGGATATTAGATGCCCTTTGTTCTC   228

Qy   181  TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229  TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG   288

Qy   241  AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289  AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA   348

Qy   301  GTCAGAAGTCTTGTAGGTGTGGTCACTTTGCTGAAGTGCGAGGTGGTAAGAGAGAAAGCA   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349  GTCAGAAGTCTTGTAGGTGTGGTCACTTTGCTGAAGTGCGAGGTGGTAAGAGAGAAAGCA   408

Qy   361  ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409  ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG   468

Qy   421  GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCCTCGAAGCACAAGCCCGTGGATCCCC   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469  GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCCTCGAAGCACAAGCCCGTGGATCCCC   528

Qy   481  CAATTACAGTATGCCTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529  CAATTACAGTATGCCTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT   588

Qy   541  GGAGGGGACTTGCTGTCCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589  GGAGGGGACTTGCTGTCCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA   648

Qy   601  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCCGTTCATCTGATGGGATACGTG   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCCGTTCATCTGATGGGATACGTG   708

Qy   661  CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGCAGCACCATCAAGCGGTG   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   709  CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGCAGCACCATCAAGCGGTG   768

Qy   721  GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769  GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT   828

Qy   781  GGGACCCCAGATTACATACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAGGC   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829  GGGACCCCAGATTACATACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAGGC   888

Qy   841  ACCTACGGCCTGGACTGTGACTGTGCTGCAGTGGCGTCAGTGGGCGTGCCTATGGAGATGATTTAT   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889  ACCTACGGCCTGGACTGTGACTGGTCGTCAGTGGGCGTGGGGCGTGCCTATGGAGATGATTTAT   948

Qy   901  GGGAGATCCCCTTCGCCGGAGAGGGAACCTTCTGCCAGAACCTTCAATAACATTATGAATTTC   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949  GGGAGATCCCCCTTCGCCGGAGAGGGAACCTTCTGCCAGAACCTTCAATAACATTATGAATTTC  1008

Qy   961  CAGCCGGTTTTTGAAATTTCCGATGAGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1009  CAGCCGGTTTTTGAAATTTCCGATGAGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT  1068

Qy  1021  CAAAGCTTGTTGTGTGCGCGCCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1069  CAAAGCTTGTTGTGTGCGCGCCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1128

Qy  1081  TTCTTCCTCTAAAATTGACTGGAACAATCTGTAACCTCTCCTCCCCCCTTCGTTCCCACCC  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1129  TTCTTCCTCTAAAATTGACTGGAACAACACATTCGTAACCTCTCCTCCCCCCTTCGTTCCCACC  1188

Qy  1141  CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCA  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1189  CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCA  1248

Qy  1201  TCCTCTCCGTGCCAGCTGAGCCCTCCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1249  TCCTCTCCGTGCCAGCTGAGCCCTCCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG  1308

Qy  1261  TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTGTCGGGTCTG  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1309  TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTCTGTGTCGGGTCTG  1368

Qy  1321  GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCATCAAAAGAACAAAGAGAGCTA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1369  GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCATCAAAAGAACAAAGAGAGCTA  1428

Qy  1381  CAAGACTCTCAGGACAAGTGTCACAAGGT  1409
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Db  1429  CAAGACTCTCAGGACAAGTGTCACAAGAT  1457
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RESULT 6
US-10-262-511-3
; Sequence 3, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917

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;      PRIOR FILING DATE: 2001-10-09
;      PRIOR APPLICATION NUMBER: 60/381,642
;      PRIOR FILING DATE: 2002-05-17
;      PRIOR APPLICATION NUMBER: 60/328,029
;      PRIOR FILING DATE: 2002-10-09
;      PRIOR APPLICATION NUMBER: 60/381,038
;      PRIOR FILING DATE: 2002-05-16
;      PRIOR APPLICATION NUMBER: 60/328,056
;      PRIOR FILING DATE: 2001-10-09
;      PRIOR APPLICATION NUMBER: 60/373,260
;      PRIOR FILING DATE: 2002-04-17
;      PRIOR APPLICATION NUMBER: 60/373,826
;      PRIOR FILING DATE: 2002-04-19
;      PRIOR APPLICATION NUMBER: 60/327,435
;      PRIOR FILING DATE: 2001-10-05
;      Remaining Prior Application data removed - See File Wrapper or PALM.
;      NUMBER OF SEQ ID NOS: 439
;      SOFTWARE: CuraSeqList version 0.1
;
; SEQ ID NO 3
;      LENGTH: 1870
;      TYPE: DNA
;      ORGANISM: Homo sapiens
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: (2)..(1870)
US-10-262-511-3

Query Match       92.3%;    Score 1398.2;    DB 17;    Length 1870;
Best Local Similarity    99.8%;    Pred. No. 0;
Matches 1400;    Conservative    0;    Mismatches    3;    Indels    0;    Gaps    0;

Qy       7 ATGTTGAAGTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGTCTGCTGAACCCATT  66
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14 ATGTTGAAGTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGTCTGCTGAACCCATT  73

Qy      67 GCCAACCGGCCCTCCAGGCTGAATCGTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTCTCTTTGAA  126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 GCCAGCCGGCCCTCCAGGCTGAATCGTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTCTCTTTGAA  133

Qy     127 CAGCAGATGTCTCCTCTTTCCCGAGAGGGATATTAGATGCACGTGAGCAACTTTGTCCGGAAGTAT  186
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 CAGCAGATGTCTCCTCTTTCCCGAGAGGGATATTAGATGCACGTGAGCAACTTTGTCCGGAAGTAT  193

Qy     187 GAATGCAGTCAGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT  246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GAATGCAGTCAGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT  253

Qy     247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA  306
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA  313

Qy     307 AGTCTTGTAGGTTGGTCACTTTGCTGAAGTGGTGTAAGAGAGAAAGCAACCGGG  366
            |||||||||||||||||||||||||||||||||||||||||||||
Db     314 AGTCTTGTAGGTTGGTCACTTTGCTGAAGTGGTGTAAGAGAGAAAGCAACCGGG  373

Qy     367 GACATCTATGCTATGAAAGTGATGAAGAAGCGCTTATTGGCCCAGGAGCAGTTTCA  426
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     374 GACATCTATGCTATGAAAGTGATGAAGAAGCGCTTATTGGCCCAGGAGCAGTTTCA  433

Qy     427 TTTTTTGACGAAGAGCGGAACATATTATCTCGAGCACAAGCCCGTTCCCCAATTA  486
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 TTTTTTGACGAAGAGCGGAACATATTATCTCGAGCACAAGCCCGTTCCCCAATTA  493

Qy     487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG  546
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db     494 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG  553

Qy     547 GACTTGCTGTCACTTTGAATAGATAGATGGACCAGTTAGATGAAAACCTGATACAGTTT  606
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     554 GACTTGCTGTCACTTTGAATAGATAGATGGACCAGTTAGATGAAAACCTGATACAGTTT  613

Qy     607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA  666
            ||||||||||||||||||||||||||||||||||||||||||||
Db     614 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA  673

Qy     667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGTGGGATTT  726
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     674 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGCGTGGGATTT  733

Qy     727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC  786
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     734 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC  793

Qy     787 CCAGATTACATGGCTTCCTGAAGTGCTGACTGTGAGTGATGAGGATGGAAAAGGCCACCTAC  846
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db     794 CCAGATTACATGGCTTCCTGAAGTGCTGACTGTGAGTGATGAGGATGGATGGAAAAGGCCACCTAC  853

Qy     847 GGCCTGGACTGGACTGTGGTCAGTGGCCGTGAGTGGCCGTGATTGCCTATGAGATGATTATGGGAGA  906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     854 GGCCTGGACTGGACTGTGGTCAGTGGCCGTGAGTGGCCTATGAGATGATTATGGGAGA  913

Qy     907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCCGG  966
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     914 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCCGG  973

Qy     967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC  1026
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     974 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC  1033

Qy    1027 TTGTTGTGCGGCCAGAAAGAGACGTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC  1086
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    1034 TTGTTGTGCGGCCAGAAAGAGACGTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC  1093

Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCCTTCGTTCCCACCCTCAAG  1146
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCCTTCGTTCCCACCCTCAAG  1153

Qy    1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT  1206
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    1154 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT  1213

Qy    1207 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCCGGGTGAAGAACTGCCGGTTGTGTGGGGTTTTCG  1266
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1214 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCCGGGTGAAGAACTGCCGGTTGTGTGGGGTTTTCG  1273

Qy    1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCGCGGGTCTGGACTCC  1326
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    1274 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCGCGGGTCTGGACTCC  1333

Qy    1327 CCTGCCAAGACTAGCTCCATGGAAAGAAAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC  1386
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1334 CCTGCCAAGACTAGCTCCATGGAAAGAAAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC  1393

Qy    1387 TCTCAGGACAAGTGTCACAAGGT  1409
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Db    1394 TCTCAGGACAAGTGTCACAAGAT  1416
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RESULT 7
US-10-028-946-3
;      Sequence 3, Application US/10028946
;      Publication No. US20020123622A1
;      GENERAL INFORMATION:
;      APPLICANT: Yu, Xuanchuan
;      APPLICANT: Miranda, Maricar
;      APPLICANT: Friddle, Carl Johan
;      TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polynucleotides Encoding t
;      FILE REFERENCE: LEX-0289-USA
;      CURRENT APPLICATION NUMBER: US/10/028,946
;      CURRENT FILING DATE: 2001-12-20
;      PRIOR APPLICATION NUMBER: US 60/258,335
;      PRIOR FILING DATE: 2000-12-27
;      NUMBER OF SEQ ID NOS: 4
;      SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 3
;      LENGTH: 5877
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;  TYPE: DNA
;  ORGANISM: homo sapiens
US-10-028-946-3

  Query Match       92.3%;  Score 1398.2;  DB 13;  Length 5877;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1400;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      7 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy     67 GCCAACCGGGCCTGAATCGTTCTTCCGAGAAGGGATATAGATGCCCTCTTGTTCTCTTGAA 126
            |||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCAGCCGGGGCCTGAATCGTTCTTCCGAGAAGGGATATAGATGCCCTCTTGTTCTCTTGAA 120

Qy    127 CAGCAGATGTCTCCTGCTCGGAGGGATATTAGATGCACGTGAGCAACTTGTCCGGAAGTAT 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGATGTCTCCTGCTCGGAGGGATATTAGATGCACGTGAGCAACTTGTCCGGAAGTAT 180

Qy    187 GAATGCAGTCAGCCTCTGATGAGAAGTGAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAATGCAGTCAGCCTCTGATGAGAAGTGAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy    247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCGAAAGGACTTCGGAGTCAGA 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCGAAAGGACTTCGGAGTCAGA 300

Qy    307 AGTCTTGTAGGTGTGTCACTTGCTGAGTGCAGGTGCAGGTGGTAAGAGAAGCACCCGGG 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGTCTTGTAGGTGTGTCACTTGCTGAGTGCAGGTGCAGGTGGTAAGAGAAGCACCCGGG 360

Qy    367 GACATCTATGCTATGAAAGTGATGAACGAAGAGGCTTTATTGGCCAGGAGCAGGTTTCA 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACATCTATGCTATGAAAGTGATGAACGAAGAGGCTTTATTGGCCAGGAGCAGGTTTCA 420

Qy    427 TTTTTGAGGAAGAGCGGAACATATTCTGAAGCACAAGCCCGTGGATCCCCAATTA 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTTTTGAGGAAGAGCGGAACATATTCTGAAGCACAAGCCCGTGGATCCCCAATTA 480

Qy    487 CAGTATGCCTTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGTATGCCTTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540

Qy    547 GACTTGCTCGTCACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACTTGCTCGTCACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy    607 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy    667 GACATCAAGCCTGAGAACATTCTCGTTGACCGGACAGGACACATCAAGCTGGTGGATTTT 726
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GACATCAAGCCTGAGAACATTCTCGTTGACCGGACAGGACACATCAAGCTGGTGGATTTT 720

Qy    727 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy    787 CCAGATTACATGGCTCCTGAAGTGCTGATGAACGGGATCGAAAGGCACCTAC 846
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCAGATTACATGGCTCCTGAAGTGCTGATGAACGGGATCGAAAGGCACCTAC 840

Qy    847 GGCCTGGACTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGCCTGGACTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 900

Qy    907 TCCCCCCTTCGGCAGAGGGAACCTGCCAGAACTTCAAATAAACATTATGAATTTCCAGCGG 966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TCCCCCCTTCGGCAGAGGGAACCTGCCAGAACTTCAAATAAACATTATGAATTTCCAGCGG 960

Qy    967 TTTTTGAAATTTCCAGATGACCCCAAAGTGACCTTCTGATCGTGACTTTCTGATTCAAAGC 1026
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTTGAAATTTCCAGATGACCCCAAAGTGACCTGAAGTGAGCAGTGACTTCTGATTCAAAGC 1020

Qy   1027 TTGTTGTGCGGCCAGAAGAAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTCTTC 1086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTGTTGTGCGGCCAGAAGAAGAGACTGAAGTTGAAGGTCTTGCCATCCTTCTTC 1080

Qy   1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1146
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1140

Qy   1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTTGGGTTTCATCCTCT 1206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCT 1200

Qy   1207 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGTTTCG 1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCG 1260

Qy   1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC 1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC 1320

Qy   1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAGAGACTACAAGAC 1386
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAGAGACTACAAGAC 1380

Qy   1387 TCTCAGACAAGTGTCACAAGT 1409
            |||||||||| ||||||||||
Db   1381 TCTCAGACAAGTGTCACAAGAT 1403


RESULT 8
US-10-791-666-3
;  Sequence 3, Application US/10791666
;  Publication No. US2004020929741
;  GENERAL INFORMATION:
;    APPLICANT: Yu, Xuanchuan
;    APPLICANT: Miranda, Maricar
;    APPLICANT: Friddle, Carl Johan
;    TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
;    FILE REFERENCE: LEX-0289-USA
;    CURRENT APPLICATION NUMBER: US/10/791,666
;    CURRENT FILING DATE: 2004-03-02
;    PRIOR APPLICATION NUMBER: US/10/028,946
;    PRIOR FILING DATE: 2001-12-20
;    PRIOR APPLICATION NUMBER: US 60/258,335
;    PRIOR FILING DATE: 2000-12-27
;    NUMBER OF SEQ ID NOS: 4
;    SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 3
;    LENGTH: 5877
;    TYPE: DNA
;    ORGANISM: homo sapiens
US-10-791-666-3

  Query Match       92.3%;  Score 1398.2;  DB 18;  Length 5877;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1400;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      7 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy     67 GCCAACCGGGCCTGAATCGTTCTTCCGAGGGAAACCACCCTTTATGACTCAA 126
            |||| ||||| |||||||||||||||||||||||||||||||||||||||||
Db     61 GCCAGCCGGGGCCTGAATCGTTCTTCCGAGGGAAACACCCTTTATGACTCAA 120

Qy    127 CAGCAGAATGTCTCCTCCAGAAGCCTGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTGAA 186
            ||||||| ||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTTGAA 180

Qy    187 GAATGCAGTCAGCCTCTGATGAGAAGTGAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
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Db 1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCGGGTCTGGACTCC 1320

Qy 1327 CCTGCCAAGACTAGCTCCATGAAGAAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 CCTGCCAAGACTAGCTCCATGAAGAAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1380

Qy 1387 TCTCAGGACAAGTGTCACAAGGT 1409
         |||||||||||||||||||||||
Db 1381 TCTCAGGACAAGTGTCACAAGAT 1403

RESULT 9
US-10-028-946-1
; Sequence 1, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-1

Query Match   92.3%;   Score 1398.2;   DB 13;   Length 6165;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 66
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy   67 GCCAACCGGGCCTCCAGGCGCTGAATCGTCTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCAGCCGGGCCTCCAGGCGCTGAATCGTCTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy 127 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTCTTGTCTCTTGAA 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTCTTGTCTCTTGAA 180

Qy 187 GAATGCAGTCAGCCTGCTCTGATGAAGTTACAGGAGCTCGAGCAACTTTGTCCGGAAGTAT 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GAATGCAGTCAGCCTGCTCTGATGAAGTTACAGGAGCTCGAGCAACTTTGTCCGGAAGTAT 240

Qy 247 TCCGACACCATAGCTGAGTTACACTTGCTCAGTGGTCAGGTGGTAAGAGAAAGCAACCGGG 306
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TCCGACACCATAGCTGAGTTACACTTGCTCAGTGGTCAGGTGGTAAGAGAAAGCAACCGGG 300

Qy 307 AGTCTTGTAGGTTGTGGCGCTGTGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCAGGTTCA 366
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGTCTTGTAGGTTGTGGCGCTGTGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCAGGTTCA 360

Qy 367 GACATCTATGCTATGAAAGTGATGAAAAGTGATGAAGAAGAAGAGGCGGAACATATATCTCGAAGCACAAGCCGTGGATCCCCAATTA 426
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACATCTATGCTATGAAAGTGATGAAAAGTGATGAAGAAGAAGAGGCGGAACATATATCTCGAAGCACAAGCCGTGGATCCCCAATTA 420

Qy 427 TTTTTGAGGAAGAGCGGAACAAATCACCTTTATCTCGTCATGGAAATATCACCTTTATCTCGTCATGGAAATATCAGCCTGAGGG 486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TTTTTGAGGAAGAGCGGAACAAATCACCTTTATCTCGTCATGGAAATATCACCTTTATCTCGTCATGGAAATATCAGCCTGAGGG 480

Qy 487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAAATATCAGCCTGAGGGG 546
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAAATATCAGCCTGAGGGG 540

[left column]

Db 181 GAATGCAGTCAGCCTGCTCTGATGAAGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy 247 TCCGACACCATAGCTGAGTTACAGGAGCTTCGCAGAAGGACTTCGAGCAACTTGGAAGTCAGA 306
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TCCGACACCATAGCTGAGTTACAGGAGCTTCGCAGAAGGACTTCGAGCAACTTGGAAGTCAGA 300

Qy 307 AGTCTTGTAGGTGTGGTCACTTGCTCAGTGGTCAGGTGGTAAGAGAAAGCAACCGGG 366
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGTCTTGTAGGTGTGGTCACTTGCTCAGTGGTCAGGTGGTAAGAGAAAGCAACCGGG 360

Qy 367 CAGTATGCCTTTCAGGACAAAAATCAGCGGGATATCAGTGGAATATCAGCCTGGAGGG 426
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CAGTATGCCTTTCAGGACAAAAATCAGCGGGATATCAGTGGAATATCAGCCTGGAGGG 420

Qy 427 GACTGCTGCTGTCACTTTTGAATAGATGAGGACCAGTTAGATAGAAACCTGATACAGTTT 486
Db 421 GACTGCTGCTGTCACTTTTGAATAGATGAGGACCAGTTAGATAGAAACCTGATACAGTTT 480

Qy 487 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 546
Db 481 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 540

Qy 607 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGCGACACATCAAGCTGGTGGATTTT 666
Db 601 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy 727 GGATCTGCCGCGAAAATGAATCAAACAAGAGTGAATGCCAAACTCCCGATTGGGACC 786
Db 661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGCGACACATCAAGCTGGTGGATTTT 720

Qy 787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAGGCACCTAC 846
Db 721 GGATCTGCCGCGAAAATGAATCAAACAAGAGTGAATGCCAAACTCCCGATTGGGACC 780

Qy 847 GGCCTGGACTGTGACTGGTGTGCTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 906
Db 781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGGATGGAAAGGCACCTAC 840

Qy 907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGGAACCTCCAGAACCTGACTTTCTGATTCAAAGC 966
Db 841 GGCCTGGACTGTGACTGGTGTGCTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 900

Qy 967 TTTTTGAAATTTCAGAGTCTTGTGTGCGCATCCTTTGCTGCCATCCTTTCTTC 1026
Db 901 TCCCCCTTCGCAGAGGGAACCTCTGCCAGGAACCTCCAGAACCTGACTTTCTGATTCAAAGC 960

Qy 1027 TTGTTGTGTCGGCCAGAAGAGAGAGAGACTGAAGTTTGAAGGTCTTGCGCCATCCTTTCTTC 1086
Db 961 TTTTTGAAATTTCAGAGTCTTGTGTGCGCATCCTTTGCTGCCATCCTTTCTTC 1020

Qy 1087 TCTAAAATTGACTGGAACAACATGCCCAATTTGATGAACCAGAAGAATTCGTAACTCTCT 1146
Db 1021 TTGTTGTGTCGGCCAGAAGAGAGAGAGACTGAAGTTTGAAGGTCTTGCGCCATCCTTTCTTC 1080

Qy 1147 CCGACGATGACACCTTCAGGCCCTGAGCCCTGCCGTTTGCCGTTTCATCCTCT 1206
Db 1081 TCTAAAATTGACTGGAACAACATGCCCAATTTGATGAACCAGAAGAATTCGTAACTCTCT 1140

Qy 1207 CCGTGCCAGCTGAGCCCTGCCGTTTGTGGGTTTTCG 1266
Db 1141 CCGACGATGACACCTTCAGGCCCTGAGCCCTGCCGTTTGCCGTTTCATCCTCT 1200

Qy 1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCGGGTCTGGACTCC 1325
Db 1201 CCGTGCCAGCTGAGCCCTGCCGTTTGTGGGTTTTCG 1260

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;   PRIOR APPLICATION NUMBER: US/10/028,946
;   PRIOR FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: US 60/258,335
;   PRIOR FILING DATE: 2000-12-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1
;   LENGTH: 6165
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-791-666-1

Query Match           92.3%;   Score 1398.2;   DB 18;   Length 6165;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1400;   Conservative  0;   Mismatches  0;   Indels  3;   Gaps  0;
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Qy    7 ATGTTGAAGTTCAAATATGGAGCGCCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGTTGAAGTTCAAATATGGAGCGCCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy   67 GCCAACCGGCCTCCAGCTGAATCTGTCTTCTTCCAGGGGAAACACCACCCTTTATGACTCAA 126
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCAGCGCGGCCTCCAGCTGAATCTGTCTTCTTCCAGGGGAAACACCACCCTTTATGACTCAA 120

Qy  127 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

Qy  187 GAATGCAGTCAGCCTCGTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GAATGCAGTCAGCCTCGTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy  247 TCCGACACCATAGCTGAGTTACAGGAGTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAAGACTTCGAGGA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCCGACACCATAGCTGAGTTACAGGAGTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAAGACTTCGAGGA 300

Qy  307 AGTCTTGTAGGTTGTGTCACTTTGCTGCAGTGGCAGTGGTAAGAGAAAGCAACCGGG 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGTCTTGTAGGTTGTGTCACTTTGCTGCAGTGGCAGTGGTAAGAGAAAGCAACCGGG 360

Qy  367 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCCAGGTTTCA 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCCAGGTTTCA 420

Qy  427 TTTTTGAGGAAGAGCGGAACATCACCTTTATCTCGTCTGTTGAATATCAGCCGGAGGG 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TTTTTGAGGAAGAGCGGAACATCACCTTTATCTCGTCTGTTGAATATCAGCCGGAGGG 480

Qy  487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCTGTCATGGGGTCTGGACTCC 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCTGTCATGGGGTCTGGACTCC 540

Qy  547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTT 600

Qy  607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 660

Qy  667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720

Qy  727 GGATCTGCCGGCGAAAATGAATTCAAACAAGATGGTGAATGCCCAAACTCCCGATTGGGACC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GGATCTGCCGGCGAAAATGAATTCAAACAAGATGGTGAATGCCCAAACTCCCGATTGGGACC 780

Qy  787 CCAGATTACATGGCTCTGACTGCTGAGTCAGTGTGTGATGAGAACGGGGATGGAAAAGGCACCTAC 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCAGATTACATGGCTCTGACTGCTGAGTCAGTGTGTGATGAGAACGGGGATGGAAAAGGCACCTAC 840

Qy  847 GGCCTGACTGCTGACTGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GGCCTGACTGCTGACTGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGA 906
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Qy  547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTAGATGAAAAACCTGATACAGTTT 600

Qy  607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 660

Qy  667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720

Qy  727 GGATCTGCCGGCGAAAATGAATTCAAACAAGATGGTGAATGCCCAAACTCCCGATTGGGACC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GGATCTGCCGGCGAAAATGAATTCAAACAAGATGGTGAATGCCCAAACTCCCGATTGGGACC 780

Qy  787 CCAGATTACATGGCTCTGACTGCTGAGTCAGTGTGTGATGAGAACGGGGATGGAAAAGGCACCTAC 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCAGATTACATGGCTCTGACTGCTGAGTCAGTGTGTGATGAGAACGGGGATGGAAAAGGCACCTAC 840

Qy  847 GGCCTGACTGTGACTGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GGCCTGACTGTGACTGTGGTCAGTGGGCCGTGATTGCCTATGAGATGATTTATGGGAGA 900

Qy  907 TCCCCCTTCCGCAGAGGAACCTTCGCCAGACCTTCAATAACAATATTATGAATTTCCAGCCG 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TCCCCCTTCCGCAGAGGAACCTTCGCCAGACCTTCAATAACAATATTATGAATTTCCAGCCG 960

Qy  967 TTTTGAAATTTCCAGATGACGACCCCAAAGTGAGCAGTGACTTTCTTGATTCTGATTCAAAGC 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TTTTGAAATTTCCAGATGACGACCCCAAAGTGAGCAGTGACTTTCTTGATTCTGATTCAAAGC 1020

Qy 1027 TTGTTGCGGCCAGAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGTTCTTGCTGCCATCCTTTCTTC 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTGTTGCGGCCAGAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGTTCTTGCTGCCATCCTTTCTTC 1080

Qy 1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCCACCCTTCCCACCCTCAAG 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCCACCCTTCCCACCCTCAAG 1140

Qy 1147 TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCTGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy 1207 CCGTTGCCAGCTGAGCCCTGAGCCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGTTTTCG 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 CCGTTGCCAGCTGAGCCCTGAGCCTTCTCGGGTGAAGAACTGCCGTTTGTGTGGGTTTTCG 1260

Qy 1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCTGGACTCC 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCGAGTCTGTTGTGTCTGGACTCC 1320

Qy 1327 CCTGCCAAGACTAGCTCCATGGGAAAAGAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 CCTGCCAAGACTAGCTCCATGGGAAAAGAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC 1380

Qy 1387 TCTCAGGACAAGTGTCACAAGGT 1409
          |||||||||||||||||||||| |
Db 1381 TCTCAGGACAAGTGTCACAAGAT 1403
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RESULT 10
US-10-791-666-1
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;   Sequence 1, Application US/10791666
;   Publication No. US2004/0209297A1
;   GENERAL INFORMATION:
;   APPLICANT: Yu, Xuanchuan
;   APPLICANT: Miranda, Maricar
;   APPLICANT: Friddle, Carl Johan
;   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
;   FILE REFERENCE: LEX-0289-USA
;   CURRENT APPLICATION NUMBER: US/10/791,666
;   CURRENT FILING DATE: 2004-03-02
```

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Qy  121  ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGATATTAGATGCCCTCTTTGTTCTC  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133  ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGATATTAGATGCCCTCTTTGTTCTC  192

Qy  181  TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  193  TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG  252

Qy  241  AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253  AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA  312

Qy  301  GTCAGAAGTCTTGTAGGTTGGTCACTTTGCTGGAAGTGCAGGTGGTAAGAGAAAAGCA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  313  GTCAGAAGTCTTGTAGGTTGGTCACTTTGCTGGAAGTGCAGGTGGTAAGAGAAAAGCA  372

Qy  361  ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  373  ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG  432

Qy  421  GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  433  GTTTCATTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC  492

Qy  481  CAATTACAGTATGCCTTCAGGACACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT  540
         ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db  493  CAATTACAGTATGCCTTCAGGACAAAAAATCACCTTTATCTGATGGAATATCAGCCT  552

Qy  541  GGAGGGGACTTGCTCGTCACTTTGAATAGATATGAGGACCAGTTAGTGAGAAACCTGATA  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  553  GGAGGGGACTTGCTCGTCACTTTGAATAGATATGAGGACCAGTTAGTGAGAAACCTGATA  612

Qy  601  CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCTTCACAGCGTTCATCTGATGGGATAGTG  660
         |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db  613  CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCTTCACAGCGTTCATCTGATGGGATAGTG  672

Qy  661  CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGACCAGCAGCACATCAAGCTCGTG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  673  CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGACCAGCAGCACATCAAGCTCGTG  732

Qy  721  GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  733  GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT  792

Qy  781  GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  793  GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC  852

Qy  841  ACCTACGGCCTGGACTGTGACTGGGCGGTCAGTGGGCGGTGATTGCCTATGAGATGATTTAT  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  853  ACCTACGGCCTGGACTGTGACTGGGCGGTCAGTGGGCGGTGATTGCCTATGAGATGATTTAT  912

Qy  901  GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  913  GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC  972

Qy  961  CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCACGTGACTTTCTTGATCTGATT  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  973  CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCACGTGACTTTCTTGATCTGATT  1032

Qy  1021 CAAAGTCGTTGTGTGCGGCCAGAAAGAGAGACTGAAGGTCTTGAAGGTCTTGCTGCCATCCT  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1033 CAAAGTCGTTGTGTGCGGCCAGAAAGAGAGACTGAAGGTCTTGAAGGTCTTGCTGCCATCCT  1092

Qy  1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACCTCTCCCCCCTTCGTTCCCACC  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1093 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACCTCTCCCCCCTTCGTTCCCACC  1152

Qy  1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAAGAAGAATTCGTGGGTTTCA  1200
         |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1153 CTCAAGTCTGACGATGACACCTCCAATTTGATGAACCAAGAAGAATTCGTGGGTTTCA  1212

Qy  1201 TCCTCTCCGTGCCAGCCCTGAGCCCTCCGAGGCTTCTCCGGGTGAAGAACTGCCGTTGTGTGGGG  1260
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Db  841  GGCCTGGACTGTGACTGGGCGGTCAGTGGGCGGTGATTGCCTATGAGATGATTTATGGGGAGA  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  907  TCCCCTTCGCAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAGATGATTTATGGGGCGG  966
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  TCCCCTTCGCAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATGAGATGATTTATGGGGCGG  960

Qy  967  TTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGAGTGAGCAGTGAGTCTTTGATTCAAAGC  1026
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGAGTGAGCAGTGAGTCTTTGATTCAAAGC  1020

Qy  1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGGTTTGAAGGTCTTTGTTGCTGCCATCCTTTCTTC  1086
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGGTTTGAAGGTCTTTGTTGCTGCCATCCTTTCTTC  1080

Qy  1087 TCTAAAATTGACTGGAACAACATTCGTAACCTCTCCTCCCTTCGTTCCCACCCTCAAG  1146
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TCTAAAATTGACTGGAACAACATTCGTAACCTCTCCTCCCTTCGTTCCCACCCTCAAG  1140

Qy  1147 CCGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCT  1206
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CTGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTGGGTTTCATCCTCTCT  1200

Qy  1207 CCGTCCAGCTGAGCCCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGGTTTCG  1266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 CCGTGCCAGCTGAGCCCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGGTTTCG  1260

Qy  1267 TACAGCAAGGCACTCGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC  1326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TACAGCAAGGCACTCGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC  1320

Qy  1327 CCTGCCAAGACTAGCTCCATGGAAAAAGAAAACTTCTCATCAAAGAGCAAAAGAGCTACAAAGAC  1386
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CCTGCCAAGACTAGCTCCATGGAAAAAGAAAACTTCTCATCAAAGAGCAAAAGAGCTACAAAGAC  1380

Qy  1387 TCTCAGGACAGTGTCACAAGGT  1409
         |||||||||||||||||||||
Db  1381 TCTCAGGACAGTGTCACAAGAT  1403
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RESULT 11
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
US-10-017-216-1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match   92.3%;   Score 1397.8;   DB 13;   Length 6574;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1402;   Conservative 0;   Mismatches 0;   Indels 7;   Gaps 0;

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Qy  1    GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCGTCGGTGCTGCTGAA  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13   GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCGTCGGTGCTGCTGAA  72

Qy  61   CCCATTGCCAACCGGGCCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCCTTTATG  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  73   CCCATTGCCAACCGGGCCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCCTTTATG  132
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RESULT 12
US-10-325-430-10
; Sequence 10, Application US/10325430
; Publication No. US20030153325A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceutical, Inc
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPI01-294P1RNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-325-430-10

Query Match   92.3%;   Score 1397.8;   DB 16;   Length 6574;
Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1402;   Conservative 0;   Mismatches 0;   Indels 7;   Gaps 0;

RESULT 13
US-10-757-262-51
; Sequence 51, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:

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; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 1589, 15995, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 17827, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)...(6180)
US-10-757-262-51

Query Match        92.3%;   Score 1397.8;   DB 18;  Length 6574;
Best Local Similarity 99.5%;  Pred. No. 0;
Matches 1402;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 72

Qy   61 CCCATTGCCAACCGGCGCCTCCAGGTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
         |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Db   73 CCCATTGCCAGCCGGCGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 132

Qy  121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTC 192

Qy  181 TTTGAAGAATGCAGTCAGCTCAGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  193 TTTGAAGAATGCAGTCAGCTCAGCCTGCTCTGATGAAGATTAAGCACGTGACAACTTGTCCGG 252

Qy  241 AAGTATTCCGACACCATAGCTGAGTTACAGGACTCGGCAAGGACTTCGAA 300
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  253 AAGTATTCCGACACCATAGCTGAGTTACAGGACTCGGCAAGGACTTCGAA 312

Qy  301 GTCAGAAGTCTTGTAGGTGTGGTCACTTGCTGAAGTGCAGTGGTCAGTGGTAAGAGAGAAAGCA 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  313 GTCAGAAGTCTTGTAGGTGTGGTCACTTGCTGAAGTGCAGTGGTCAGTGGTAAGAGAGAAAGCA 372

Qy  361 ACCGGGGACATCTATGCTATGAAAGTGATGAGAAGAGAGGCTTTATTGGCCCAGGAGCAG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  373 ACCGGGGACATCTATGCTATGAAAGTGATGAGAAGAGAGGCTTTATTGGCCCAGGAGCAG 432

Qy  421 GTTTCATTTTTTGAGGAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  433 GTTTCATTTTTTGAGGAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCC 492

Qy  481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 540
         |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  493 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTGAGGAATATCAGCCT 552

Qy  541 GGAGGGGACTTGCTCGTCGTGTCACTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  553 GGAGGGGACTTGCTCGTCGTGTCACTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 612

Qy  601 CAGTTTACCTAGCTGAGCTGATTTGGCTGTTGACCGACACAGGACACATCAAGCTGGTG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  613 CAGTTTACCTAGCTGAGCTGATTTGGCTGTTGACCGACACAGGACACATCAAGCTGGTG 672

Qy  661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGACCACAGCACATCAAGCTGGTG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  673 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGACCACAGCACATCAAGCTGGTG 732

Qy  721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  733 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 792

Qy  781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  793 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGC 852

Qy  841 ACCTACGGCCTGACTGGTGTCAGTGGCGTGATTGCCTATGAGATGATTTAT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  853 ACCTACGGCCTGACTGGTGTCAGTGGCGTGATTGCCTATGAGATGATTTAT 912

Qy  901 GGGAGATCCCCCTTCGGCGAGGAGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  913 GGGAGATCCCCCTTCGGCGAGGAGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTC 972

Qy  961 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  973 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1032

Qy 1021 CAAAGCTTGTTGTGCGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1033 CAAAGCTTGTTGTGCGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT 1092

Qy 1081 TTCTTCTCTAAAATTGACTGGAACACATTGAAGTTGAACAACATTCGTAACTCTCCTCCGCCCTCGTTCCCACC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1093 TTCTTCTCTAAAATTGACTGGAACACATTGAAGTTGAACAACATTCGTAACTCTCCTCCGCCCTCGTTCCCACC 1152

Qy 1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1153 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA 1212

Qy 1201 TCCTCTCCGTGCCAGCTGAGCCCTGAGGCCCTCAGGCTTCTCGGTGAAGAACTGCCCGTTTGTGGGG 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1213 TCCTCTCCGTGCCAGCTGAGCCCTGAGGCCCTCAGGCTTCTCGGTGAAGAACTGCCCGTTTGTGGGG 1272

Qy 1261 TTTTCACGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTCGTGTGTCGGGTCTG 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1273 TTTTCACGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTCGTGTGTCGGGTCTG 1332

Qy 1321 GACTCCCCTGCCAAGACTAGCTTCTCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1333 GACTCCCCTGCCAAGACTAGCTTCTCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1392

Qy 1381 CAAGACTCTCAGGACAAGTGTCACAGGT 1409
         ||||||||||||||||||||||||||
Db 1393 CAAGACTCTCAGGACAAGTGTCACAAGAT 1421
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RESULT 14
US-10-017-216-3
; Sequence 3, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELER-LIBERMANN, Rosana
;  TITLE OF INVENTION: 13245, A No. US2002016O483Alel Human Myotonic Dystrophy Type Prot
;  TITLE OF INVENTION: Kinase and Uses Thereof
;  FILE REFERENCE: 10147-57U1
;  CURRENT APPLICATION NUMBER: US/10/017,216
;  CURRENT FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 60/242,429
;  PRIOR FILING DATE: 2000-10-23
;  SOFTWARE: Patentin Ver. 2.1
;  NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 3
;  LENGTH: 6159
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-017-216-3

Query Match             91.9%;  Score 1391.8;  DB 13;  Length 6159;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1396;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy      7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGATGCTGCTGCTGAACCCATT 66
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGATGCTGCTGCTGAACCCATT 60

Qy     67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA 120

Qy    127 CAGCAGATGTCTCCTCTTCCCGAGAAGAGGGATATTAGAGTGCCCTCTTTGTTCTCTTTGAA 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGATGTCTCCTCTTCCCGAGAAGAGGGATATTAGAGTGCCCTCTTTGTTCTCTTTGAA 180

Qy    187 GAATGCAGTCAGCCTGCTCTGATGAAGACTGAAGCACGTGGCAACTTGTCCGGAAGTAA 246
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAATGCAGTCAGCCTGCTCTGATGAAGACTGAAGCACGTGGCAACTTGTCCGGAAGTAT 240

Qy    247 TCCGACACCATAGCTGAGTTACAGGAGACTCCAGCCTTCGGCAAAGGACTTCGAACTTCAGA 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCCGACACCATAGCTGAGTTACAGGAGACTCCAGCCTTCGGCAAAGGACTTCGAACTTCAGA 300

Qy    307 AGTCTTGTAGGTTGTGTGTCACTTTGCTGAAGTGATGAAGAGAAGGCTTATTGGCCCAGGAGCACCCGGG 366
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Db    301 AGTCTTGTAGGTTGTGTGTCACTTTGCTGAAGTGATGAAGAGAAGGCTTATTGGCCCAGGAGCACCCGGG 360

Qy    367 GACATCCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
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Db    361 GACATCCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy    427 TTTTTTGAGAAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 486
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Db    481 CAGTATGCCTTTCAGGACAACAAAAAATCACCTTTATCTCGATGGAGGAATATCAGCCTGGAGGG 540

Qy    547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACTTGCTGTCACTTTTGATTTGAATAGATAGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy    607 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGATACGTGCATCGA 666
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Db    601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGATACGTGCATCGA 660

Qy    667 GACATCAAGCCTGAGAACATTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTT 726
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Db    661 GACATCAAGCCTGAGAACATTCGTTGACCGCCACAGGACACATCAAGCTGTGGGATTTT 720

Qy    727 GGATCTGCGCGCGAAAATGAATTCAAACAAGATGGTCAAACTCCCGATTGGGACC 786
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Db    721 GGATCTGCGCGCGAAAATGAATTCAAACAAGATGGTCAAACTCCCGATTGGGACC 780

Qy    787 CCAGATTACATGGCTCCTGAGTGCTGACTGTGTGACTGTGATGAACGGGATGAAAAGGCACCTAC 846
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Db    781 CCAGATTACATGGCTCCTGAGTGCTGACTGTGTGACTGTGATGAACGGGATGAAAAGGCACCTAC 840

Qy    847 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTATGGGAGA 906
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Db    841 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCATGAGATGATTATGGGAGA 900

Qy    907 TCCCCCTTCGCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
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Db    901 TCCCCCTTCGCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960

Qy    967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
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Db    961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020

Qy   1027 TTGTTGTGCGGCCAGAAAAGACGACTGAAGTTGAAGGTCTTTGCTCCATCCTTTCTTC 1086
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Qy   1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1146
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Db   1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy   1207 CCGTGCCAGCTGAGCCCCTCAGGGCTTCTCCGGGTGAAGAACTGCGCGTTGTGGGGTTTTCG 1266
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Qy   1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCGTGTCTGGACTCC 1326
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Db   1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTCGTGTCTGGACTCC 1320

Qy   1327 CCTGCCAAGACTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1386
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Db   1321 CCTGCCAAGACTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1380

Qy   1387 TCTCAGGACAAGTGTCACAAGT 1409
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RESULT 15
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT: Silos-Santiago, Inmaculada
;  APPLICANT: Rosenfeld, Julie Beth
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
;  TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
;  TITLE OF INVENTION: 32838,336 and 52908
;  FILE REFERENCE: MPI01-294P1RNM
;  CURRENT APPLICATION NUMBER: US/10/325,430
;  CURRENT FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/341,953
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;  LENGTH: 6162
;  TYPE: DNA
;  ORGANISM: Homo sapiens
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;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(6162)
US-10-325-430-11

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Best Local Similarity 99.5%;   Pred. No. 0;
Matches 1396;   Conservative  0;   Mismatches  7;   Indels  0;   Gaps  0;

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Qy     67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
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Qy    307 AGTCTTGTAGGTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAAAGCAACCGGG 366
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Db    541 GACTTGCTGTCACTTTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 600

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Db    721 GGATCTGCCCGCGAAAATGAATTCAAACAAGAGTGGTGAATGCCAAACTCCCGATTGGGACC 780

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Qy    907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCCAGCGG 966
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Search completed: March 19, 2005, 18:10:54
Job time : 833.8 secs
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              GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      March 19, 2005, 07:56:21 ; Search time 267.502 seconds
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Title:       US-10-724-594-1
Perfect score: 1515
Sequence:    1 ggggaggatgtgaagtcaa........tctgagccgcctgatccgta 1515

Scoring table: IDENTITY NUC
             Gapop 10.0 , Gapext 1.0

Searched:    1202784 seqs, 81813B359 residues

Total number of hits satisfying chosen parameters:   2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
             Maximum Match 100%
             Listing first 45 summaries

Database :   Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                      SUMMARIES
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Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	1515	100.0	1515	4	US-09-804-471A-1	Sequence 1, Appli
2	1515	100.0	1515	4	US-10-238-709-1	Sequence 1, Appli
3	1398.2	92.3	5877	4	US-10-028-946-3	Sequence 3, Appli
4	1398.2	92.3	6165	4	US-10-028-946-1	Sequence 1, Appli
5	963.2	63.6	2162	4	US-09-774-528-419	Sequence 419, App
6	760.8	50.2	1133	4	US-09-916-204-1	Sequence 1, Appli
7	760.8	50.2	1133	4	US-10-282-048-1	Sequence 1, Appli
8	234.6	15.5	2423	4	US-09-949-016-2640	Sequence 2640, Ap
9	225.6	14.9	2726	2	US-08-422-699A-12	Sequence 12, Appl
10	225.6	14.9	2726	2	US-08-422-706B-12	Sequence 12, Appl
11	218.8	14.4	2511	2	US-08-422-699A-8	Sequence 8, Appli
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13	218.4	14.4	3182	4	US-08-484-044-11	Sequence 11, Appl
14	216.2	14.3	174493	4	US-09-804-471A-3	Sequence 3, Appli
15	216.2	14.3	174493	4	US-10-238-709-3	Sequence 3, Appli
16	194	12.8	2706	2	US-08-630-822A-61	Sequence 61, Appl
17	194	12.8	2706	3	US-09-005-069-61	Sequence 61, Appl
18	194	12.8	2706	3	US-09-171-156A-20	Sequence 20, Appl
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21	186	12.3	4363	2	US-08-685-576-5	Sequence 5, Appli
22	184.4	12.2	4848	4	US-09-976-594-295	Sequence 295, App
23	178.8	11.8	48763	4	US-09-916-204-3	Sequence 3, Appli
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33	125.4	8.3	1498	3	US-09-509-902A-6	Sequence 6, Appli
34	125.4	8.3	1961	3	US-09-509-902A-15	Sequence 15, Appl
35	125.4	8.3	5276	4	US-09-233-857-2	Sequence 2, Appli
36	121	8.0	3018	2	US-08-860-150-6	Sequence 6, Appli
37	121	8.0	3018	2	US-09-338-132-6	Sequence 6, Appli
38	114.6	7.6	1935	2	US-08-878-989-11	Sequence 11, Appl
39	114.6	7.6	1935	3	US-09-272-796-11	Sequence 11, Appl
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42	113	7.5	3213	4	US-09-442-102-5	Sequence 5, Appli
43	110.4	7.3	1251	4	US-09-248-796A-4400	Sequence 4400, Ap
44	108	7.1	2160	3	US-09-588-256-1	Sequence 1, Appli
45	104.6	6.9	5720	3	US-09-442-100-1	Sequence 1, Appli

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                      ALIGNMENTS

RESULT 1
US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION:  ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 1515
;  TYPE: DNA
;  ORGANISM: Human
US-09-804-471A-1

Query Match            100.0%;  Score 1515;  DB 4;  Length 1515;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1515;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GGGGAGGATGTGAAGTTCAAAATGATGAGGCGGGAATCCTTGGATGCGTGGTGCTGCTGAA 60
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Qy    61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
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Qy   181 TTTGAAGAATGCAGTCAGTCAGCCTCGAGTTACAGCGAGCTCCAGCCTTCGGCAACTTGTCCGG 240
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Qy   1501 GCCGCCTGATCCGTA 1515
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Db   1501 GCCGCCTGATCCGTA 1515

RESULT 2
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; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
;   APPLICANT: WEBSTER, Marion et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001164DIV
;   CURRENT APPLICATION NUMBER: US/10/238,709
;   CURRENT FILING DATE: 2002-09-11
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1515
;   TYPE: DNA
;   ORGANISM: Human
US-10-238-709-1

Query Match   100.0%; Score 1515; DB 4; Length 1515;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1515; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGATGCTGAA 60

Qy   61 CCCATTGCCAACCGGCCTCCCTTCGCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGCCAACCGGCCTCCCTTCGCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120

Qy   121 ACTCAACAGCAGATGTCTCCTTCCCGAGAAGGGATATTAGATGATGAGCAACTTGTGTCTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACTCAACAGCAGATGTCTCCTTCCCGAGAAGGGATATTAGATGATGAGCAACTTGTGTCTC 180

Qy   181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAGTTACAGAGACGTGAGCAACTTGTCCGG 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAGTTACAGAGACGTGAGCAACTTGTCCGG 240

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGCCTTCGGCAAAGGACTTCGAA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGTATTCCGACACCATAGCTGAGTTACAGCCTTCGGCAAAGGACTTCGAA 300

Qy   301 GTCAGAAGTCTTGTAGGTGTGTGTCACTTGCTCAGAGGTGGTGCAGGGAAAGCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTCAGAAGTCTTGTAGGTGTGTGTCACTTGCTCAGAGGTGGTGCAGGGAAAGCA 360

Qy   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCAGGAGCAG 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCAGGAGCAG 420

Qy   421 GTTTCATTTTTTGAGGAAGAGACCGGAACAAAAATCACCTTTATTCTGTCATGGAATATCAGCCT 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTTTCATTTTTTGAGGAAGAGACCGGAACAAAAATCACCTTTATTCTGTCATGGAATATCAGCCT 480

Qy   481 CAATTACAGTAGTGCCTTTCAGGACACAAAACTGAGTAGATAGGACCAGTAGATGAAAACCTGATA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAATTACAGTAGTGCCTTTCAGGACACAAAACTGAGTAGATAGGACCAGTAGATGAAAACCTGATA 540

Qy   541 GGAGGGGACTTCGTGTCACTTTTGAATAGATAGAGGACCAGTTGTCACAGGGATACGTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAGGGGACTTCGTGTCACTTTTGAATAGATAGAGGACCAGTTGTCACAGGGATACGTG 600

Qy   601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTG 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTG 660

Db   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCAGGAGCAG 420

Qy   421 GTTTCATTTTTTGAGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTTTCATTTTTTGAGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 480

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 540

Qy   541 GGAGGGGACTTCGTGTCACAAGGTGTCACAAGGTGTCACAGGTGGGATATTATTTCGGCCCGGCCTTCCTGC 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAGGGGACTTCGTGTCACAAGGTGTCACAAGGTGTCACAGGTGGGATATTATTTCGGCCCGGCCTTCCTGC 600

Qy   661 CATCGAGACATCAAGCCTGAGACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATCGAGACATCAAGCCTGAGACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720

Qy   721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780

Qy   781 GGGACCCCAGATTACATAGGCTCCTGACTGTGTCTGTCAGTGGGCGTGACTGGGCATGAGATGAATTAT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGGACCCCAGATTACATAGGCTCCTGACTGTGTCTGTCAGTGGGCGTGACTGGGCATGAGATGAATTAT 840

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGGCTGATTGGGGCTGATTGCCTATGGGATGGATTTAT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGGCTGATTGGGGCTGATTGCCTATGGGATGGATTTAT 900

Qy   901 GGGAGATCCCCTTGCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGGAGATCCCCTTGCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960

Qy   961 CAGCGGTTTTTGAAATTCCAGATGAGCAGTCAGTTGAAGGTCTTTGCTTGCTGTCCATCCT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CAGCGGTTTTTGAAATTCCAGATGAGCAGTCAGTTGAAGGTCTTTGCTTGCTGTCCATCCT 1020

Qy   1021 CAAAGCTTGTTGTGCGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGAAGGTCTCTTGCTTGTCCTCCACC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAAAGCTTGTTGTGCGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGAAGGTCTCTTGCTTGTCCTCCACC 1080

Qy   1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCGTAACTCGTCCCCCCTTCGTTCCACC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCGTAACTCGTCCCCCCTTCGTTCCACC 1140

Qy   1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGACCAGAGAAGAATTCGTGGGTTTCA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGACCAGAGAAGAATTCGTGGGTTTCA 1200

Qy   1201 TCCTCTCCGTGCGTTGAGCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTTGTGGGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTCTCCGTGCGTTGAGCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTTGTGGGG 1260

Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGAGTCGGGTCTG 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGAGTCGGGTCTG 1320

Qy   1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGCTA 1380

Qy   1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTGC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTGC 1440

Qy   1441 TCCAGGATCCTCCCGTTCCGTCCGTATATGCCAAGGGATCCCGGCCCCGGGGCGCGGCCTGCCTGCTCTGA 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TCCAGGATCCTCCCGTTCCGTCCGTATATGCCAAGGGATCCCGGCCCCGGGGCGCGGCCTGCCTGCTCTGA 1500

; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match   92.3%;   Score 1398.2;   DB 4;   Length 5877;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1400; Conservative   0; Mismatches   0; Indels   3; Gaps   0;

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Qy         7 ATGTTGAAGTTCAAATATGGAGCGCGAATCCTTGGATGCTGGTGCTGTGCTGAACCCATT 66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGTTGAAGTTCAAATATGGAGCGCGAATCCTTGGATGCTGGTGCTGTGCTGAACCCATT 60

Qy        67 GCCAACCGGCCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCCAGCGCCGGGCCTCCAGGCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy       127 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTCTTGTTCTTCTTTGAA 186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTCTTGTTCTTCTTTGAA 180

Qy       187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy       247 TCCGACACCATAGCTGAGTTACAGGAGCTTCGGCAAAGGACTTCGAAGTCAGA 306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TCCGACACCATAGCTGAGTTACAGGAGCTTCGGCAAAGGACTTCGAAGTCAGA 300

Qy       307 AGTCTTGTAGGTTGTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGG 366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AGTCTTGTAGGTTGTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGG 360

Qy       367 GACATCTATGCATGGAAGTGATGAAGAAGAGCTTTATTGGCCCAGGAGCAGGTTTCA 426
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GACATCTATGCATGGAAGTGATGAAGAAGAGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy       427 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCCAATTA 486
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCCAATTA 480

Qy       487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGGTCATGGAATATCAGCCTGGAGGG 546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGGTCATGGAATATCAGCCTGGAGGG 540

Qy       547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy       607 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy       667 GACATCAAGCCTGAGAACATTCTCGTTGACCCGACCGGCCAAACTCCCGATTGGGACC 726
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GACATCAAGCCTGAGAACATTCTCGTTGACCCGACCGGCCAAACTCCCGATTGGGACC 720

Qy       727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy       787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTAC 846
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGCACCTAC 840

Qy       847 GGCCTGGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGGGCCTATGGGAGA 906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCCGACCGGCCACAGGACGACATCAAGCTGGTG 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCCGACCGGCCACAGGACGACATCAAGCTGGTG 720

Qy       721 GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
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Db       721 GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780

Qy       781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGAAAAGGC 840

Qy       841 ACCTACGGCCTGGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGGGCCTATGGGAGATGATTAT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACCTACGGCCTGGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGGGCCTATGGGAGATGATTAT 900

Qy       901 GGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTCTGCCAGAGAGGAACCTCTGCCAGAGACCTTCGGGAGATCCCCTTCGCAGAGGAACCTGCCAGAACCTCAATAACATTATGATGAATTTC 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTCAATAACATTATGATGAATTTC 960

Qy       961 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020

Qy      1021 CAAAGTTGTTGTTGTGCGGCCAGAAGAGAGACTGAAGGTTGAAGGTCTTTGCCATCCT 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 CAAAGTTGTTGTTGTGCGGCCAGAAGAGAGACTGAAGGTTGAAGGTCTTTGCCATCCT 1080

Qy      1081 TTCTTCTCTAAAATTGACTGAACAACAACATTCGTAACTCTCCCCCCCTTCGTTCCACC 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TTCTTCTCTAAAATTGACTGAACAACAACATTCGTAACTCTCCCCCCCTTCGTTCCACC 1140

Qy      1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCA 1200

Qy      1201 TCCTCTCCGTGCCAGTGAGCCCTCAGGCTTCTCCGGTGAAGAACTGCCCGTTTGTGTGGGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TCCTCTCCGTGCCAGTGAGCCCTCAGGCTTCTCCGGTGAAGAACTGCCCGTTTGTGTGGGG 1260

Qy      1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTGAGTCGGGGTCTG 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTGAGTCGGGGTCTG 1320

Qy      1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380
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Db      1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380

Qy      1381 CAAGACTCTCAGGACACAAGTGTCACAAGGTATTTATTTCCCGCAGCCGGCCTCCTTCCTTGC 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CAAGACTCTCAGGACACAAGTGTCACAAGGTATTTATTTCCCGCAGCCGGCCTCCTTCCTTGC 1440

Qy      1441 TCCAGGATCCTCCCCGTCCGTATATGCCAAGGGATCCGCAAGGGAAGGGCCGCTGGCTCTGA 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TCCAGGATCCTCCCCGTCCGTATATGCCAAGGGATCCGCAAGGGAAGGGCCGCTGGCTCTGA 1500

Qy      1501 GCCGCCTGATCCGTA 1515
             |||||||||||||||
Db      1501 GCCGCCTGATCCGTA 1515
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RESULT 3
US-10-028-946-3
; Sequence 3, Application US/10028946
Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: NO. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946

Db 841 GGCCTGGACTGTGACTGGTGCGTCAGTGGGCGTGATTGCCTGACTTCAATAACAACATTATGATGAATTCCAGCGG 900
Qy 127 CAGCAGATGTCTCCTCTTCCCGAGAAGGGGATATTAGAATGCCCTCTTTGTCTCTTTGAA 186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CAGCAGATGTCTCCTCTTCCCGAGAAGGGGATATTAGAATGCCCTCTTTGTCTCTTTGAA 180

Qy 187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy 247 TCCGACACCATAGTCGAGTTACAGAGGCTCCAGCCTTCGGCCAACAAAGACTTCGAAGTCAGA 306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TCCGACACCATAGTCGAGTTACAGAGGCTCCAGCCTTCGGCCAACAAAGACTTCGAAGTCAGA 300

Qy 307 AGTCTTGTAGGTTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGG 366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGTCTTGTAGGTTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGG 360

Qy 367 GACATCTATGCTATGGAAGTGATGAAGAAGAGGCTTTATTGGCCACAAGCCCGTGGATCCCCAATTA 426
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACATCTATGCTATGAAGTGATGAAGAAGAGGCTTTATTGGCCACAAGCCCGTGGATCCCCAATTA 420

Qy 427 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 486
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Db 421 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 480

Qy 487 CAGTATGCCTTCAGGACAAAAATCACCTTTATCTCGTCATGGAAATATCAGCCTGGAGGG 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CAGTATGCCTTCAGGACAAAAATCACCTTTATCTCGTCATGGAAATATCAGCCTGGAGGG 540

Qy 547 GACTTGCTGTCACTTTGAATGAGAGATATGAGGACCAGTTAGATGGGATACGTGCATCGA 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GACTTGCTGTCACTTTGAATGAGAGATATGAGGACCAGTTAGATGGGATACGTGCATCGA 600

Qy 607 TACCTAGCTGAGCTGATTTTGGCTGTTCACCGACACAGGACACATCAAGCTGGTGGATTT 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACCGACACAGGACACATCAAGCTGGTGGATTT 660

Qy 667 GACATCAAGCCTGAGAACATTCGTCGTTGACCTGACCTGAGAACACTGGTAAGCAAGATGGTGAATGCCAAACTCCCGATTGGGACC 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GACATCAAGCCTGAGAACATTCGTCGTTGACCTGAGAACACTGGTAAGCAAGATGGTGAATGCCAAACTCCCGATTGGGACC 720

Qy 727 GGATCTCGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 GGATCTCGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy 787 CCAGATTACATGGCTCCTGAGCTGTCGACTGTGATGAACGACGATGGAAAAGCACCTAC 846
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Db 781 CCAGATTACATGGCTCCTGAGCTGTCGACTGTGATGAACGACGATGGAAAAGCACCTAC 840

Qy 847 GGCCTGGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGGAGATGATTTATGGGAGA 906
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GGCCTGGACTGTGACTGGTCAGTGGGCGTGATTGCCTATGGAGATGATTTATGGGAGA 900

Qy 907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACAACTTCAATAACAACTTCCAGCGG 966
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACAACTTCCAGCGG 960

Qy 967 TTTTTGAAATTCCAGATGACCCCAAAGTCCTTTGGATGCGTGCTGCTCAAGCCTTTCAAAGC 1026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 TTTTTGAAATTCCAGATGACCCCAAAGTCCTTTGGATGCGTGCTGCTCAAGCCTTTCAAAGC 1020

Qy 1027 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGTCTTTGCTGCCATCCTTTCTTC 1086
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGTCTTTGCTGCCATCCTTTCTTC 1080

Qy 1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTCGTTCCACCCTCAAG 1146
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Db 1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTCGTTCCACCCTCAAG 1140

Qy 1147 TCCGACGATGACACCTCACTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCTGACGATGACACCTCACTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy 1207 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1260

Qy 1267 TACAGCAAGGCACTGGGATTCTTGTGGTAGATCTGAGTCGTGTTGTGTCGGGTCTGGACTCC 1326
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TACAGCAAGGCACTGGGATTCTTGTGGTAGATCTGAGTCGTGTTGTGTCGGGTCTGGACTCC 1320

Qy 1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAAAGAAAACTTCTCATCAAAGACAAAGAGCTACAAGAC 1386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAAAGAAAACTTCTCATCAAAGACAAAGAGCTACAAGAC 1380

Qy 1387 TCTCAGGACAAGTGTCACAAGGT 1409
         ||||||||||||||||||
Db 1381 TCTCAGGACAAGTGTCACAAGAT 1403

RESULT 4
US-10-028-946-1
; Sequence 1, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-028-946-1

; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens

Query Match   92.3%; Score 1398.2; DB 4; Length 6165;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1400; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   7 ATGTTGAAGTCAAATATGGACGCGCGAATCCTTTGGATGCGTGCTGCTCGTGCTGCTCGAACCCATT 66
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGTTGAAGTCAAATATGGACGCGCGAATCCTTTGGATGCGTGCTGCTCGTGCTGCTCGAACCCATT 60

Qy   67 GCCAACCGGGCTCCAGGCTGAATCGTCTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCAGCCGGGCCGGCCTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 120

Db   1201 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGGTTGTGTGGGGGTTTCG 1260

Qy   1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCC 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCC 1320

Qy   1327 CCTGCCAAGACTAGCTCCATGGAAAGAAAGAAGAGCTACAAAGAGCTACAAGAC 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCTGCCAAGACTAGCTCCATGGAAAGAAAGAAGAGCTACAAAGAGCTACAAGAC 1380

Qy   1387 TCTCAGGACAAGTGTCACAAGGT 1409
          |||||||||||||||||||||||
Db   1381 TCTCAGGACAAGTGTCACAAGAT 1403

RESULT 5
US-09-774-528-419

Query Match   63.6%; Score 963.2; DB 4; Length 2162;
Best Local Similarity   99.7%; Pred. No. 1.1e-311;
Matches 965; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGCTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   358 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGCTGAA 417

Qy   61 CCCATTGCCAACCGGCCTTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   418 CCCATTGCCAACCGGCCTTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATG 477

Qy   121 ACTCAACAGCAGATGTCTCCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTTGTTCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   478 ACTCAACAGCAGATGTCTCCTTTCCCGAGAAGGGGATATTAGATGCCCTCTTTGTTCTC 537

Qy   181 TTTGAAGAATGCAGTCAGCCTCAGCCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   538 TTTGAAGAATGCAGTCAGCCTCAGCCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 597

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGAGGACTTCGAA 300
          |||||||||||||||||||||||||||||||||||||||||

Db   598 AAGTATTCCGACACCATAGCTGAGTTACAGAGGACTTCGAA 657

Qy   301 GTCAGAAGTCTTGTAGTTGTGGTCACTTTGTCAGTGGTAAGGAGGAGAAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   658 GTCAGAAGTCTTGTAGTTGTGGTCACTTTGTCAGTGGTAAGGAGGAGAAAGCA 717

Qy   361 ACCGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGACCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   718 ACCGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG 777

Qy   421 GTTTCATTTTTGAGGAGAGCGGAACATATATCGAAGCACAAGCCAAGCCCGTGGATCCCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   778 GTTTCATTTTTTGAGGAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 837

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 897

Qy   541 GGAGGGGACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   898 GGAGGGGACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGAGATGAAAACCTGATA 957

Qy   601 CAGTTTTACCTAGCTGAGCTGATTTGGCTTCATCGGTCATCTGATGGGATACGTG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   958 CAGTTTTACCTAGCTGAGCTGATTTGGCTTCATCGGTCATCTGATGGGATACGTG 1017

Qy   661 CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGTG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 1077

Qy   721 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 1137

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGAACGGGATGAAAAGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGAACGGGATGAAAAGGC 1197

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGTTGAGTGGAGCGGATTGCCTATGAGATGATTTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 ACCTACGGCCTGGACTGTGACTGGTGTTGAGTGGAGCGGATTGCCTATGAGATGATTTAT 1257

Qy   901 GGGAGATCCCCTTCGCCAGAGGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 GGGAGATCCCCTTCGCCAGAGGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTC 1317

Qy   961 CAGCGGTT 968
          ||||||||
Db   1318 CAGGTGTT 1325

RESULT 6
US-09-916-204-1

Query Match   50.2%; Score 760.8; DB 4; Length 1133;
Best Local Similarity   99.7%; Pred. No. 5.3e-244;

US-10-282-048-1

Query Match   50.2%; Score 760.8; DB 4; Length 1133;
Best Local Similarity   99.7%; Pred. No. 5.3e-244;
Matches 762; Conservative   0; Mismatches   2; Indels   2; Gaps   0;

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Qy      1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     48 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 107

Qy     61 CCCATTGCCAACCGGCCTCCAGGCTGAATCGTTCTTCCCAGGGGAAACCACCCTTTATG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    108 CCCATTGCCAGCCGGCCTCCAGGCTGAATCGTTCTTCCCAGGGGAAACCACCCTTTATG 167

Qy    121 ACTCAACAGCAGATGTCTCCTTCCCGAGAAGGGATATTAGATGCACGTGAGCAACTTGTCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    168 ACTCAACAGCAGATGTCTCCTTCCCGAGAAGGGATATTAGATGCACGTGAGCAACTTGTCTC 227

Qy    181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGAGATTAAGCAACTTGTCCGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    228 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGAGATTAAGCAACTTGTCCGG 287

Qy    241 AAGTATTCCGACACCATAGCTGAGTTACAGGACCTCAGCCTTCGGCAAAGGACTTCGAA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 AAGTATTCCGACACCATAGCTGAGTTACAGGACCTCAGCCTTCGGCAAAGGACTTCGAA 347

Qy    301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAGTGCAGTGTCGCAGTGTAAGAGAGAAAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAGTGCAGTGTCGCAGTGTAAGAGAGAAAGCA 407

Qy    361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCCAGGAGCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    408 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCCAGGAGCAG 467

Qy    421 GTTTCATTTTTTGAGGAAGAGCGGAACAAAAATCACCTTTATCTGGTCGTTATCTCGAAGCACAAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    468 GTTTCATTTTTTGAGGAAGAGCGGAACAAAAATCACCTTTATCTGGTCGTTATCTCGAAGCACAAGCCCT 527

Qy    481 CAATTACAGTAGTGCCTTTCAGGACACAGTTAGGATGATGAGGACCAGTTAGAATGAAAACCTGATA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 CAATTACAGTAGTGCCTTTCAGGACACAGTTAGGATGATGAGGACCAGTTAGAATGAAAACCTGATA 587

Qy    541 GGAGGGGACTTGCTGTCTGAGCTGATTTTGGCTGTGTCACAGCGTTCATCTGATGGGATACGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 GGAGGGGACTTGCTGTCTGAGCTGATTTTGGCTGTGTCACAGCGTTCATCTGATGGGATACGTG 647

Qy    601 CAGTTTTACCTAGCTGAGCTGAGTTTGGCTGTTCACAGGTTCATCTGATGGGATACGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 CAGTTTTACCTAGCTGAGCTGAGTTTGGCTGTTCACAGGTTCATCTGATGGGATACGTG 707

Qy    661 CATCGAGACATCAAGCCTGAGAAATTGAATTCAAACAAGAGCACATCAAGCGTCTGTG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    708 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGGACAACATCAAGCGTCTGTG 767

Qy    721 GATTTTGGATCTGCCGCGCGAAAATGAATTCAAACAAGATGGTGAA 764
          || ||||||||||||||||||||||||||||||||||||||||| ||
Db    768 GATTTTGGATCTGCCGCGCGAAAATGAATTCAAACAAGATGGTAAA 811
```

RESULT 8
US-09-949-016-2640
; Sequence 2640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768

RESULT 7
US-10-282-048-1
; Sequence 1, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
;   APPLICANT: WEI, Ming-Hui et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001164CIP-DIV
;   CURRENT APPLICATION NUMBER: US/10/282,048
;   CURRENT FILING DATE: 2002-10-29
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1133
;   TYPE: DNA
;   ORGANISM: Human

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;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2640
;  LENGTH: 2423
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-2640

Query Match          15.5%;     Score 234.6; DB 4;   Length 2423;
Best Local Similarity 52.5%;     Pred. No. 2.9e-67;
Matches 591;  Conservative   0; Mismatches 519;  Indels  15;  Gaps     3;

Qy    158 TATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAATTA 217
              |  ||||||  || || ||| |  ||   ||||||| || |  | |  |||||||||
Db   1021 TACTCGATATACTCATCTGCCTTTATGATGATCAATAATTCTCCATTGATGAAGAGAGA 1080

Qy    218 AGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCC 277
              ||     ||  |  |  |     || | | ||  ||| |||||| | || ||  ||
Db   1081 AGAACATTCTCGATACCTAGAATGGGCTAAACCATTTACTTCTAAAGTGAAACAAATGC 1140

Qy    278 AGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTGTGTCACTTTGCTGAAG 337
              ||| ||  || |||| |  |   | | |   | |||  |  || |||||||| ||||
Db   1141 GATTACATAGAGAGACTTTGAAATATTAAAGGTGATTGGTCGAGGAGCTTTGGGGGAGG 1200

Qy    338 TGCAGGTGGTAAGAGAGAAAGCAACCCGGGGACATCTATGCTATGAAGTGATGAAGAAGA 397
              | | ||||  |  ||||| ||| |    |||| ||||| |||||||||| |||| |
Db   1201 TTGCTGTAGTAAAACTAAAAAATGCAGATAAAGTGTTTGCCATGAAAATATTGAATAAAT 1260

Qy    398 AGGCTTTATTGGCCCAGGAGCAGCAGGTTTCATTTTTGAGGAAGAGCGGAACATATTATCTC 457
              ||   |||  ||  | |  | || | | | || | |||||| | |  |  | || |
Db   1261 GGGAAATGCTGAAAAGAGCTGAGACAGCATGTTTCGTGAAGAAAGGGATGTATTAGTGA 1320

Qy    458 GAAGCACAAGCCCGTGGATCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTT 517
              |||     | |||| |||  | | | || | | |  ||| | || | | ||||| ||
Db   1321 ATGGGAGACAATAAATGGATTACAACCTTGCACTATGCTTTTCCAGGATGACAATAACTTAT 1380

Qy    518 ATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGG 577
              |  |||  |  | ||| ||  |   ||  ||| | | |   | | || |||||| |
Db   1381 ACCTGGTTATGGATTATTATGTGTGGGGATTTGCTTACTCTACTGAGCAAATTTGAAG 1440

Qy    578 ACCAGTTAGATGAAAACCTGATACAGTTTACCTAGCTGAGCTGATTTTGGCTGTGTTCACA 637
              || | | || || | |    || | ||||  ||    | |    | ||||| || ||
Db   1441 ATAGATTGCCTGAACGATATGGCTAGATTTTTACTTGGCTGAGATGGTGATAGCAATTGACT 1500

Qy    638 GCGGTTCATCTGATGGGATACGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACC 697
              |||||  | |   | |   | |  | ||||| | |  |  | || | | ||| ||
Db   1501 CAGTTCATCATCTACCATTATGTACACAGAGACACATTAAACCTGACAATATACTGAACAAGA 1560

Qy    698 GCACAGGACACATCAAGCTCGTGGATTTTGGATCTCGCGCGCGAAAATGAATTCAAACAAGA 757
              |||  |||   | | |  | | |     |||  | | | |   |  |   | |  ||
Db   1561 TGAATGGACATATTCGGTTGAAATGCTTTACGGAGAATCGGAGAATCGGAGAATGGAA 1620

Qy    758 TGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGGCTGTCCTGAAGTGCTGACTG 817
              || ||     |  ||   |  |||   | | | |||| |  | ||| | ||| || | |
Db   1621 CGGTTCAGTGCTCAGTGGCTGTGTAGGAAACTCCAGATTATATCTCTCTGAAATCCTTCAAG 1680

Qy    818 TGATGAACGGGGATGGAAAAGGCCACCTACGGCCTCAGGTCCTCGACTGGTCAGTCAGTGGGCG 877
              || ||  |   | | ||||    ||   |      |  ||||| ||||| || |||||
Db   1681 CCATGGAAG---ATGGAAAAGGGAGATATGGACCTGAATGTGACCTGGTCTTTGGGGG 1737

Qy    878 TGATTGCCTATGAGATGATTTATGGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAA 937
              || ||  ||  | || | |  |  || || |   |||| | |||| |  | |||||||
Db   1738 TCTGTATGTATGAAAATGCTTTACGGAGGAATCGAGAAAACACCATTTTATGCAGAAGATGTGGGATGA 1797

Qy    938 CCTTCAATAACATTATGAATTTCCAGCCGGTTTTTTGAAATTTCCAG--ATGACCCCAAAG 994
              || || || || || || |  ||||| | |  |||| ||| || || |  |   | |
Db   1798 CATACGGAAAAATCATGAACCACACAAAGAGAGAGGTTTTCAGTTTCCAGCCCAAGTGACTGATG 1857

Qy    995 TGAGCAGTGACTTTCTTGATCTGATTCAAGCTTGTTGTGTGCGGCCAGAAAGAGAGAGACT-- 1052
              ||| ||  |  | || |   | | | |  ||    |  || |  | |||
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Db   1858 TGTCTGAAAATGCTAAGGATCTTATTCGAAGGCTCATTGTGAGCAGGAACATCGACTTG 1917

Qy    1053 -------GAAGTTGAAGGTCTTGCTGCCATCCTTTCTTCCTCTAAAATTGACTGGACA 1105
                     |||||  || | ||| | ||  |||| ||| ||  |||||||||||||
Db   1918 GTCAAAATGGAATAGAAGACTTTAAGAAACACCCATTTTTCAGTGAGTTGATTGGGATA 1977

Qy    1106 ACATTGTAACTCTCCTCCCCCCCCTTGCTTCCTCGTTCCACCCTCAAGTCCGACGATGACACCTCCA 1165
              | ||||||    || || || || || ||| | | || | || |  || |   | | ||||
Db   1978 ATATTCGGAACTGTGAAGCACTTATATTCCAGAAGTTAGTAGCCCACAGATACATCGA 2037

Qy    1166 ATTTTGATGAACCAGGAAGAGAATTCGTGGGTTCATCCTCGTGCCAGCTGAGCCCCT 1225
              |||   ||  |  |   |  ||||    || |||     | ||| | || || ||||
Db   2038 ATTTTGATGTAGATGATGATGTGTTAAAAAATTCTGAAACGATGCCCCCAACACATA 2097

Qy    1226 CAGGCTTCTCCGGGTGGAAGAACTGCCCGTTGTGGGGTTTTCGTACA 1270
              ||| ||  | |     | || ||| | || | |||||||   ||
Db   2098 CTGCATTTTCTGGCCACCATCTGCCATTGTGTTGGTTTTTACATATA 2142
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RESULT 9
US-08-422-699A-12
;  Sequence 12, Application US/08422699A
;  Patent No. 5955265
;  GENERAL INFORMATION:
;     APPLICANT: Brook, J. David
;     APPLICANT: Housman, David E.
;     APPLICANT: Shaw, Duncan J.
;     APPLICANT: Harley, Helen G.
;     APPLICANT: Johnson, Keith J.
;     TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
;     TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
;     NUMBER OF SEQUENCES: 14
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;        STREET: Two Militia Drive
;        CITY: Lexington
;        STATE: Massachusetts
;        COUNTRY: US
;        ZIP: 02713
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/08/422,699A
;        FILING DATE:
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 08/422,706
;        FILING DATE:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US 08/023,612
;        FILING DATE: 26-FEB-1993
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US 07/839,255
;        FILING DATE: 20-FEB-1992
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: PCT/US93/01545
;        FILING DATE: 19-FEB-1993
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: PCT/GB93/00253
;        FILING DATE: 05-FEB-1993
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: GB9202485.0
;        FILING DATE: 06-FEB-1992
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Granahan, Patricia
;        REGISTRATION NUMBER: 32,227
;        REFERENCE/DOCKET NUMBER: MIT-5830A2
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 617-861-6240
;        TELEFAX:  617-861-9540
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Db     1143 TCTTTGGCTCGACTGGGATGTCTCCGGGACGTGCCCCCCTTTACACCGGATTTCG 1202
                |||  ||     ||||       ||||| |  ||||||||||||
Qy     1145 AGTCCGACGATGCACACCTCCAATTTTGA 1172
                |  |||||  |  |  ||| ||| ||
Db     1203 AAGGTGCCACCGACACATGCAACTTCGA 1230


RESULT 10
US-08-422-706B-12
; Sequence 12, Application US/08422706B
; Patent No. 5977333
; GENERAL INFORMATION:
;      APPLICANT: Brook, J. David
;      APPLICANT: Housman, David E.
;      APPLICANT: Shaw, Duncan J.
;      APPLICANT: Harley, Helen G.
;      APPLICANT: Johnson, Keith J.
;      TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
;      TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
;      NUMBER OF SEQUENCES: 14
;      CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;        STREET: Two Militia Drive
;        CITY: Lexington
;        STATE: Massachusetts
;        COUNTRY: US
;        ZIP: 02713
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/08/422,706B
;        FILING DATE: 14-APR-1995
;        CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US 08/284,543
;        FILING DATE: 08-AUG-1994
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US 08/023,612
;        FILING DATE: 26-FEB-1993
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: US 07/839,255
;        FILING DATE: 20-FEB-1992
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: PCT/US93/01545
;        FILING DATE: 19-FEB-1993
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: PCT/GB93/00253
;        FILING DATE: 05-FEB-1993
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: GB9202485.0
;        FILING DATE: 06-FEB-1992
;      ATTORNEY/AGENT INFORMATION:
;        NAME: Granahan, Patricia
;        REGISTRATION NUMBER: 32,227
;        REFERENCE/DOCKET NUMBER: MIT-5830A2
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 617-861-6240
;        TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 12:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 2726 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: double
;        TOPOLOGY: linear
US-08-422-706B-12

Query Match    14.9%;  Score 225.6;  DB 2;  Length 2726;
Best Local Similarity    54.0%;  Pred. No. 3.3e-64;
Matches  534;  Conservative    0;  Mismatches  439;  Indels  15;  Gaps  3;
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;  INFORMATION FOR SEQ ID NO: 12:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 2726 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: double
;        TOPOLOGY: linear
US-08-422-699A-12

Query Match    14.9%;  Score 225.6;  DB 2;  Length 2726;
Best Local Similarity    54.0%;  Pred. No. 3.3e-64;
Matches  534;  Conservative    0;  Mismatches  439;  Indels  15;  Gaps  3;

Qy     200 CTGACCTCGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG 259
               |||   ||||||  | |  || |  |||   |||  |||| || |  |||||
Db     243 CCGAACTGGCCCAGGACAAGTACGTGGCCGACTTCTTGCAGTGGGCGGCCCATCCGTGG 302

Qy     260 CTGAGTTACAGGAGGCTCCAGCCTTCCGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTT 319
               ||| ||||||| |   |     |||   ||| ||| |||  | ||  || ||| |
Db     303 TGAGGCTTAAGGAGGTCCGACTGCAGAGGGACGGACTTCGAGATTCTGAAGGTGATCGGAC 362

Qy     320 GTGGTCACTTTGCTGAAGTGCGAGTTGGTAAGAGAGAAGCAACCGGGGACAATCTATGCTA 379
               ||||| ||| ||||  | ||||| || |  ||| | || ||  |||  |||| ||
Db     363 GCGGGGCGTTCAGCGAGGTAGCCGTAGTGAAGATGAAGCAGCAGGTGTATGCCA 422

Qy     380 TGAAAGTGATGAAGAGAGAAGGCTTTATTGGCCCAGAGCAGTTTCATTTTTTGAGGAAG 439
               ||||||| |||  ||| | ||  ||  ||| ||  || ||    ||  |||||  |||
Db     423 TGAAGATCATGAACAAGTGGGACATCCTGAGACAGGGGCGAGGTGTGTCCGTGCTTCCGTGAGG 482

Qy     440 AGCGGAACATATTATTCTCGAAGCACACAGCCCGTGGATCCCCAATTACAGTATGCCTTTC 499
               || | | |||| |  ||  || ||||| || ||  ||| ||  |||||||| || || |
Db     483 AGAGGGACGTGTTGGTGAATGGGACGGCGGTGAGCAGCTGCACTTCGCCCTTCC 542

Qy     500 AGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTGCTGTCAC 559
               ||| |||| |||  ||  |||||||  ||  ||| |||  ||| ||| ||  || || |||
Db     543 AGGATGAGAACTACCTGACCTGGTCATGGAGTATTACGGTGGCGGGGACCTGACAC 602

Qy     560 TTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTGAGC 619
               |||   | | | | | |||   |||||||| || | |||  || ||||| | || ||||
Db     603 TGCTGAGCAAGTTGGGGAGGAGGGATTCCGGGCCGAGATGGGCCGCGCTTCTACCTGGGCGGAGA 662

Qy     620 TGATTTTGGCTGTTCACAGCGTTCATCTGATGGATACGTGCATCGAGAGATCAAGCCTG 679
               |||| ||| | | | || || |    || |  ||  || | |||  ||| || | || ||
Db     663 TTGTCATGGCCATAGACTCCGGTGCACCGGCTTGGCTACGTGCACAGGGACAACAAACCCG 722

Qy     680 AGAACATTCTCCTTGCACCAGGACCAGTTAGATGAAAACCTGATACAGTTTTGGATCTGCCGGCGA 739
               ||||||||| | |||| ||||| | || || |  |||||  |||| || || |||| |||
Db     723 ACAACATCCTGCTGGACCGCGTGTGGCCACATCCGCCTGTGGCTCGGCTCTTGCCTCA 782

Qy     740 AAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACATGG 799
               ||| | |  |||  || || ||| ||  || ||| ||  ||||| ||||| | || | ||
Db     783 AGCTGCGGGGCCAGCAGGAGATGGAACGGTCGTCGTCGGGGCACCCCAGACTACCTGT 842

Qy     800 CTCCTGAAGTGCTGA---CTGTGATGAACGGGATGGAAAGGCACCTACGGCTTGGACT 856
               |   |||| ||| ||   || |   ||| | |||     | |||| || | || |||
Db     843 CCCCCGAGATCCTGCACCGGTCTGGGCCGGTGGGCGTGGGGCCGCAGCAGCGCCCTTCT 902

Qy     857 GTGACTGGTGGTCAGTCAGTGGCCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCTTCG 916
               ||||| ||||||  ||| || | |||    |  | ||| ||| ||  ||| |||  | |
Db     903 GTGACTGGTGGGCGCTGGGTGTATTCGCCTATGAAATGTTCATGGCCTTCATTGCAGCGGTTGCTGT 962

Qy     917 CAGAGGGAACCTCTGCCGAGAACCTTCAATAACCATTATGAATTTCCAGCGGTTTTTGAAAT 976
               |||||| ||  ||  | ||| |||  ||  | || |||||||  |||    | | |||||
Db     963 ACGCCGGATTCCACGGCGGAGAACGTCCACTACCAAGGAGGCGACACCCCTCTC 1022

Qy     977 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTGATCGATCGAAAGCTTGTGTGT 1033
               ||||  | ||  |||||| ||||     |||||| |||| ||  | ||| |||
Db     1023 TGCCGGTGGTGACGCAGAGGGGTCCCTGAGGAGCTCCGAGACTTCATTCAGCCGGTTGCTGT 1082

Qy     1034 GCGGGCCAGCAGAAAGAGAGACTGAAGTTTCAAAGTGTCTTTGCTGC------CATCCTTTCT 1084
               | |||||  |||||||| ||||  |||  | ||||  |  |||||        ||||| |||
Db     1083 GTCCCCCGGAGACACGGCTGGGCGGAGCAGGCGACTTCCGGACAACATCCCCTTTCA 1142

Qy     1085 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCCCTTCGTTCCCACCCTCA 1144
```

Patent No. 5955265
GENERAL INFORMATION:
    APPLICANT: Brook, J. David
    APPLICANT: Housman, David E.
    APPLICANT: Shaw, Duncan J.
    APPLICANT: Harley, Helen G.
    APPLICANT: Johnson, Keith J.
    TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
    TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
    NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
        STREET: Two Militia Drive
        CITY: Lexington
        STATE: Massachusetts
        COUNTRY: US
        ZIP: 02713
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/422,699A
        FILING DATE:
        CLASSIFICATION:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/422,706
        FILING DATE:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/023,612
        FILING DATE: 26-FEB-1993
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/839,255
        FILING DATE: 20-FEB-1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/US93/01545
        FILING DATE: 19-FEB-1993
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/GB93/00253
        FILING DATE: 05-FEB-1993
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: GB9202485.0
        FILING DATE: 06-FEB-1992
    ATTORNEY/AGENT INFORMATION:
        NAME: Granahan, Patricia
        REGISTRATION NUMBER: 32,227
        REFERENCE/DOCKET NUMBER: MIT-5830A2
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 617-861-6240
        TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2511 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
        NAME/KEY: CDS
        LOCATION: 1..1746
US-08-422-699A-8

Query Match   14.4%; Score 218.8; DB 2; Length 2511;
Best Local Similarity 54.5%; Pred. No. 6e-62;
Matches 511; Conservative   0; Mismatches 412; Indels 15; Gaps 3;

Qy   250 GACACCATAGCTGAGTTACAGGAGCTTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGT 309
Db   43 GCCATCGTCGGTGAGGCTTAAGGAGGTCCGACTTGCAGAGGACCAACCGCGGGAC 102
Qy   310 CTTGTGTAGTTGGTTGGTCACTTTGCTGAGGTCGAAGTGCTGAGGTGCGTGAGAGAAGCAACCGCGGGAC 369

Qy   200 CTGCTCTGATGAAGAGTTAAGCAGCGTGAGCAACTTGTCCGGAAGAAGTATTCCGACACCATAG 259
Db   243 CCGAACTGGCCCAGGACAAGCAAGTACGTGCCGACTTCTTGCAGTGGGCGGGAGCCCATCGTGG 302
Qy   260 CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTGTAGGTT 319
Db   303 TGAGGCTTAAGGAGGTCCGACTGCAGAGGGACGACTTCGAGATTCTGAAGTGATCGGAC 362
Qy   320 GTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGACACATCTATGCTA 379
Db   363 GCGGGGCGGTTCAGCGAGGTAGCGGTAGTGAAGATGAAGCAGCGGCCAGGTGTATGCCA 422
Qy   380 TGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGGAAG 439
Db   423 TGAAGATCATGAACAAGTGGACATGCTGAAGAGGGGCGAGGTGTCGTGCTTCCGTGAGG 482
Qy   440 AGCGGAACATATTATCTCGAGACCACAGCCCGTGGATCCCCAATTACAGTATGCCTTTC 499
Db   483 AGAGGGACGTGTGTTGGTGAATGGGGACCGGCCGGTGAGGGGGACTTGCTGTCAC 542
Qy   500 AGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCAC 559
Db   543 AGGATGAGAACTACCTGTCATCGAGTATTACGTGGGCGGGGACCTGCTGACAC 602
Qy   560 TTTTGAATAGATATGAGGACCAGTTAGATGAGAAAACCTGATACAGTTTACCTAGCTGAGC 619
Db   603 TGCTGAGCAAGTTTGGGGAGCGGATTCCGGCCGAGATGGGCGCGCTTCTACCTGGCCGGAGA 662
Qy   620 TGATTTGGCTGTCTTCACAGCGTTCATCTGATGGGAGTCGCATCGAGACATCAAGCCTG 679
Db   663 TTGTCATGGCCATAGACTCCGGTGCACCGGCGTTGGCTACGTGCACAGGGACATCAAACCCG 722
Qy   680 AGAACATTCTCGTTGACCGGACACAGAGACAATCAAGCTGGTGTCGGATTTTGGATCTGCCGCGA 739
Db   723 ACAACATCTCTGCTGACCGTGCGTGGCCACATCCGCATCTTCGGCTTCGGCTTCTTGCCTCA 782
Qy   740 AAATGAATTCAAACAACAAGATGTGAATGCCAAACTCCCAGATTGGGACCCCAGATTACATGG 799
Db   783 AGCTGCGCGGCCAGATGGAACGGTGCGGTCGCGTGGTCGGTCGCGTGTCGCACCCCAGACTACCTGT 842
Qy   800 CTCCTGCAAGTGCTGA---CTTGTGATGAACGGGGATGCGAAAAGGCACCTACGGCGCTGGACT 856
Db   843 CCCCCGAGATCTGCGAGGCTGTGGGCGGTGGCCTGGGCAGCAGGCTACACGGGCCCGAGT 902
Qy   857 GTGACTGGTGGTCAGTGGCGCTGAATTGCCTATGAGATGATTTATGGGAGAGATCCCCCTTCG 916
Db   903 GTGACTGGTGGGCGCTGCGGGTGTATTCGCCCATGAAATGTTCTATGGGCAGACGCGCCCTTCT 962
Qy   917 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTTGAAAT 976
Db   963 ACGCGGATTCCACGCGGCGGGAGACCTATGGCAAGATCGTCCACTACAGGAGCACCTCTCTC 1022
Qy   977 TTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTGATCTGATTCAAAGCTTGTTGT 1033
Db   1023 TGCCCGCTGGTGGACGGAGGGGGTCCCTGAGGAGGCTCGAGACTTCATTCAGCGGTTGCTGT 1082
Qy   1034 GCGGGCCAGAAGAGAGACTGAAGTTTGAAGGTGTCTTTGCTGC--------CATCCTTTCT 1084
Db   1083 GTCCCCCGGAGACGAGACACGCGTGGGCCGGGGTGGAGCAGGCGACTTCCCGGACAACATCCCTTCT 1142
Qy   1085 TCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCA 1144
Db   1143 TCTTTGGCCTTCGGACTGGAATGCTTCCGGGACAGCGCTGCCCCCCTTTACACCGGATTTCG 1202
Qy   1145 AGTCCGACGATGACACCTCCAATTTTGA 1172
Db   1203 AAGGTGCCACCGACACATGCAACTTCGA 1230

RESULT 11
US-08-422-699A-8
; Sequence 8, Application US/08422699A

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746
US-08-422-706B-8

Query Match   14.4%;   Score 218.8;   DB 2;   Length 2511;
Best Local Similarity   54.5%;   Pred. No. 6e-62;
Matches 511;   Conservative 0;   Mismatches 412;   Indels 15;   Gaps 3;

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Qy   250 GACACCATAGCTGAGTTACAGAGCTTCAGCCTTCGGCCAAAGGACCTTCGGAAGTCAGAAGT 309
             ||| |||  |||| |||||| ||||||||||||||  ||||||||||||||
Db    43 GCCATCGGTGGTGAGGCTTAAGGAGGTCCGACTTGCAGGTCGAGAGATTCGAAG 102

Qy   310 CTTGTAGGTTGGTGTCACTTTGCTGACGAGCTTCGGAAGTGCAGGTCGAGAGAGCAAGAAAGCAACCGGGAC 369
             |||  |||||    |||     |||  ||||    ||||||||
Db   103 GTGATCGGACGCGGGGCGTTCAGCGAGGTAGCGGTAGTGAAGATGAAGCAGAGAGTCGTGC 162

Qy   370 ATCTATGCTATGAAAGTGATGATGAAGAGAGAGAAGGCTTTATTGGCCCAGGAGAGAAGCAGGTTTCATTT 429
             ||  ||||||||||||  ||||||
Db   163 GTGTATGCCATGAAGATCATGAACAGTGGGAATGGGCGGATCATGGGACATGGGACCGGGAGTGTCGTGC 222

Qy   430 TTTGAGGAAGAGCGGAACATATATTATCTCGAAGCACAGCCCGTGGATCCCCAATTACAG 489
             ||||  ||||||||  ||||||||||||||||||||||||||
Db   223 TTCCGTGGAGGAGGACGTGTTGGTGAATGGGCATCATGAATGGGACATGGGACCGGGCGGGGAC 282

Qy   490 TATGGCCTTTCAGGACAAAAATCACCTTATCTGGTCATGAATATCAGCCTGGAGGGGAC 549
             ||||||  ||||||||| ||||||||||||||||||
Db   283 TTCGGCCTTTCCAGGATGAGAACTACCTGTACCGTGACCTGGAGTATTACGTGGGCGGGGAC 342

Qy   550 TTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGTAGATGAAAACCTGATACAGTTTTAC 609
             ||||||||| |||| |||| |||||
Db   343 CTGCTGACACTGCTGAGCAAGTTGGGGAGCGGATTCCGGCCGGAGACGTGCATCGACGAC 402

Qy   610 CTAGCTGAGCTGATTTTGGCCTTCACAGCGTCATCGATGGGATACGTGCATCGAGAC 669
             |||||||||  ||| |||||||||||||||  |||||||  ||||||
Db   403 CTGGCGGAGATTGTCATGGCCATAGACTCGGTGCACCGGCTCACGTGCACAGGGAC 462

Qy   670 ATCAAGCCTGAGAACATTCTCGTTGACCAGACACATCCAAGCTGGTGTGATTTTGGA 729
             ||||   || ||||||  |||||||| ||||  ||||||||||||||||
Db   463 ATCAAACCGCAACACATCCTCTGCTGGACCTGTGGCCACATCCGCCTGGCGACTTCGGC 522

Qy   730 TCTGCCCGCGAAAATGAATTCAAACACAGAGATGTGCAATGCCAAACTCCCGATTGGGACCCCA 789
             ||  |||||  |||||||||||| |||||||  ||||||||||||||||
Db   523 TCTTGCCTCAAGCTGCGGCAGATCCCGGGCGTGCTCGGCGGCCGTGTGTGGGCGCACCCCCA 582

Qy   790 GATTACAATGGCTCCTGA---AGTGCTGACTGTGATGAACGGGATGAAAAGGCACTAC 846
             ||| ||| |||||||||     ||||||||||||||  |||||||||||||||||
Db   583 GACTAACCTGTCCCCGAGATCCTGTGGGGCCGTGGGCGTCGGGCGCAGCTAC 642

Qy   847 GGCCTGGACTGTGACTGGTGTCAGTGGGCGCTGATTGCCATGAGAGATGATTTATGGGAGA 906
             ||  ||| |||| |||||   ||||| ||| |||||||
Db   643 GGGCCCGCAGTGCACTGTGACTGGTGGCGCGCTGGTGTATTCCCTATGAATAACATTTCAATGGCGG 702

Qy   907 TCCCCCTTCGGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
             ||||||  |  |||||| |||||||||||||||  ||||||||||
Db   703 ACGCCCTTCTACGCGGATTCCACGGCGGACGTCTCCACTACAGGAG 762

Qy   967 TTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCGATTCAA 1023
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Db   763 CACCTCTCTGCCGCGTGGTGACGAGAAGGGGTCCCTGACGAGAGGCTCGAGACTTCATTCAG 822

Qy  1024 AGCTTGTGTGTGCGGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC-------- 1074
             |||||  | ||||  ||||||||| |||||  |||||||
Db   823 CGGTTGCTGTGTGTCCCCGAGACACCGCTGGGCCCGGGGTGGAGCAGCGACTTCCCGGACA 882

Qy  1075 CATCCTTCTTCTTCTCTCTCAAAATTGACTGGGCATCGTGGAACAACATTCGTAACTCTCTCCCCCCTTCGTT 1134
             |||||||||||| ||||||||||||||
Db   883 CATCCCTTCTTCTTCTTGGCCTCGACGATGACACCTCCGGATGGTCTCCGGGACACCTCCAATTTGA 942

Qy  1135 CCCACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1172
             |||||||||||||  |||  |||||| ||||||||||
Db   943 CCGGATTTCGAAGGTGCCACCGCCACCACATGCAACTTCCA 980
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RESULT 12
US-08-422-706B-8
; Sequence 8, Application US/08422706B
; Patent No. 5977333
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

APPLICATION NUMBER: US/08/484,044
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-044-11

Query Match   14.4%;   Score 218.4; DB 1; Length 3182;
Best Local Similarity   54.5%;   Pred. No. 9.6e-62;
Matches 510; Conservative   0; Mismatches 411; Indels 15; Gaps 3;

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Qy    252  CACCATAGCTGAGTTACAGGAGCTTCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCT  311
Db    743  CATCGTGGTGAGGCTTAAGGAGTTCCGACTGGAGGTTCCGAGATTCGAAGT  802

Qy    550  TTGCTGTCACTTTGAATAGATGAGGACCAGTTAGATGAGAAAACCTGATACAGTTTTAC  609
Db    343  CTGCTGACACTGCTGAGCAAGTTTGGGGAGCGGATTCCGGCCGAGATGGGGCGCTTCTAC  402

Qy    312  TGTAGGTTGTGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACAT  371
Db    803  GATCGGACGCGGGGCGTTCAGCGAGGTAGCGGTAGTGAAGCAGACGGGCCAGGT  862

Qy    610  CTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGAC  669
Db    403  CTGGCGGAGATTGTCATGGCCATAGACTCGGTGCACCGGCTTGGCTACGTGCACAGGGAC  462

Qy    372  CTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGCCCAGGAGCAGGTTTCATTTTT  431
Db    863  GTAATGCCATGAAGATCATGAACAAGTGGACATGCTGAAGAGGGGCAGGTGTCGTGCTT  922

Qy    670  ATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGA  729
Db    463  ATCAAACCCGACAACATCCTGCTGGACCCGTGTGGGCCACTCCGCTTGGCCGACTTCGGC  522

Qy    432  TGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTACAGTA  491
Db    923  CCGTGAGGAGGAGGACGTGTTGGTGAATGGGGACCGGCGGCCGTCGATCACGCAGCTGCACTT  982

Qy    730  TCTGCCGCGAAAATGAATTCAAACAACAAGATGCTGAATGCCAAACTCCCGATTGGGACCCCA  789
Db    523  TCTTGCCTCAAGCTGCGGGCAGATGAACGGTCGCGTCGGTGGTGTGGGCGTGGGCACCCCA  582

Qy    492  TGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTT  551
Db    983  CGCCCTTCCAGGATGAGAACTACCTGTACCTGGTCATGCATGGGGCGGGGACCT  1042

Qy    790  GATTACATGGCTCCTGA---AGTGCTGACTGTGATGAACGGGATGGAAAGGCACCTAC  846
Db    583  GACTACCTGTCCCCCGAGATCCTGCGAGGCTGTGGCGGGGTGGGCCTGGGACAGGCAGCTAC  642

Qy    552  GCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCT  611
Db    1043 GCTGACACTGCTGAGCAAGTTTGGGGATGGCGGATTCCGGCCGAGATGGGGATACGTGCATCGAGACAT  1102

Qy    847  GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA  906
Db    643  GGGCCCGAGTGTGACTGGTGACTGGTGGCGCGCTGGGTGTATTCGCCTATGAAATGTTCTATGGCGAG  702

Qy    612  AGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGAACGGGATCGGGGATGGAAAAGGCACCTACGG  671
Db    1103 GGCGGAGATTGTCATGCCATAGACTCGGTGCACCGGCTTGGCTACGGCTGGTGGTGATTTTGATC  1162

Qy    907  TCCCCCTTCCGAGGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG  966
Db    703  ACGGCCCTTCTACGCGGATTCCACGCGGGAGACCTATGGCAGCCTATGGGCCAGAAGAGGAG  762

Qy    672  CAAGCCTGAGAACATTCTCGGTGACCGGCACACATCAAGCTGGTGGATTTTGGATC  731
Db    1163 CAAACCCGACACAACATCCTGCTGGACCCGTGTGCCACATCCCGCTTGCCGACTTCGGCTC  1222

Qy    967  TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAA  1023
Db    763  CACCTCTCTCGTGCGCTGGTGTCGGACGAGGGGCTCGAGGACTTCATTCAG  822

Qy    732  TGCCGGCGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAACTCCAGATTGGGACCCCAGA  791
Db    1223 TTGCCTCAAGCTGCGGGCAGATGGAACGGTCGCGGTTGGCTGTGGGCGTGGGGCACCCCAGA  1282

Qy    1024 AGCTTGTTGTGTCGGCCCAGAAAGAGAGGACTGAAGTTTGAAGGTCTTTGCTCGC------  1074
Db    823  CGGTTGCTGTGTCCCCGGAGACCAGCGCTCGGGCTGGAGCGAGGCAGGCGACTTCCGGACA  882

Qy    792  TTACATGGCTCCTGA---AGTGCTGACTGTGATGAACGGGGAGGAAAAGGCACCTACGG  848
Db    1283 CTACCTGTCCCCGAGATCCTGGGCGTGGGGCGTGGGGACCAGCAGCTACGG  1342

Qy    1075 CATCCTTTCTTTCTCTAAAATTGACTGGAACAATTCGTAACTCTCCCCCCTTCGTT  1134
Db    883  CATCCCTTCTTCTTTGGCCTCGACTGGATGTCTCCGGGACAGGCGTGCCCCCCTTTACA  942

Qy    849  CCTGAGCTGTGACTGGTGGTCAGTGGGCGTGATTGCTATGAGATGAATTTATGGGAGATC  908
Db    1343 GCCGAGTGTGACTGGTGGTGGGCGTGGGCGTGGTATTCGCCTATGAAATGTTCTATGGGCGAC  1402

Qy    1135 CCACCCTCAAGTCCGACGATGACACCTCCAATTTGA  1172
Db    943  CCGGATTTCGAAGGTGCCACCGGACACTTCGA  980

Qy    909  CCCCTTCCGAGGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTT  968
```

RESULT 13
US-08-484-044-11
; Sequence 11, Application US/08484044
; Patent No. 5552282
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizzuti, Antonio
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```
Db   1403 GCCCTTCTACGCGGATTCCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAGCA 1462

Qy    969 TTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT---GACTTTCTTGATCTGATTCAAAG 1025
               |||||||  ||||  ||  |  |  ||  |  |   |   |||||
Db   1463 CCTCTCTCGCCGCTGGTGGACGAAGGGGTCCCTGAGGAGGCTCGAGACTTCATTCAGCG 1522

Qy   1026 CTTGTTGTGCGGCCAGAAAGAGAGAGACTGAAGTTGAAGGTCTTTGCTGC---------CA 1076
               ||||||  |||  ||||||||||   ||  |  |  ||||
Db   1523 GTTGCTGTGTCCCCGGAGACACGGCTGGGCCGGGGTGGGACAGGGGACTTCCGGACACA 1582

Qy   1077 TCCTTTCTTCTCTAAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCC 1136
               ||||||||| |||  |||||      |  ||||| || | ||||
Db   1583 TCCCCTTCTTCTTTGGCCTGGACTGGGATGGTCTCCGGGACAGCGTGCCCCCCTTTACACC 1642

Qy   1137 CACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1172
               |||||||| ||||  |||| |||  ||| |||
Db   1643 GGATTTCGAAGGTGCCACCGACACATGCAACTTCGA 1678

RESULT 14
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;   APPLICANT: WEBSTER, Marion et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match        14.3%;    Score 216.2;  DB 4;  Length 174493;
Best Local Similarity  96.5%;    Pred. No. 8.7e-60;
Matches  221;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy   1287 TCTTGGTAGATCTGAGTCTGTTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCAT 1346
               |||||||| |  |||||||| ||||||||||||||||||||||||||||||||
Db  171282 TTTTCTCTACCTAGGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCAT 171341

Qy   1347 GGAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCAGGACAAGTGTCACAA 1406
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  171342 GGAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCAGGACAAGTGTCACAA 171401

Qy   1407 GGTATTTATTTCCGCAGCCGGCCTCCTTCCTTGCTCCAGGATCCTCCGGTCCGTATATGC 1466
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  171402 GGTATTTATTTCCGCAGCCGGCCTCCTTCCTTGCTCCAGGATCCTCCGGTCCGTATATGC 171461

Qy   1467 CAAGGGATCCGCCCGGGGCCGCCGCCCGCTGGCTCGAGCCGCCGCCTGATCCGTA 1515
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  171462 CAAGGGATCCGCCCGGGGCCGCCGCCCGCTGGCTCGAGCCGCCGCCTGATCCGTA 171510

RESULT 15
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
;   APPLICANT: WEBSTER, Marion et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
```

Right column:

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; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Query Match        14.3%;    Score 216.2;  DB 4;  Length 174493;
Best Local Similarity  96.5%;    Pred. No. 8.7e-60;
Matches  221;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy   1287 TCTTGGTAGATCTGAGTCTGTTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCAT 1346
               |||||||| |  |||||||| ||||||||||||||||||||||||||||||||
Db  171282 TTTTCTCTACCTAGGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCAT 171341

Qy   1347 GGAAAGAAACTTCATCAAAAGCAAAGAGCTACAAGACTTCAGGACAAGTGTCACAA 1406
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1407 GGTATTTATTTCCGCAGCCTCCTTCCTTGCTCCAGGATCCTCCGGTCCGTATATGC 1466
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Db  171402 GGTATTTATTTCCGCAGCCGGCCTCCTTCCTTGCTCCAGGATCCTCCGGTCCGTATATGC 171461

Qy   1467 CAAGGGATCCGCCCGGGGCCGCCGCCCGCTGGCTCGAGCCGCCGCCTGATCCGTA 1515
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Search completed: March 19, 2005, 14:35:00
Job time : 271.502 secs
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:45:41 ; Search time 4592.53 Seconds
                                         (without alignments)
                                         12556.766 Million cell updates/sec

Title: US-10-724-594-1
Perfect score: 1515
Sequence: 1.ggggagatgtgtgaagtcaa.........tctgagccgcctgatccgta 1515
Scoring table: IDENTITY NUC
             Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_htc:*
             4: gb_est3:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	602.6	39.8	698	5	BP146990	BP146990 BP146990
	2	521.2	34.4	1085	5	BM904785	BM904785 AGENCOURT
	3	478	31.6	492	7	CR746615	CR746615 CR746615
	4	452.8	29.9	600	9	BG808196	BG808196 2082-86 M
	5	425.4	28.1	485	7	CR746792	CR746792 CR746792
	6	423.8	28.0	427	4	BG944539	BG944539 ax51fi1.x
	7	413.2	27.3	617	7	BQ417810	BQ417810 ik51b06.y
	8	380	25.1	481	7	CN682405	CN682405 E0164B04-
	9	378	25.0	479	7	CN678533	CN678533 E0112C12-
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	11	344.2	22.7	821	4	BI654262	BI654262 603280370
	12	329.2	21.7	450	9	CG501400	CG501400 OST45250
	13	328.8	21.7	423	9	BF344814	BF344814 602014091
	14	327	21.6	449	9	CG501399	CG501399 OST45249
	15	318.2	21.0	512	9	CG652891	CG652891 OST417039
c	16	314.2	20.7	340	2	BF380737	BF380737 IL2-UT007
	17	312.6	20.6	582	5	BX516291	BX516291 BX516291
	18	281.6	18.6	521	1	AI882189	AI882189 ul31e08.y
	19	281.4	18.6	355	8	CC325092	CC325092 XL068 Bay
c	20	278.6	18.4	539	2	AW525215	AW525215 UI-R-BJOp
c	21	276.4	18.2	325	3	BC008127	BC008127 Homo sapi
	22	272.6	18.0	336	9	CG869028	CG869028 AB0155 Sa
c	23	270.8	17.9	321	2	BF932611	BF932611 RC5-NT018
c	24	262.4	17.3	335	2	BF763211	BF763211 IL2-CS004
c	25	262.4	17.3	524	7	CK841805	CK841805 UI-R-BJOp
	26	251.8	16.6	423	2	BB827314	BB827314 BB827314
	27	251.4	16.6	398	2	BY018641	BY018641 BY018641
	28	246.4	16.3	385	9	CG655761	CG655761 OST426725
	29	246.2	16.3	289	6	BF944809	BF944809 PM3-NN117
	30	246	16.2	508	6	CB783081	CB783081 AMGNNUC:N
	31	245.8	16.2	547	7	CF744826	CF744826 UI-M-GV0-
	32	245.4	16.2	647	7	CF744580	CF744580 UI-M-GV0-
	33	244.8	16.2	801	5	BU475240	BU475240 603844069
	34	244.8	16.2	847	5	BU467302	BU467302 603373635
	35	243.4	16.1	807	6	CK147448	CK147448 AGENCOURT
	36	240.8	15.9	401	6	BY602044	BY602044 BY602044
	37	238.8	15.8	2688	3	BC024150	BC024150 Mus muscu
	38	237.2	15.7	2862	3	BC056615	BC056615 Mus muscu
	39	236	15.6	1478	9	AY408842	AY408842 Mus muscu
	40	233.6	15.4	605	5	BP168081	BP168081 BP168081
	41	233.4	15.4	563	6	CD310916	CD310916 StrPu691.
	42	231.6	15.3	370	5	BY021399	BY021399 BY021399
	43	231.4	15.3	423	2	BB823725	BB823725 BB823725
	44	225.2	14.9	1600	3	BC038993	BC038993 Homo sapi
	45	222	14.7	400	1	AL360718	AL360718 AL360718

ALIGNMENTS

RESULT 1
BP146990
LOCUS   BP146990   698 bp   mRNA   linear   EST 30-DEC-2003
DEFINITION BP146990 full-length enriched swine cDNA library, adult ovary Sus
            scrofa cDNA clone OVRM10025B09 5', mRNA sequence.
ACCESSION   BP146990
VERSION   BP146990.1 GI:40396461
KEYWORDS   EST.
SOURCE   Sus scrofa (pig)
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 698)
  AUTHORS   Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
            Okumura,N., Hamasima,N. and Awata,T.
  TITLE   PEDE (Pig EST Data Explorer): construction of a database for ESTs
            derived from porcine full-length cDNA libraries
  JOURNAL   Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT   Contact: Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department
            National Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
            Email: huenishi@affrc.go.jp
            EST project with full-length enriched cDNA libraries carried out in
            Animal Genome Research Program (Japan) by National Institute of
            Agrobiological Sciences and STAFF-Institute
            Single pass sequencing of clones derived from oligo-capped cDNA
            library
            Vector sequences were eliminated by RepeatMasker version 2002/07/13
            and crossmatch version 0.990319
            Low quality bases were trimmed based on the quality values.
FEATURES   Location/Qualifiers
     source   1..698
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="OVRM10025B09"
                     /tissue_type="ovary"
                     /dev_stage="adult"
                     /clone_lib="full-length enriched swine cDNA library, adult
                     ovary"
ORIGIN
Query Match   39.8%;   Score 602.6; DB 5; Length 698;
Best Local Similarity   91.4%;   Pred. No. 2.9e-172;

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12279 row: d column: 07
High quality sequence stop: 510.

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FEATURES             Location/Qualifiers
     source          1..1085
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5557590"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
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ORIGIN

Query Match   34.4%;   Score 521.2;   DB 5;   Length 1085;
Best Local Similarity 99.3%;   Pred. No. 2.8e-147;
Matches 534; Conservative   0; Mismatches   3; Indels   1; Gaps   1;

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Qy   873 GGGCGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCTTCGCAGAGGGAACCTCTGC 932
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Db     1 GGGCGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCTTCGCAGAGGGAACCTCTGC 60

Qy   933 CAGAACCTTCAATAACATTATGAAATTTCCAGCGGTTTTGAAATTTCCAGATGACCCCAA 992
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CAGAACCTTCAATAACATTATGAAATTTCCAGCGGTTTTGAAATTTCCAGATGACCCCAA 120

Qy   993 AGTGAGCAGTGACTTTCTGATTCGATCCGCATCCTTTCTTCTCTAAAATTGACTGGAACAACATTCG 1052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGAGCAGTGACTTTCTGATTCGATCCGCATCCTTTCTTCTCTAAAATTGACTGGAACAACATTCG 180

Qy  1053 GAAGTTTGAAGGTCTTTGCTGCGCATCCTTTCTTCTCTAAAATTGACTGGAACAACATTCG 1112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAAGTTTGAAGGTCTTTGCTGCGCATCCTTTCTTCTCTAAAATTGACTGGAACAACATTCG 240

Qy  1113 TAACTCTCCTCCCCCTTCGTCCCACCCTCCGTCCCACCCTCCAAGTCGACGATGACACCCTCCAATTTTGA 1172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TAACTCTCCTCCCCCTTCGTCCCACCCTCCGTCCCACCCTCCAAGTCGACGATGACACCCTCCAATTTTGA 300

Qy  1173 TGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCCAGCTGAGCCCCTCAGCGCTT 1232
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Db   301 TGAACCAGAAGAATTCGTGGGTTTCATCCTCCGTGCCCAGCTGAGCCCCTCAGCGCTT 360

Qy  1233 CTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTTTGTCGTACAGCAAGCAAGGCACTGGGGATTCTTGG 1292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTCGGGTGAAGAACTGCCGTTTGTGGGGTTTGTGGGGTTTGTCGTACAGCAAGCAAGGCACTGGGGATTCTTGG 420

Qy  1293 TAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAAA 1352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAAA 480

Qy  1353 GAAACTTCTCATCAAAA-GCAAAGAGCTACAGAGACTCAGGACAGTGTCACAAGT 1409
             |||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   481 GAAACTTCTCATCAAAAGGCAAAGAGCTACCAGAGACTACCAGACACAGTGTCACAAGAT 538
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RESULT 3
```
CR746615
LOCUS       CR746615       492 bp    mRNA    linear    EST 30-AUG-2004 ;
DEFINITION  CR746615 NIH_MGC_72 Homo sapiens cDNA clone IMAGp998D712279 ;
            IMAGE:5557590 5', mRNA sequence.
ACCESSION   CR746615
VERSION     CR746615.1  GI:51659741
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

Matches 638;   Conservative   0;   Mismatches   60;   Indels   0;   Gaps   0;

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Qy   412 CAGGAGCAGTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCG 471
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CAGGAGCAGTTTCATTTTTGAGGAAGAGCGGAACATCTTATCCCGGAGCACAAGCCCT 60

Qy   472 TGGATCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA 531
             ||||||||  |||| ||||||||||||||||||  ||||||||||||||||||||||
Db    61 TGGATCCCCCAGTTACAGTATGCCTTTCAGGACAAACATAACCTTTATCTGGTCATGGAA 120

Qy   532 TATCAGCCTGGAGGGACTTGCTGTCTCACTTTTGAATAGATATGAGGACCAGTTAGATGAA 591
             |||| ||||||||| |||||||||||||| |||||||||||||||||||||||||||||
Db   121 TATCAGCCTGGAGGGGATTTGCTGTCTCACTTTTGAATAGATATGAGGACCAATTAGATGAA 180

Qy   592 AACCTGATACAGTTTACCTTAGCTGACTGAGCTTTTGGCTGTTGGCTGTTCACAGCGTTCATCTGATG 651
             |||| |  ||||||||||| ||||||||  |||  ||||||||| |||||||||||||||
Db   181 AATATGATACAGTTTTACCTTAGCTGAAATGATTTTGGCTGTTGGCTGTTCACAGCGTTCATCAGATG 240

Qy   652 GGATACGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATC 711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GGATATGTACATCGAGACATCAAGCCTGAGAACATTCTCATCGAACCGGGACACATC 300

Qy   712 AAGCTGGTGGATTTTGGATCTGCCCGCGAAAATGAATTCAAACAACAAGATGGTGAATGCCAAA 771
             |||||||||||||| ||||||||||||||||  ||||||||  |||||||||||||||||||
Db   301 AAGCTGGTGGACTTTGGATCAGCTGCTAAGATGAACTCAAATAAGATGGTGAATGCCAAA 360

Qy   772 CTCCCGATTGGGACCCCCAGATTACATGGCTCCTGAGTGCTGACTGCTGATGATGAACGGGGAT 831
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   361 CTCCCGGTTGGGACCCCCAGATTACATGGCCTAGACTGTGATCGTGATCGTGATGGGGAT 420

Qy   832 GGAAAAGGCACCTACGGCCTGACTGGTCGTGGTCGGGGCCTGATTGCCTATGAG 891
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   421 GGAAAAGGTGCCTATGGCCTAGACTGTGATTGGTCGTCGTCGGAGTATTGCTTATGAG 480

Qy   892 ATGATTTATGGAGATCCCCCTTCGCCATTCACTGAGGGAACCTCAGCCAGAACCTTCAATAACATT 951
             ||||| |||||||| ||||||||||||||||||||||||||| ||||||||||||||||
Db   481 ATGGTTTATGGAAGGTCCCCCATTCACTGAGGAACCTCAGCCAGAACCTTCAATAACATC 540

Qy   952 ATGAATTTCCAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTCGACGAGCAGTGACTTTCTT 1011
             ||||||||||||||||| |||||||||||||||||||| |||||||||||||||||||||
Db   541 ATGAATTTCCAGCGGTTTTTGAAGTTTCCAGATGACCCCAAAGTTAGCAGTGAATTGCTT 600

Qy  1012 GATCTGATTCAAAGCTGTGTGTGCGGCCAGAAAGAGAGACTTGAAGGTCTTTGC 1071
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   601 GATCTGATCCAAAGNTTATTGTGCGGCCAGAAAGAGAGAGACTTGAAGGTTTGAAGGCCCTTTGC 660

Qy  1072 TGCCATCCTTTCTTCTCTAAAATTGACTGGAACAACAT 1109
             ||||||||||||||||||||| |||||||||||||||
Db   661 TGTCATCCTTTCTTCTCTAAAATCGACTGGAATAACAT 698
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RESULT 2
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BM904785
LOCUS       BM904785     1085 bp    mRNA    linear    EST 12-MAR-2002
DEFINITION  AGENCOURT_6659306 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557590
            5', mRNA sequence.
ACCESSION   BM904785
VERSION     BM904785.1  GI:19355164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
```

```
REFERENCE   1 (bases 1 to 492)
AUTHORS     Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
            Peters,M., Radelof,U. and Schneider,D.
TITLE       I.M.A.G.E. cDNA Clone Collection
JOURNAL     Unpublished (2004)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD: IMAGp998D0712279.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES    Location/Qualifiers
  source    1..492
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGp998D0712279 ; IMAGE:5557590"
            /tissue_type="melanotic melanoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_72"
            /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2 kb.  Library constructed by Life
            Technologies."

ORIGIN

Query Match             31.6%;  Score 478;  DB 7;  Length 492;
Best Local Similarity   98.6%;  Pred. No. 3.3e-134;
Matches   481;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     864 GTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGGATCCCCCTCGCAGAGGG 923
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       5 GCGGTNNGCGGGGCGTGATTGCCTATGAGATGATTTATGGGAGGATCCCCCTCGCAGAGGG 64

Qy     924 AACCTCTGCCAGAACCTTCAATACACATTACATTATGAATTTCCAGCGGTTTGAAATTTCCAGA 983
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 AACCTCTGCCAGAACCTTCAATAACACATTATGAATTTCCAGCGGTTTGAAATTTCCAGA 124

Qy     984 TGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATCTGATTCAAAAGCTTGTGTGCGGCCAGAA 1043
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 TGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATCTGATTCAAAAGCTTGTGTGCGGCCAGAA 184

Qy    1044 AGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTGACTGGAA 1103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTCTAAAATTGACTGGAA 244

Qy    1104 CAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTTCCGACGATGACACCTC 1163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 CAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTTCCGACGATGACACCTC 304

Qy    1164 CAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCC 1223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCC 364

Qy    1224 CTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGG 1283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 CTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGG 424

Qy    1284 GATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTC 1343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 GATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGACTAGCTC 484

Qy    1344 CATGGAAA 1351
           ||||||||
Db     485 CATGGAAA 492


RESULT 4
BG808196
LOCUS       BG808196    600 bp    mRNA    linear    EST 20-DEC-2001
DEFINITION  2082-86 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
ACCESSION   BG808196
VERSION     BG808196.1  GI:17955172
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 600)
AUTHORS     Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE       Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
JOURNAL     Nucleic Acids Res. 29 (24), 4983-4993 (2001)
MEDLINE     21671825
PUBMED      11812828
COMMENT     Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES    Location/Qualifiers
  source    1..600
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /tissue_type="neural retina"
            /dev_stage="embryonic day 14.5 post-fertilization"
            /clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Query Match             29.9%;  Score 452.8;  DB 4;  Length 600;
Best Local Similarity   86.6%;  Pred. No. 1.9e-126;
Matches   499;  Conservative   0;  Mismatches   77;  Indels   0;  Gaps   0;

Qy       1 GGGGAGGATGTTGAAGTTCAAATATGAGACGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60
           ||||||||||||||||||| |||||| |||||||||||||||| |||||||||||||||
Db      25 GGAGAGATGTTGAAGTTCAAGTTCAAGTATGGTGCGGAACCCGCGGGAAACCACCCTTATG 84

Qy      61 CCCATTGCCAACCGGCCTCCAGGCTGAATCTGTTCTTCTTCTCCAGGGGAAACCGCCCCCATG 120
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||
Db      85 CCCATTGCCAGTGCGGCCTCCAGGCTAAATCTCTTCTTCTTCCAGGGGAAACCGCCCCCATG 144

Qy     121 ACTCAACAGCAGAATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db     145 ACTCAACAGCAGAATGTCTCGTCTTTCCCGGGAAGGGATGCCAGCAGATGAGCTGCTCTC 204

Qy     181 TTTGAAGAATGCAGTCAGTCAGCTGTCTGATGAAGATTAAGCACGTGAGCAATTTGTCGG 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TTTGAAGAGTGCAGCGCAACCCGCCGAGTTGCGGGAGCTGCAGCTGAGCACGCTTGTCCAG 264

Qy     241 AAGTATTCCGACACCATAGCTGAGTTACAGAGCTTCCAGCCTCAAAGGACTTCGAA 300
           ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     265 AAGTATTCCGACACCATAGCCGAGTTGCGGGAGCTGCAGCCGTGCAGCCGTGCGGAGACTTCGAA 324

Qy     301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTCGTGAAGTGCAGGTGTAAGAGAGAAGCA 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 GTTCGAAGCCTTGGCGGCTGGTCACTTGTCGGCTGTGGTGTTAGGAGAGAAGGCG 384

Qy     361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGGAGAAGGGCTTTATTGGCCCAGGAGCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 ACCGGGGACGTCTATGCCATGAAAATCATGAGAAGATCATGAGAAGAGAGAGGCTTGCTGCCCAGGAACAG 444

Qy     421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCCTGAAGCACAAGCCCCGTGGATCCCC 480
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Db    445 GTTTCATTTTTCGAGGAGGAGGAACATATTATCTTCGAGCACGAGTCCTTGGATCCCC 504
Qy    481 CAATTACAGTATGCCTTTCAGGACAAAAAATCACCTTTATCTGGTGGTCATGGAATATCAGCCT 540
           |||||||| ||||||||||||||| |||||||||||||||||||||  |||||| |||||||
Db    505 CAGTTACAGTACGCCTTTCAGGACAAAAATAACCTTTACCTGGTCATGGAATATCAGCCT 564
Qy    541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGAG 576
           |||||||| ||| |||  ||||  |||  ||||| |||
Db    565 GGAGGGGGATTTGCTGTCGCCTTCTGAACAGATACGAG 600

RESULT 5
CR746792
LOCUS        CR746792            485 bp    mRNA    linear    EST 30-AUG-2004
DEFINITION   CR746792 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGp998E239412 ;
             IMAGE:4149886 5', mRNA sequence.
ACCESSION    CR746792
VERSION      CR746792.1  GI:51660027
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 485)
  AUTHORS    Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
             Peters,M., Radelof,U. and Schneider,D.
  TITLE      I.M.A.G.E. cDNA Clone Collection
  JOURNAL    Unpublished (2004)
COMMENT      Contact: Inge Arlart
             R2PD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Heubnerweg 6, D-14059 Berlin, Germany
             Email: www.rzpd.de
             R2PD; IMAGp998E239412.
             R2PDLIB; I.M.A.G.E. cDNA Clone Collection;
             Contact: Inge Arlart
             R2PD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Heubnerweg 6, D-14059 Berlin, Germany
             Tel: +49 30 32639 100
             Fax: +49 30 32639 111
             www.rzpd.de
             This clone is available royalty-free from RZPD;
             contact RZPD (clone@rzpd.de) for further information. Seq primer:
             M13r, Primer purchase: TTTCACACAGAAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source      1..485
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGp998E239412 ; IMAGE:4149886"
                 /tissue_type="glioblastoma with EGFR amplification"
                 /lab_host="DH10B (T1 phage-resistant)"
                 /clone_lib="NCI_CGAP_Brn64"
                 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                 Average insert size 1.57 kb. Constructed by Life
                 Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Query Match    28.1%;    Score 425.4;  DB 7;  Length 485;
Best Local Similarity 99.8%;  Pred. No. 4.1e-118;
Matches  426;   Conservative  0;  Mismatches  1;   Indels  0;  Gaps  0;

Qy     1 GGGGGAGGAGTGTTGAAGTTCAAATATGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    59 GGGGGAGATGTTGAAGTTCAAATATGAGGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 118
Qy    61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 CCCATTGCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 178
Qy   121 ACTCAACAGCAGATGTCTCCTTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 ACTCAACAGCAGATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 238
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Qy   181 TTTGAAGAATGCAGTGCAGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 240
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Db   239 TTTGAAGAATGCAGTGCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 298
Qy   241 AAGTATTCCGACACCATAGCTGAGTACAGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
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Db   299 AAGTATTCCGACACCATAGCTGAGTACAGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 358
Qy   301 GTCAGAAGTCTTGTAGGTTGGTGTCACTTTGCTGAAGTGGTAAGAGAAAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGGTCAGGTGGTAAGAGAAAAGCA 418
Qy   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAG 420
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Db   419 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGGCTTATTGGCCCAGGAGCAG 478
Qy   421 GTTTCAT 427
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Db   479 GTTTCAT 485

RESULT 6
BG944539
LOCUS        BG944539                    427 bp    mRNA     linear    EST 15-JAN-2003
DEFINITION   ax51fl1.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library)
             Homo sapiens cDNA clone ax51fl1 random, mRNA sequence.
ACCESSION    BG944539
VERSION      BG944539.1  GI:11434911
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 427)
  AUTHORS    Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
  TITLE      Gene expression in proliferating human erythroid cells
  JOURNAL    Genomics 59 (2), 168-177 (1999)
  MEDLINE    99339981
  PUBMED     10409428
COMMENT      Contact: Jeffery L. Miller
             Laboratory of Chemical Biology
             National Institute of Diabetes and Digestive and Kidney Diseases
             Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
             20892, USA
             Tel: 301 402 2373
             Fax: 301 435 5148
             Email: jm7f@nih.gov
             DNA Sequencing and analyses by National Institutes of Health
             Intramural Sequencing Center (NISC).
             Plate: 51 row: f column: 11
             Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source      1..427
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="ax51fl1"
                 /sex="unknown"
                 /tissue_type="blood"
                 /cell_type="Erythroid Cells"
                 /cell_line="Primary Culture of Peripheral Blood
                 Mononuclear Cells"
                 /dev_stage="Progenitor; EPO responsive CD71+++"
                 /lab_host="SOLR"
                 /clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
                 library)"
                 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
                 Site 2: EcoRI; 65,000 proliferating erythroid cells from
                 the buffy coat of a blood donation were obtained by flow
                 cytometric separation after a 5-day culture period in the
                 presence of erythropoietin. Total RNA was purified from
                 the sorted cell population using TRIzol reagent. RNA (0.3
```

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.

Location/Qualifiers

FEATURES
source   1..617
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv x CD1"
/db_xref="taxon:10090"
/dev_stage="p.c. 14.5"
/lab_host="E. coli-DH12S (GIBCO)"
/clone_lib="Kaestner ngn3 wt"
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S_ Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and Sal I linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-Sall sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORT1, T7 promoter is 5'."

ORIGIN

Query Match   27.3%;   Score 413.2;   DB 5;   Length 617;
Best Local Similarity   86.1%;   Pred. No. 2.4e-114;
Matches   457;   Conservative   0;   Mismatches   74;   Indels   0;   Gaps   0;

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Qy    1 GGGGAGATGTTGAAGTTCAAATATGGAGCCGGAATCCTTTGGATCGTGGTCGTCTCGTGAA  60
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Db   87 GGAAAGATGTTGAAGTTCAAGTTCAAGTATGGTGTGGGAACCCGCCCGAGGGCCAGTCCTCCGAG 146

Qy   61 CCCATTGCCAACCGGAGCCTCCAGGCTGAATCGTGTTCTTCTTCCGGAGAAGGGATATTTATG 120
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Db  147 CCCATTGCCAGTCGGGCCTCCGGGCTAAATCTTCTTCTTCCGGAGAAGGGAAACCGCCCCTCATG 206

Qy  121 ACTCAACAGCAGATGTCTCCTTTCCCGGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
          ||||||||||||||||||||||||||||||||||||||
Db  207 ACTCAACAGCAGATGTCTGCTCTTTCCCGGAGAAGGGATGCTAGACGCCCCTCTTCGCTCTC 266

Qy  181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTTCCGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  267 TTTGAAGAGTGCAGCCAACCGGCCTGATGAAGATGAAGCACGTGAGCAGCTTTGTTCCAG 326

Qy  241 AAGTATTCCGACACCATAGCTGAGTTACAGAGCTTCCAGCCTTCCGGCAAAGGACTTCGAA 300
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Db  327 AAGTATTCCGACACCATAGCCGAGTTGCGGGAGCTGCAGCCGTGCAGCGAGACTTCGAA 386

Qy  301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360
          ||||||||||||||||||||||||||||||
Db  387 GTTCGAAGCCTTGTGGGGCTGTGGGTCGTGTCACTTCGGTGAAGTGCAGGTGGTGNTAGAGAAGGCG 446

Qy  361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAG 420
          ||||||||||||||||||||||||||
Db  447 ACCGGGGACGTCTATGCCATGAAAATCATGAAGAGAAGAAGGCTTTGCTGCGGCCCAGGACAG 506

Qy  421 GTTTCATTTTTGAGGAAGAGCGGAACACATATTATCTGACAGCACGGCCTGGATCCCC 480
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Db  507 GTTTCATTTTTCGAGGAGGAGCAGCAGCACATATTATTCTCGGAGCACGAGTCCTTGGATCCCC 566

Qy  481 CAATTACAGTATGCCCTTCAGGACAAAAAATCACCTTTATCTGGTCATGGAA 531
          |||||||||||||||||||||||||||||||
Db  567 CAGTTACAGTACGCCCTTTCAGGACAAAAAAATAACCTTTACCTGGTCATGGAA 617
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---

ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
http://www.nisc.nih.gov/)."

ORIGIN

Query Match   28.0%;   Score 423.8;   DB 4;   Length 427;
Best Local Similarity   99.5%;   Pred. No. 1.2e-117;
Matches   425;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

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Qy  148 CGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTCAGCCTGCTCTG 207
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Db    1 CGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTCAGCCTGCTCTG  60

Qy  208 ATGAAGATTAAGCACGTGAGCAACTTTGTTCCGGAAGTATTCCGACACCATAGCTGAGTTA 267
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATGAAGATTAAGCACGTGAGCAACTTTGTTCCGGAAGTATTCCGACACCATAGCTGAGTTA 120

Qy  268 CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGGAGTCTTGTAGGTTGTGGTCAC 327
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Db  121 CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGGAGTCTTGTAGGTTGTGGTCAC 180

Qy  328 TTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG 387
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Db  181 TTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG 240

Qy  388 ATGAAGAGAAGGCTTTATTGGCCCAGGAGCAGCAGGTTTCATTTTTGAGGAAGAGCGGAAC 447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATGAAGAGAAGGCTTTATTGGCCCAGGAGCAGCAGGTTTCATTTTTGAGGAAGAGCGGAAC 300

Qy  448 ATATTATCTCGAAGCACAAGCACCCGTGGATCCCGTGGATCCCGTGGATCCCCAATTACAGTATGCCCTTTCAGGACAAA 507
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  301 ATATTATCTCGAAGCACAAGCACCCGTGGATCCCTGATCCCCAATTACAGTATGCCTTTCAGGACAAA 360

Db  508 AATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTTGCTGTCACTTTGAAT 567

Db  361 AATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTGCTGTCACTTTGAAT 420

Qy  568 AGATATG 574
          |||||||
Db  421 AGATATG 427
```

RESULT 7
BQ417810
LOCUS   BQ417810   617 bp   mRNA   linear   EST 23-MAY-2002
DEFINITION   ik51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:O88937 O88937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
; mRNA sequence.
ACCESSION   BQ417810
VERSION   BQ417810.1   GI:21123011
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 617)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE   Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
COMMENT   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute

```
RESULT 8
CN682405
LOCUS       CN682405            481 bp    mRNA    linear   EST 17-MAY-2004
DEFINITION  E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
            density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04
            IMAGE:30782511 5', mRNA sequence.
ACCESSION   CN682405
VERSION     CN682405.1  GI:47448856
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 481)
AUTHORS     Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE       Transcriptome analysis of mouse stem cells and early embryos
JOURNAL     PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: E0164 row: B  column: 04
            Seq primer: M13 Reverse
            High quality sequence stop: 481
            POLYA=No.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="129sv/EvTac"
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                     /db_xref="taxon:10090"
                     /clone="NIA:E0164B04 IMAGE:30782511"
                     /sex="Male"
                     /tissue_type="Embryonic Stem Cell"
                     /cell_line="129.3 ES cells"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
                     h, low-density) cDNA library (Long)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001) [PMID: 11544199]). ES
                     cells were plated at density 3x10³/cm2, on gelatin-coated
                     plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
                     medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
                     0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
                     beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
                     streptomycin. Double-stranded cDNAs were synthesized with
                     an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     2ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.8 kb. The library was
                     constructed by Yulan Piao."

ORIGIN

Query Match          25.1%;  Score 380;  DB 7;  Length 481;
Best Local Similarity  88.0%;  Pred. No. 3.2e-104;
Matches  426;  Conservative  0;  Mismatches  55;  Indels  3;  Gaps  1;

Qy   297 CGAAGTCAGAAGTCTTGTAGGTGTGGTCACTTGCTGAAGTGCCAGGTGGGTAAGAGAA 356
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Db     1 CGAAGTTCGAAGCCTTGTGGGCTGTGGTCACTTCGCTGAAGTGCCAGGTGCCAGTGGGTAGAGAA 60

Qy   357 AGCAACCGGGACATCTATGCTATGAAAGTGATGAGAGAGAGGCTTTATTGCCCAGGA 416
             || ||||||| || ||||| ||||| ||  ||||| |||||||||| | ||| ||||
Db    61 GGCGACCGGGGACGTCTATGCCATGAGAAATCATGAGAAGAGAGGCTTTGCTCGGCCCAGGA 120

Qy   417 GCAGGTTCATTTTTGAGGAAGAGCGGGACAGATATTATCTCGAAGACACAAGCCCGTGGAT 476
             ||||||||||||||| ||| || ||||||||||||||||||| || | ||||| ||||||
Db   121 ACAGGTTTCATTTTTCGGAGGAGGAGGACAGATATTATCTCGGAGCACGAGTCCTTCGGAT 180

Qy   477 CCCCCAATTACAGTAGTGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCA 536
             |||| |||||||||  ||||||||||||||||||| |||||||| ||||||||||||||||
Db   181 CCCCAGTTACAGTACGCCTTTCAGGACAAAAATAACCTTTACCTGGTCATGGAATATCA 240

Qy   537 GCCTGGAGGGAGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCT 596
             |||||||||| || |||||||| |  || || |||| |||||||| |||||||| |  |
Db   241 GCCTGGAGGGGGATTTGCTGTCGCCTTCGAACAGATACGAGGACCAATTAGATGAGAGCAT 300

Qy   597 GATACAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATA 656
             || ||||||||||| |||||||||||||||| |||| ||||||| || | ||||||||||
Db   301 GATCCAGTTTTACCTTGCTGAGCTGATTTTGCGTGTTCCACAGCGTGCACCAGATGGGATA 360

Qy   657 CGTGCATCGAGACATCAAGCCTGAGAACATCTCGTTGACCCGCCACAGGACACATCAAGCT 716
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Db   361 TGTGCATCGAGACATCAAGCCCGAGAACATCCTCATCGACCGACGGGGACACATCAAGCT 420

Qy   717 GGTGGAATTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC 776
             ||||| |||||||||  |||   ||||||||||||||| ||     ||| || |||||||||
Db   421 GGTGGATTTTGGATCAGCCGTAAGATGAATTCAAATAA---GGTCGATGCGAAACTCCC 477

Qy   777 GATT 780
             ||||
Db   478 CATT 481


RESULT 9
CN678533
LOCUS       CN678533            479 bp    mRNA    linear   EST 17-MAY-2004
DEFINITION  E0112C12-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
            density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12
            IMAGE:30777539 5', mRNA sequence.
ACCESSION   CN678533
VERSION     CN678533.1  GI:47444984
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 479)
AUTHORS     Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
            VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
            Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
            Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
            Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
            Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
            Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
            D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE       Transcriptome analysis of mouse stem cells and early embryos
JOURNAL     PLoS Biol. 1 (3), 410-419 (2003)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Db   301 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  360
         GATCCAGTTTACCTGCTGAGCTGATTTGGCTGTCCACAGCGTGCACCAGATGGGATA

Qy   657 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  716
         CGTGCATCGAGACATCAAGCCTGAGAACATTCGTTGACGCGAACACATCAAGCT

Db   361 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  420
         TGTGCATCGAGACATCAAGCCCGAGACACATCCTCATCGACGCGGGACACATCACAGCT

Qy   717 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  776
         GGTGGATTTGGATCTGCCGGGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC

Db   421 |||||||||||||||||||||||||||||||||||||||||||||||||||  477
         GGTGGATTTGGATCAGCCGCCTAAGATGAATTCAAATAA---GGTGGATGCCAAACTCCC

Qy   777 GA 778
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Db   478 CA 479
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RESULT 10
BF562826
LOCUS        BF562826              490 bp    mRNA       linear   EST 12-DEC-2000
DEFINITION   UI-R-BJ0p-aip-b-06-0-UI.r1 UI-R-BJ0p Rattus norvegicus cDNA clone
             UI-R-BJ0p-aip-b-06-0-UI 5', mRNA sequence.
ACCESSION    BF562826
VERSION      BF562826.1  GI:11672556
KEYWORDS     EST.
SOURCE       Rattus norvegicus (Norway rat)
  ORGANISM   Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.
REFERENCE    1  (bases 1 to 490)
  AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE      Normalization and subtraction: two approaches to facilitate gene
             discovery
  JOURNAL    Genome Res. 6 (9), 791-806 (1996)
   MEDLINE   97044477
    PUBMED   8889548
COMMENT      Contact: Soares, MB
             Coordinated Laboratory for Computational Genomics
             University of Iowa
             375 Newton Road,  4156  MEBRF,  Iowa City, IA 52242, USA
             Tel: 319 335 8250
             Fax: 319 335 9565
             Email: bento-soares@uiowa.edu
             cDNA Library Preparation: M.B. Soares Lab Clone distribution:
             clones will be available through Research Genetics (www.resgen.com)
             This clone is also available through the I.M.A.G.E. Consortium at
             LLNL (info@image.llnl.gov). IMAGE ID: 1797673
             Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-BJ0p"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ0p
                     library is a subtracted library derived from the UI-R-AAl,
                     UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AE1, UI-R-AP1, and
                     UI-R-AG1 libraries. These libraries represent tissues from
                     rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
                     at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
                     canal at 15 dpc, and ventricle at 13 dpc. The tag is a
                     string of 5-6 nucleotides present between the Not I site
                     and the oligo-dT track. The library was constructed as
                     described by Bonaldo, Lennon and Soares, Genome Research
                     6: 791-806, 1996."
ORIGIN
```

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Query Match         23.2%;  Score 351.4;  DB 2;  Length 490;
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Left column:

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          Email: cdna@lgsun.grc.nia.nih.gov
          Plate: E0112  row: C  column: 12
          Seq primer: M13 Reverse
          High quality sequence stop: 479
POLYA=No.
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                     /mol_type="mRNA"
                     /strain="129sv/EvTac"
                     /db_xref="niaEST:E0112C12-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:E0112C12 IMAGE:30777539"
                     /sex="Male"
                     /tissue_type="Embryonic Stem Cell"
                     /cell_line="129.3 ES cells"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
                     h, low density) cDNA library (Long)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site 2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
                     cells were plated at density 3x103/cm2, on gelatin-coated
                     plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
                     medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
                     0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
                     beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
                     streptomycin. Double-stranded cDNAs were synthesized with
                     an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGGCGGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     2ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.8 kb. The library was
                     constructed by Yulan Piao."
ORIGIN
```

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Query Match         25.0%;  Score 378;  DB 7;  Length 479;
Best Local Similarity     88.0%;  Pred. No. 1.3e-103;
Matches  424;  Conservative    0;  Mismatches   55;  Indels    3;  Gaps    1;

Qy   297 CGAAGTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAA  356
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Db     1 CGAAGTCGAAGCCCTTGTGGGCTGTGGTCACTTCGCTGAGCGTGCAGGTGGTTAGAGAGAA   60

Qy   357 AGCAACCGGGACACTCTATGCTATGAAAGTGATGAAGAAGAAGAGGCTTATTGGCCCAGGA  416
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GGCGACCGGGGACGTCTATGCCATGAAAATCATGAAGAACAGAGAAGAGGCTTTGCTGGCCCCAGGA  120

Qy   417 GCAGGTTTCATTTTTGAGGAAGAGCCGGAACATATTATCTCGAAGCACAGCCCGTGGAT  476
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Db   121 ACAGGTTTCATTTTTCGAGGAGGAGGAACATATTATCTCCGGAGCACGAGTCCTTGGAT  180

Qy   477 CCCCAATTACAGTATGCCTTCAGGACGACAAAAATCACCTTTATCTGGTCATGGAATATCA  536
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Db   181 CCCCCAGTTACAGTACGCCCTTTCAGGACGACAAAAATAACCTTTACCTTGGTCATGGAATATCA  240

Qy   537 GCCTGGAGCGGGGACTTGCGTCCTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCT  596
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Db   241 GCCTGGAGGGGGATTTGCTGTCGCTTCGGCTTCTGAACAGATACGACGGACCAATTAGAGAGAGCAT  300

Qy   597 GATACAGTTTTACCTAGCTGAGCTGATTTGGCTGTCGTTCACAGCGTTCATCTGATGGGATA  656
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/clone_lib="NCI_CGAP_Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
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ORIGIN

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Query Match            22.7%;   Score 344.2;   DB 4;   Length 821;
Best Local Similarity  84.5%;   Pred. No. 3.5e-93;
Matches 469;   Conservative  0;   Mismatches  78;   Indels  8;   Gaps  7;

Qy    1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA  60
         ||||||||||||||||||||||||||||||||| |||| ||||||| |||| |||||||
Db  101 GGAGAGATGTTGAAGTTCAAGTATGGTGTGCGGAACCCGCCCGAGGCCCAGTGCCTCCGAG 160

Qy   61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
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Db  161 CCCATTGCCAGTCGGGCCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATG 220

Qy  121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
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Db  221 ACTCAACAGCAGATGTCTGCTCTTTCCCGGAAGGGATGCTAGACGCCCTCTCGCTCTC 280

Qy  181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGCAACTTGTCCGG 240
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Db  281 TTGGAAGAGTGCAGCCAACCGCCCTGATGAAGATGAAGCACGTGAGCAGCTTAGTCCAG 340

Qy  241 AAGTATTCCGACACCATAG-CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGA 299
         |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db  341 AAGTATTCCGACACCATAGCCGAGTTGCGGGAGCTGCAGCCCTCGGCGAGAGACTTCGA 400

Qy  300 A-GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGCAGGTGG-TAAGAGAGAAA 357
         | ||||||||||||||||||||||||||||| ||| |||||||| ||||||||||||||||
Db  401 AGGTTCGAAGCCTTGTGCAGCGTGGGTCGTGGTCACTTCGCTGAAGTGCAGGTGGTTACGAGAGAAG 460

Qy  358 GCAACCGGGGACAATCCATATGCTATGAAAGTGATGA-AGAAGAAGCTTTATTGGCCCAGGA 416
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Db  461 GCGACCGGGGACGTCTATGCCATGAAAATCATGACAGAGAAGAAGGCTTTGCTTGGCCCAGGA 520

Qy  417 GCAGGTTCATTTTTGAGGAGAGCGAA-CATATTATCTCGAAGCACAAGCCCGTGGA 475
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  521 ACAGGTTCATTTTTCGAGGAGGAGGAACCATATTATCTCGGAGCACGAGTCCTTGGA 580

Qy  476 TCCCCCAATTACAGTATGCCTTTCAGGA-CAAAAATCACCTTATCTGGTCATGG--AAT 532
         ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db  581 TCCACCAGTTACAGTACGCCCTTTCAGGACCCAAAAATAAACTTTACCTGGTCATGGACACT 640

Qy  533 ATCAGCCTGGAGGGG 547
         |||||||||||||||
Db  641 ATCAGCCTGATGGG 655
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RESULT 12
CG501400
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CG501400
LOCUS       CG501400                          450 bp    mRNA    linear    GSS 01-OCT-2003
DEFINITION  OST45250 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45250,
            mRNA sequence.
ACCESSION   CG501400
VERSION     CG501400.1  GI:37275069
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
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Best Local Similarity  85.6%;  Pred. No. 1.8e-95;
Matches 391;  Conservative  0;  Mismatches 66;  Indels  0;  Gaps  0;

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Db   34 GGAGAGATGTTGAAGTTCAAGTATGGAGTGCGGAACCCGTCCGAGGCCAGTGCCCCCGAG  93

Qy   61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 CCCATTGCCAGTCGGGCCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATG 153

Qy  121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
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Db  154 ACTCAACAGCAGATGTCTGCTCTTTCCCGGAAGGGATATTAGATGCCCTCTTTGTTCTC 213

Qy  181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGCAACTTGTCCGG 240
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Db  214 TTGGAAGAGTGCAGCCAACCGCCCTGATGAAGATAAAGCACGTGAGCAGCTTCGTCCGG 273

Qy  241 AAGTATTCCGACACCATAGTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
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Db  274 AAGTATTCGACGATAGCCGAGTTACGGGAGCTCCAGCCGTCGTGAGGGACTTCGAA 333

Qy  301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360
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Db  334 GTGCGAAGTCTTGTGGGCTGGTCGTGGTGGTTTAGAGAGAAAGGCC 393

Qy  361 ACCGGGGACAATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 420
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Db  394 ACCGGGGATGTCTACGCCATGAAAATCATGAAGATCATGAAGAAGAAGGCGGCTTTGCGGGCCCAGGAGCAG 453

Qy  421 GTTTCATTTTTTGAGGAAGAGCGGAACACATATTATCTC 457
         ||||||||||||||||| ||||||||||||||||||||
Db  454 GTTTCATTTTTCGAGGAGGAGGAACACATATTATCCC 490
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RESULT 11
BI654262
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LOCUS       BI654262                          821 bp    mRNA    linear    EST 12-SEP-2001
DEFINITION  603280370F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5310496 5',
            mRNA sequence.
ACCESSION   BI654262
VERSION     BI654262.1  GI:15568498
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11786 row: 1 column: 17
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
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                     /clone="MAGE:5310496"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="5 months"
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TITLE   Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
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Best Local Similarity 90.0%; Pred. No. 1.1e-88;
Matches 352; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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Qy   1184 AGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCGCTTCAGGCTTCTCGGGTGAAG 1243
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Db     62 AGAATTCGTGGGTTTCATCCTCTGTGTGCCAGCTGAGCGCCTTCAGGCTTCTCGGGTGAAG 121

Qy   1244 AACTGCCGTTTGTGGGGTTTTCGTACAGCAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGT 1303
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Qy   1424 CCGGCCTCCTTCCTTGCTCCAGGATCCTCCAGGATCCTCCAGTCAATATGCCAAGGGAATCCGCCCGGG 1483
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Qy   1484 GCCGTGCTGCTCGAGCCGCCTGATCCGT 1514
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RESULT 13
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DEFINITION 602014091F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149886
          5', mRNA sequence.
ACCESSION   BF344814
VERSION   BF344814.1 GI:11292270
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 423)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE
  JOURNAL   Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9412 row: e column: 23
High quality sequence stop: 423.

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     Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match   21.7%; Score 328.8; DB 2; Length 423;
Best Local Similarity 95.7%; Pred. No. 1.4e-88;
Matches 360; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

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Db     48 GGGGAGATGTTGAAGTTCAAATATGGAGGCGGGAATCCTTCGGATGCTGGTGCTGCTGAA 107

Qy     61 CCCATTGCCAACCGGCCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
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Db    108 CCCATTGCCAGCCGGCCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 167

Qy    121 ACTCAACAGCAGATGTCTCCCTCTTCCCGAGGAGGATATTAGATGCCCCTCTTTGTTCTC 180
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Db    168 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGGAGGATATTAGATGCCCCTCTTAGTGTCTC 227

Qy    181 TTTGAAGAATGCAGTCAGCCTGCTCTG--ATGAAGATTAAGCACGTG--AGCAACTTGT 236
          |||||||||||||||||||||||||    ||| |||||||||||||  |||||||| ||
Db    228 TTTGAAGAATGCAGTCAGCCTGCTCGTCATGCAAGATTAAGCACGTGCAGCAACCTTTGT 287

Qy    237 CCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTT 296
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Db    288 CCGGAAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTT 347

Qy    297 CGAAGTCAGAAGTCTTGTGAGTGTGTGCACTTTGCTCACTTTGCTGAAGTGGTAAGAGAGAA 356
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Db    348 CGAAGTCAGAAGTCTTGTGAGTGTGTGCACTTTGCTCACTTTGCTGAAGTGGTAAGAGAGAC 407

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DEFINITION OST45249 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45249,
          mRNA sequence.
ACCESSION   CG501399
VERSION   CG501399.1 GI:37275067
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 449)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

REFERENCE
AUTHORS   Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
            Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q. Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
TITLE   Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT   OmniBank
            Contact: Zambrowicz BP
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   21.0%; Score 318.2; DB 9; Length 512;
Best Local Similarity   92.0%; Pred. No. 2.6e-85;
Matches 346; Conservative   0; Mismatches   29; Indels   1; Gaps   1;

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Db   8 CTCCTCCCCCCTTCG-TCCCCNCCTCAAGTCGACGATGACACCTCCAATTTGATGAAC 66

Qy   1178 CAGAGAAGAATTCGTGGGTTTCATCCTCCTCCGTGTGCCAGCTGAGCCCCTCAGGCTTCTCCGG 1237
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Db   67 CAGAGAAGAATTCGTGGGTTTCATCCTCCTCCGTGTGCCAGCTGAGCCCCTCGGGCTTCTCCAG 126

Qy   1238 GTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGGTGAGAT 1297
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Db   127 GCGAAGAGCTGCCGTTTGTGGGGATTTTCGTACAGCAAGGCACTGGGGTATCTTGGTGAGAT 186

Qy   1298 CTGAGTCGTGTGTCGGGGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAC 1357
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Db   187 CTGAGTCGTGTCGTGTCGGGACTCGGACTCCCCCGCCAAGGTTAGCTCCATGNAAAAGAAAC 246

Qy   1358 TTCTCATCAAAAGCAAAGAGCTCTCAGGACAACAAGTGTCACAAGGTATTTATTT 1417
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Db   247 TTCTCATCAAAAGCAAAGAGCTCCAGGACAACAAGTGTCACAAGGTATCTCATCT 306

Qy   1418 CCGCAGCCGGCCTCCTTCGTTGCTCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCG 1477
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Db   307 CCACAGCCGGCCTACGTTCCTTGCTCCAGGATCCTCCAGTCAATATATGCCGAGGGATCTG 366

Qy   1478 CCCGGGGGCCGCTGCTG 1493
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Job time : 4599.53 secs

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DEFINITION OST417039 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST417039,
            mRNA sequence.
ACCESSION   CG652891
VERSION   CG652891.1 GI:37476740
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 06:24:41 ; Search time 767.108 Seconds
                                            (without alignments)
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Title: US-10-724-594-1
Perfect score: 1515
Sequence: 1 ggggagatgtgtgaagttcaa..........tctgagccgcctgatccgta 1515

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

SUMMARIES

Database :   N_Geneseq_16Dec04:*
                1: geneseqn1980s:*
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                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
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               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1515	100.0	1515	8	ACA61394	Aca61394 cDNA enco
2	1515	100.0	1515	10	AAD59938	Aad59938 Human kin
3	1515	100.0	1515	12	ADO40591	Ado40591 Human kin
4	1510.2	99.7	2066	6	AAD26454	Aad26454 Human kin
5	1505.8	99.4	1765	10	ABZ68726	Abz68726 Nucleotid
6	1481.8	97.8	1485	10	ABZ68725	Abz68725 Nucleotid
7	1404.2	92.7	6298	6	AAD38864	Aad38864 Human kin
8	1398.2	92.3	1870	8	ADA05643	Ada05643 Human NOV
9	1398.2	92.3	5877	7	ABQ78871	Abq78871 Human kin
10	1398.2	92.3	6156	9	AAL55217	Aal55217 Human CRI
11	1398.2	92.3	6165	6	ABQ78870	Abq78870 Human kin
12	1398.2	92.3	6165	9	AAL55214	Aal55214 Human CRI
13	1398.2	92.3	8603	9	AAL55215	Aal55215 Human CRI
14	1397.8	92.3	6574	6	AAD39191	Aad39191 Human MDP
15	1397.8	92.3	6574	10	ADF60992	Adf60992 Pain asso
16	1397.8	92.3	6574	13	ADQ89099	Adq89099 Human uro
17	1395	92.1	1870	12	ADN62808	Adn62808 Human NOV
18	1391.8	91.9	6162	10	ADF60993	Adf60993 ORF of pa
19	1388	91.6	8656	12	ADJ96544	Adj96544 Human cit
20	1382	91.2	6159	4	AAS06701	Aas06701 Polynucle

21	1375.8	90.8	6189	6	ABS63436	Abs63436 RHO/RAC-1
22	1375.8	90.8	6189	8	ADA05641	Ada05641 Human NOV
23	1375.8	90.8	6189	12	ADN62806	Adn62806 Human NOV
24	1375.8	90.8	6201	6	ABS63435	Abs63435 Human cDN
25	1375.8	90.8	6201	8	ADA05653	Ada05653 Human NOV
26	1375.8	90.8	6201	12	ADN62818	Adn62818 Human NOV
27	1158	76.4	2380	10	ABZ68776	Abz68776 Nucleotid
28	963.2	63.6	2162	8	ABX71191	Abx71191 Novel hum
29	955.4	63.1	957	11	ADN62729	Adn62729 Human cit
30	940.8	62.1	1048	5	AAS79753	Aas79753 DNA encod
31	760.8	50.2	1133	10	ADJ79946	Adj79946 Human kin
32	578.8	38.2	2896	5	ABV30132	Abv30132 Human pro
33	441.8	29.2	446	5	ABV15823	Abv15823 Human pro
34	434.4	28.7	485	5	ABV45624	Abv45624 Human pro
35	247.2	16.3	3835	8	ABT33346	Abt33346 NOVX DNA
36	247.2	16.3	3985	8	ABT33347	Abt33347 NOVX DNA
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40	246.8	16.3	4944	12	ADF95099	Adf95099 Human ser
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43	246.8	16.3	5438	12	ADJ96545	Adj96545 Human dys
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ALIGNMENTS

RESULT 1
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ID   ACA61394 standard; cDNA; 1515 BP.
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AC   ACA61394;
XX
DT   11-AUG-2003 (first entry)
XX
DE   cDNA encoding novel human kinase.
XX
KW   Human; ss; gene; gene therapy; kinase; antisense.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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PD   30-JAN-2003.
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PF   11-SEP-2002; 2002US-00238709.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-438978/41.
DR   P-PSDB; ABU10126.
XX
PT   New human kinase peptides useful as models or targets for the development
PT   of therapeutic agents that modulate kinase activity, for eliciting immune
PT   response, and in identifying compounds that modulate kinase activity or
PT   expression.
XX

PS   Claim 4; Fig 1; 207pp; English.
XX
CC   The invention relates to a novel isolated human kinase. The kinase
CC   peptides and nucleic acids are useful as models for the development of
CC   human therapeutic targets, in the identification of therapeutic proteins,
CC   and serve as targets for the development of human therapeutic agents that
CC   modulate kinase activity in cells and tissues that express the kinase.
CC   The proteins can be used to raise or to elicit another immune response,
CC   as a reagent in assays designed to determine the levels of the protein in
CC   biological fluids, as markers for tissue in which the corresponding
CC   protein is preferentially expressed, in the identification of modulators
CC   of the peptides and in pharmacogenomic analysis. The nucleic acids are
CC   useful as hybridisation probes, in constructing vectors, host cells or
CC   transgenic animals expressing all or a part of the nucleic acid, for
CC   monitoring the effectiveness of modulating compounds on the expression or
CC   activity of the transporter gene in clinical trials or in treatment
CC   regimen, in gene therapy and as antisense constructs to control
CC   transporter gene expression in cells, tissue and organisms. The present
CC   sequence represents cDNA encoding a novel human kinase
XX
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match   100.0%; Score 1515; DB 8; Length 1515;
Best Local Similarity   100.0%;
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 CCCATTGCCAACCGGCCCTCCAGGCTGAATCGTGTTCTTCCAGGGAAACCACCCTTTATG 120
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Db   61 CCCATTGCCAACCGGCCCTCCAGGCTGAATCGTGTTCTTCCAGGGAAACCACCCTTTATG 120

Qy   121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTTCTTTGTTCTC 180
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Qy   181 TTTGAAGAATGCAGTCAGCAGCCTGCTCTCGATGAAGATTAAGCACGTGCAACTTGTCCGG 240
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Qy   301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGGTCACTTTGCTGAAGTGCAGGTGGTGAAGAGAAAGCA 360
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Qy   541 GGAGGGGACTTGCTCGTGTCACTTTGAATAGATAGATGAGGACCAGTTAGAACCTGATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAGGGGACTTGCTCGTGTCACTTTGAATAGATAGATGAGGACCAGTTAGAACCTGATA 600

Qy   601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 660

Qy   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720

Qy   721 GATTTTGGATCTGCCGCGGCGAAAATGATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GATTTTGGATCTGCCGCGGCGAAAATGATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGATGAACGGGATGAACGGGATGAAAAGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGATGAACGGGATGAACGGGATGAAAAGGC 840

Qy   841 ACCTACGGCCTGGACTGCTGCACTGGTGGTGGCCTATGAGATGATTTAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCTACGGCCTGGACTGCTGCACTGGTGGTGGCCTATGAGATGATTTAT 900

Qy   901 GGGAGATCCCCCTTCGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGGAGATCCCCCTTCGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960

Qy   961 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CAGCGGTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020

Qy   1021 CAAAGCTTGTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAAAGCTTGTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080

Qy   1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1140

Qy   1141 CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAAGAATTCGTTGGGTTTCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAAGAATTCGTTGGGTTTCA 1200

Qy   1201 TCCTCTCGTGCCAGTCGAGCCCTCAGGCTTCTCGGGTGAACTGCCGTTTGTGTGGGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTCTCGTGCCAGTCGAGCCCTCAGGCTTCTCGGGTGAACTGCCGTTTGTGTGGGG 1260

Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320

Qy   1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380

Qy   1381 CAAGAGTCTCAGGACAAGTGTCCAAGGTATTTATTCCGAGCCGGCCTCCTTCCTTGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAAGAGTCTCAGGACAAGTGTCCAAGGTATTTATTCCGAGCCGGCCTCCTTCCTTGC 1440

Qy   1441 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCCGGCCCGGGCCCGTCTGGCTCTGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCCGGCCCGGGCCCGTCTGGCTCTGA 1500

Qy   1501 GCCGCCTGATCCGTA 1515
              |||||||||||||||
Db   1501 GCCGCCTGATCCGTA 1515

RESULT 2
AAD59938
ID   AAD59938 standard; cDNA; 1515 BP.
XX
AC   AAD59938;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Human; kinase protein; diagnostic; therapeutic; immune response;
KW   pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic;
KW   gene; ss.
XX
OS   Homo sapiens.

```
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FH   Key              Location/Qualifiers
FT   5'UTR            1..6
FT                    /*tag= a
FT   CDS              7..1500
FT                    /*tag= b
FT                    /product= "Human kinase protein"
FT   3'UTR            1501..1515
FT                    /*tag= c
XX
PN   US2002132322-A1.
XX
PD   19-SEP-2002.
XX
PF   13-MAR-2001; 2001US-00804471.
XX
PR   13-MAR-2001; 2001US-00804471.
XX
PA   (WEBS/)  WEBSTER M.
PA   (YANC/)  YAN C.
PA   (DFRA/)  DI FRANCESCO V.
PA   (BEAS/)  BEASLEY E M.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2003-687480/65.
DR   P-PSDB; AAE39504.
XX
PT   New isolated human kinase proteins, useful as models for developing human
PT   therapeutic targets, or for treating a disorder associated with an
PT   absence of, inappropriate or unwanted expression of the protein, e.g.
PT   cancer.
XX
PS   Claim 4; Fig 1; 0pp; English.
XX
CC   The present invention relates to human kinase proteins and nucleic acids
CC   encoding them all of which are useful in the development of human
CC   therapeutics and diagnostic composition and methods. The invention is
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents. The invention is also useful in
CC   drug screening assays, in assays to determine the biological activity of
CC   the protein, to raise antibodies and to elicit another immune response.
CC   The antibodies are useful in pharmacogenomic analysis, for inhibiting
CC   protein function and for tissue typing. The transgenic animals are useful
CC   for studying the function of kinase protein, identifying and evaluating
CC   modulators of kinase protein activity. The invention is also used in gene
CC   therapy. The present sequence is the human kinase cDNA. The human kinase
CC   gene is located on chromosome 12
XX
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1515;  DB 10;  Length 1515;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1515;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGAGAGATGTTGAAGTCAAATATGGAGCCGGAATCCTTGGATGCTGGTGCTGCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGAGAGATGTTGAAGTCAAATATGGAGCCGGAATCCTTGGATGCTGGTGCTGCTGAA 60

Qy         61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATG 120

Qy        121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180

Qy        181 TTTGAAGAATGCAGTCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCGAACTTGTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTGAAGAATGCAGTCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCGAACTTGTCCGG 240

Qy        241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCGGCAAAGGACTTCGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCGGCAAAGGACTTCGAA 300

Qy        301 GTCAGAAGTCTTGTAGGTTGGTCACTTTGCTCAGTGGTCAGTGTGTAAGAGAGAAGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAGAAGTCTTGTAGGTTGGTCACTTTGCTCAGTGGTCAGTGTGTAAGAGAGAAGCA 360

Qy        361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAGAAGGCTTTATTGGCCCAGGAGCAG 420

Qy        421 GTTTCATTTTTTGAGGAAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTTCATTTTTTGAGGAAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCC 480

Qy        481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540

Qy        541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600

Qy        601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCCACGCGTTCATCTGATCTGATGGATAGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCCACGCGTTCATCTGATCTGATGGATAGTG 660

Qy        661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGTG 720

Qy        721 GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780

Qy        781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 840

Qy        841 ACCTACGGCCTGGACTGTGACTGGTGCTGGGCGTCAGTGGGCGTGATGCCTATGAGATGATTTAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTACGGCCTGGACTGTGACTGGTGCTGGGCGTCAGTGGGCGTGATGCCTATGAGATGATTTAT 900

Qy        901 GGGAGATCCCCTTGCCAGAGGGAACCTGCCAGAACCTTCAATAACATTATGAATTC 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGGAGATCCCCTTGCCAGAGGGAACCTGCCAGAACCTTCAATAACATTATGAATTC 960

Qy        961 CAGCGGGTTTTGAAATTCCAGATGACCCCAAAGTGACAGTGACACTGTCTGATCTGATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCGGGTTTTGAAATTCCAGATGACCCCAAAGTGACAGTGACACTGTCTGATCTGATT 1020

Qy       1021 CAAAGCTTGTTGTGCGGCCAGAAAGAGACAACATTCGAACTCTCCTCCCCCCTTCGTTCCATCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAAAGCTTGTTGTGCGGCCAGAAAGAGACAACATTCGAACTCTCCTCCCCCCTTCGTTCCATCCT 1080

Qy       1081 TTCTTCTCTAAAATTGACTCGACTAAATTGACTCGACTAACTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTCTTCTCTAAAATTGACTCGACTAAATTGACTCGACTAACTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1140

Qy       1141 CTCAAGTCCGACGATGCACACCTCCAATTTTGATGAACCAGAGAGAATTCGTGGGTTTCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTCAAGTCCGACGATGCACACCTCCAATTTTGATGAACCAGAGAGAATTCGTGGGTTTCA 1200

Qy       1201 TCCTCTCCGTGCCAGCTGAGCCCTGAGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCTCTCCGTGCCAGCTGAGCCCTGAGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGG 1260

Qy       1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGAGTCTGAGTCTGTTGTCTC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGAGTCTGAGTCTGTTGTCTC 1320

Qy       1321 GACTCCCCTGCCAAGACTAGCTCCATGGGAGCTCAGGAGCTCCATCCATCGATGGAAAAGAACTTCATCAAAAGAGAGCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380

Qy    1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTTCCTTGC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGGCCTCCTTCCTTGC 1440

Qy    1441 TCCAGGATCTCCCCGTCCGTATATGCCAAGGGATCCGCCCGGGGCCGCTGCTGGCTCTGA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TCCAGGATCCTCCCGTCCCGTATATGCCAAGGGATCCGCCCGGGGCCGCTGCTGGCTCTGA 1500

Qy    1501 GCGCCTGATCCGTA 1515
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Db    1501 GCGCCTGATCCGTA 1515
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RESULT 3

ADO40591

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ID   ADO40591 standard; cDNA; 1515 BP.
XX
AC   ADO40591;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Kinase; rho/rac-interacting citron kinase; drug screening;
KW   kinase related disorder; human; chromosome 12; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT   CDS             7..1500
FT                   /*tag= b
FT                   /product= "Human kinase protein"
FT   3'UTR           1501..1515
FT                   /*tag= c
XX
PN   US2004091993-A1.
XX
PD   13-MAY-2004.
XX
PF   02-DEC-2003; 2003US-00724594.
XX
PR   13-MAR-2001; 2001US-00804471.
PR   11-SEP-2002; 2002US-00238709.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Webster M, Yan C, Di Francesco V, Beasley EM;
XX
DR   WPI; 2004-374957/35.
DR   P-PSDB; ADO40592.
XX
PT   New isolated human kinase proteins and nucleic acids, useful for
PT   developing human therapeutic targets, identifying therapeutic proteins or
PT   serve as targets for the development of human therapeutic agents that
PT   modulate kinase activity.
XX
PS   Claim 4; SEQ ID NO 1; 207pp; English.
XX
CC   The present invention provides a kinase polypeptide and its encoding
CC   polynucleotide. The polypeptide and polynucleotide of the invention are
CC   useful as models for the development of human therapeutic targets, aid in
CC   the identification of therapeutic proteins and serve as targets for the
CC   development of human therapeutic agents that modulate kinase activity in
CC   cells and tissues that express the kinase. The invention is also useful
CC   for biological assays related to kinases, in drug screening assays, for
CC   treating disorders characterized by an absence of inappropriate and
CC   unwanted expression of the protein. The present sequence is human kinase
CC   cDNA. The human kinase gene is located on chromosome 12.
XX
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```
SQ   Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

     Query Match          100.0%;  Score 1515;  DB 12;  Length 1515;
     Best Local Similarity 100.0%;  Pred. No. 0;
     Matches 1515;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GGGGGAGATGTTGAAGTTCAAATATGAGGACGGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GGGGGAGATGTTGAAGTTCAAATATGAGGACGGCGGAATCCTTTGGATGCTGGTGCTGCTGAA 60

Qy    61 CCCATTGCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCATTGCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120

Qy   121 ACTCAACAGCAGAGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACTCAACAGCAGAGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180

Qy   181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 240

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGGCTCCAGCCTTCGGCAAAGGACTTCGAA 300

Qy   301 GTCAGAAGTCTTGTAGGTGTGGTCACTTGCTGAAGTGCAGTGGTAAGGAGAGAAAGCA 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTCAGAAGTCTTGTAGGTGTGGTCACTTGCTGAAGTGCAGTGGTAAGGAGAGAAAGCA 360

Qy   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 420

Qy   421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACACAAGCCCGTGGATCCCC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACACAAGCCCGTGGATCCCC 480

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGAATATCAGCCT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGAATATCAGCCT 540

Qy   541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600

Qy   601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCATCTGATCGGGATACGTG 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCATCTGATCGGGATACGTG 660

Qy   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTG 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCCACAGGACACATCAAGCTGGTG 720

Qy   721 GATTTGGATCTGCCCGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GATTTGGATCTGCCCGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 840

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTCAGTGGCCTATGAGATGATTAT 900
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Db   841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTCAGTGGCCTATGAGATGATTAT 900

Qy   901 GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGACCTTCAATAACATTATGAATTC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGACCTTCAATAACATTATGAATTC 960

Qy   961 CAGCGGTTTTGAAATTCCAGATGAGCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CAGCGGTTTTGAAATTCCAGATGAGCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
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PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H,   Lal P,   Bandman O,   Borowsky ML,   Au-Young J,   Lu Y;
PI   Gandhi AR,   Tribouley CM,   Walia NK,   Yao MG,   Lu DAM,   Greenwald SR;
PI   Ramkumar J,   Griffin JA,   Kearney L,   Burford N,   Nguyen DB,   Tang YT;
PI   Baughn MR,   He A,   Thornton M,   Hafalia A,   Patterson C,   Gururajan R;
PI   Lo TP,   Khan F,   Recipon SA,   Azimzai Y,   Policky JL,   Ding L;
PI   Grether M,   Elliott VS,   Thangavelu K,   Batra S,   Ison CH;
XX
DR   WPI; 2002-090207/12.
DR   P-PSDB; AAB16261.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.
XX
PS   Claim 5; Page 180-181; 197pp; English.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-7 cDNA.
XX
SQ   Sequence 2066 BP; 515 A; 497 C; 516 G; 538 T; 0 U; 0 Other;

Query Match   99.7%; Score 1510.2; DB 6; Length 2066;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1512; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 GGGGAGGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGTGGTGCTGCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8 GGGGAGGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGTGGTGCTGCTGAA 67

Qy   61 CCCATTGCCAACCGGCCGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 CCCATTGCCAACCGGCCGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 127

Qy   121 ACTCAACAGCAGATGTCTCCTTCCGAGAAGGGATATTAGATGAGTGCCCTCTTTGTGTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 ACTCAACAGCAGATGTCTCCTTCCGAGAAGGGATATTAGATGAGTGCCCTCTTTGTGTCTC 187

Qy   181 TTTGAAGAATGCAGTCAGCTGCTTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 TTTGAAGAATGCAGTCAGCTGCTTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 247

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGGTCTTTGCTGCCATCCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGGTCTTTGCTGCCATCCT 1080

Qy   1081 TTCTTCTCTAAAATTGACTGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1140
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1081 TTCTTCTCTAAAATTGACTGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACC 1140

Qy   1141 CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTCA 1200
              ||||||||||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db   1141 CTCAAGTCCGACGATGACACCTCCCAATTTTGATGAACCAGAAGAATTCGTGGGTTTCA 1200

Qy   1201 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCGGGTGAAGAACTGCCGTTTGTGGGG 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCGGGTGAAGAACTGCCGTTTGTGGGG 1260

Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTCAGTCTGTTGTGTCGGGTCTG 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTCAGTCTGTTGTGTCGGGTCTG 1320

Qy   1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCATCAAAAGCAAAGAAGCTA 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCATCAAAAGCAAAGAAGCTA 1380

Qy   1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCCAGCCGGCCTCCTTCCTTGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAAGACTCTCAGGACAAGTGTCACAAGGTATTATTTCCCGAGCCGCCTCCTTCCTTGC 1440

Qy   1441 TCCAGGATCCTCCCCGTCCCGTATATGCCAAGGGATCCGCCCGGGCGGCCGTCTGGCTCTGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TCCAGGATCCTCCCCGTCCCGTATATGCCAAGGGATCCGCCCGGGCGGCCGTCTGGCTCTGA 1500

Qy   1501 GCCGCCTGATCCGTA 1515
              |||||||||||||||
Db   1501 GCCGCCTGATCCGTA 1515

RESULT 4
AAD26454
ID   AAD26454 standard; cDNA; 2066 BP.
XX
AC   AAD26454;
XX
DT   26-MAR-2002 (first entry)
XX
DE   Human kinase PKIN-7 cDNA.
XX
KW   Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;
KW   Good pasture's disease; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   14..1507
FT   /tag= a
FT   /product= "Human PKIN-7 protein"
XX
PN   WO200196547-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX

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Db  248  AAGTATTCCGACACCATAGCTCGAGTTACAGGAGCCTTCGGCGAAAGGACTTCGAA  307

Qy  301  GTCAGAAGTCTTGTGTAGGTTGTGTCACTTTGCTCAGTCGAAGTGAGTGCGAGTGAGAGAGAAGCA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  308  GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTCAGTCGAAGTGAGTGCGAGTGAGAGAGAAGCA  367

Qy  361  ACCGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  368  ACCGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAG  427

Qy  421  GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  428  GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC  487

Qy  481  CAATTACAGTAGTATGCCTTTCAGGACAACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  488  CAATTACAGTATGCCTTTCAGGACAACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT  547

Qy  541  GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGACCAGTTAGATGAAAACCTGATA  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  548  GGAGGGGACTTGCTGTCACTTTGAATAGATATGAGACCAGTTAGATGAAAAACCTGATA  607

Qy  601  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  608  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACACGGTTCATCTGATGGGATACGTG  667

Qy  661  CATCGAGACAATCAAGCCTGAGAACATTCTCGTTGACCGGCCACACAGGACACATCAAGCTGGTG  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  668  CATCGAGACAATCAAGCCTGAGAACATTCTCGTTGACCGGCCACAGGACACATCAAGCTGGTG  727

Qy  721  GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  728  GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT  787

Qy  781  GGGACCCCAGATTACATGCTCCTGAAGTGCTGACTGTGTGACTGTGATGAACGGGATGGAAAAGGC  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  788  GGGACCCCAGATTACATGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC  847

Qy  841  ACCTACGGCCTGGACTGTGACTGGTCGTGGTCAGTGGGCGTGGTGATTGCCTATGAGATGATTAT  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  848  ACCTACCGCCTGGACTGTGACTGGTCGTGGTGGTCAGTGGGCGTGGTGATTGCCTATGAGATGATTAT  907

Qy  901  GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAAATTC  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  908  GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAAATTC  967

Qy  961  CAGCCGGTTTTTGAAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTGATCTGATT  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  968  CAGCCGGTTTTTGAAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTGATCTGATT  1027

Qy  1021 CAAAGCTTGTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1028 CAAAGCTTGTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCT  1087

Qy  1081 TTCTTCTAAAATTGACTGGAACACATTCGTAACTCTCCTCCCCTTCGTTCCCACC  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1088 TTCTTCTAAAATTGACTGGAACACATTCGTAACTCGTAACTCTCCTCCCCTTCGTTCCCACC  1147

Qy  1141 CTCAAGTCCGACGATGACACACTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1148 CTCAAGTCTGACGATGACACACTCCAATTTGATGAACCAGAGAAGAAGAATTCGTGGGTTTCA  1207

Qy  1201 TCCTCTCCGTCCCGGCCAGCTGAGCCCTGGCGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG  1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1208 TCCTCTCCGTCCCGGCCAGCTGAGCCCTGGCGCTTCTCCGGGTGAAGAACTGCCGTTTGTGGGG  1267

Qy  1261 TTTTCGTACAGCAAGGCACTGGGATTCTCGTAGATCTGAGTCTGTGTCGGGTCTG  1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1268 TTTTCGTACAGCAAGGCACTGGGATTCTTCGTAGATCTGAGTCTGTGTCGGGTCTG  1327

Qy  1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGACAAACTTCTCATCAAAGCAAAGAGCTA  1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1328 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGACAAAACTTCTCATCGAAAAGCAAAGAGCTA  1387
```

Qy 1381 CAAGACTCTCAGGACAAGCAAGTGTCACAAGGTATTATTCCGAGCCGCCTCCTTCCTTGC 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1388 CAAGACTCTCAGGACAAGCAAGTGTCACAAGGTATTATTCCGAGCCGCCGCCTCCTTGC 1447

Qy 1441 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCCGCTGCTGGCTCTGA 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1448 TCCAGGATCCTCCCGTCCGTATATGCCAAGGGATCCCGCCGCGGGCGCTGCTGGCTCTGA 1507

Qy 1501 GCCGCCTGATCCGTA 1515
         |||||||||||||||
Db 1508 GCCGCCTGATCCGTA 1522

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RESULT 5
ABZ68726
ID   ABZ68726 standard; DNA; 1765 BP.
XX
AC   ABZ68726;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression; gene; ss.
XX
OS   Homo sapiens.
XX
FH            Location/Qualifiers
FT   Key
FT   CDS          1..1494
FT                /tag= a
FT                /product= "citron rho/rac-interacting kinase-short
FT                kinase"
XX
PN   WO2003004629-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
PR   25-APR-2002; 2002US-0375015P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   P-PSDB; ABP97687.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 18; 145pp; English.
XX
CC   The present sequence encodes a human citron rho/rac-interacting kinase-
CC   short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
CC   associated with the polypeptide dysfunction. The expression vector or the
CC   reagent is useful in the preparation of a medicament for modulating the
CC   activity of a human citron rho/rac-interacting kinase-short kinase in a
CC   disease, such as obesity or chronic obstructive pulmonary disease. These
CC   may also be used for treating obesity/ overweight-associated
CC   comorbidities, such as hypertension, diabetes, coronary artery disease,
CC   hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC   apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced
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CC    fertility, and depression
XX
SQ    Sequence 1765 BP; 428 A; 430 C; 444 G; 463 T; 0 U; 0 Other;

Query Match     99.4%;  Score 1505.8;  DB 10; Length 1765;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1507;  Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy        7  ATGTTGAAGTTCAAATATGAGACGCGGAATCCTTTGGATGCTGCTGCTGAACCCATT   66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1  ATGTTGAAGTTCAAATATGAGACGCGGAATCCTTTGGATGCTGCTGCTGAACCCATT   60

Qy       67  GCCAACCGGCGCTGAATCGTCTTCTTCCCAGGGAAACCACCCTTTATGACTCAA    126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  GCCAGCCGGGCGCTCCAGGCTGAATCGTCTTCTTCCCAGGGAAACCACCCTTTATGACTCAA   120

Qy      127  CAGCAGATGTCTCCTTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA    186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA    180

Qy      187  GAATGCAGTCAGCCTGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTGAGTAT    246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  GAATGCAGTCAGCCTGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTGAGTAT    240

Qy      247  TCCGACACCATAGCTGAGTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG    306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  TCCGACACCATAGCTGAGTTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG    300

Qy      307  AGTCTTGTAGGTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG    366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  AGTCTTGTAGGTGTGGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG    360

Qy      367  GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA    426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA    420

Qy      427  TTTTTGAGGAAGAGCGGAACATATTATCTGAAGCACAAGCCCGTGGATCCCCAATTA    486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  TTTTTGAGGAAGAGCGGAACATATTATCTGAAGCACAAGCCCGTGGATCCCCCAATTA    480

Qy      487  CAGTATGCCTTTCAGGACAGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG    546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  CAGTATGCCTTTCAGGACAGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG    540

Qy      547  GACTTGCTGTCACTTTGAATAGATAGAGGAGGACCAGTTAGGATGAGAAACCTGATACAGTTT    606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  GACTTGCTGTCACTTTGAATAGATAGAGGAGGACCAGTTAGGATGAGAAACCTGATACAGTTT    600

Qy      607  TACCTAGCTGAGCTGATTTTGGCTGTCACAGCGTTCATCTGATCGTGCATCGA    666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  TACCTAGCTGAGCTGATTTTGGCTGTCACAGCGTTCATCTGATCGTGCATCGA    660

Qy      667  GACATCAAGCCTGAGAACATTCTCGTTGACCAGTTAGGATGAGAAACCTGATACAGTTT    726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  GACATCAAGCCTGAGAACATTCTCGTTGACCAGTTAGGATGAGAAACCTGATACAGTTT    720

Qy      727  GGATCTGCGCCGAAAATGAATTCAAACAAGAGTGAATGCCAAACTCCCGATTGGGACC    786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  GGATCTGCGCCGAAAATGAATTCAAACAAGAGTGAATGCCAAACTCCCGATTGGGACC    780

Qy      787  CCAGATTACATGGCCTCCTGAAGTGCTGACTGTGATGAAACGGGATGGGGAAAAGGCACCTAC    846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  CCAGATTACATGGCCTCCTGAAGTGCTGACTGTGATGAAACGGGATGGGGAAAAGGCACCTAC    840

Qy      847  GGCCTGGACTGTGACTGGTGGTCGTCAGTGGGCGGCGTGATTGCCTATGAGATGATTTATCGGGAGA    906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  GGCCTGGACTGTGACTGGTGGTCGTCAGTGGGCGGCGTGATTGCCTATGAGATGATTTATCGGGAGA    900

Qy      907  TCCCCCTTCGCAGAGGAAGCCTTGCCAGAACCTCTGCCCAGAACCTTCAATAACATTAATGAATTTCCAGCGCG    966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  TCCCCCTTCGCAGAGGAAGCCTTGCCAGAACCTCTGCCCAGAACCTTCAATAACATTAATGAATTTCCAGCGCG    960

Qy      967  TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTAGTGACTTTCCTTGATCTGATTCAAAGC   1026
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Db      961  TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTAGTGACTTTCCTTGATCTGATTCAAAGC   1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1027  TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTC   1086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTTGAAGGTTCTTGCTGCCATCCTTTCTTC   1080

Qy     1087  TCTAAAATTGACTGGAACATTGTAACTCTCCTCCCCCCCTTCGTTCCACCCTCAAG   1146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  TCTAAAATTGACTGGAACATTGTAACTCGTTCCTCCCCCCCTTCGTTCCACCCTCAAG   1140

Qy     1147  TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTCGTTTCATCCTCT   1206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTCGTTTCATCCTCT   1200

Qy     1207  CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAGCAACTGCGCGTTGTGTCGGGTCGGGACTCC   1266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAGCAACTGCGCGTTGTGTCGGGTCGGGACTCC   1260

Qy     1267  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGGTCGGGACTCC   1326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGGTCGGGACTCC   1320

Qy     1327  CCTGCCAAGACTAGCTCCATGCAGAAAGAAACTTCTCATCAAAGAGCCTCCTTCCTCCAGG   1386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCTGCCAAGACTAGCTCCATGCAGAAAGAAACTTCTCATCAAAGAGCAAAGCAAAGAGTACAAAGAC   1380

Qy     1387  TCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTCCTTCCTGCTCCAGG   1446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCTCCTTCCTTCCTGCTCCAGG   1440

Qy     1447  ATCCTCCCGTCCGTATATGCCAAGGATCCGCCCGCGGGACCGCTGCGCTCTGAGCCGCC   1506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  ATCCTCCCGTCCGTATATGCCAAGGATCCGCCCGCGGGGACCGCTGCTGCGCTCTGAGCCGCC   1500

Qy     1507  TGATCCGTA   1515
             |||||||||
Db     1501  TGATCCGTA   1509
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RESULT 6
AB268725
ID   AB268725 standard; DNA; 1485 BP.
XX
AC   AB268725;
XX
DT   16-MAY-2003  (first entry)
XX
DE   Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
XX
KW   Human; citron rho/rac-interacting kinase-short kinase; obesity;
KW   chronic obstructive pulmonary disease; hypertension; diabetes;
KW   coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;
KW   gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;
KW   polycystic ovarian syndrome; fertility; depression; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1485
FT                   /*tag= a
FT                   /partial
FT                   /product= "citron rho/rac-interacting kinase-short
FT                   kinase"
XX
PN   WO200300429-A2.
XX
PD   16-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-EP007229.
XX
PR   02-JUL-2001; 2001US-0301853P.
PR   10-DEC-2001; 2001US-0337130P.
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PR   25-APR-2002; 2002US-0375015P.
XX
PA   (FARB) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221595/21.
DR   P-PSDB; ABP97681.
XX
PT   New human citron rho/rac-interacting kinase-short kinase polypeptide and
PT   polynucleotide for preventing or treating diseases associated with the
PT   polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
PT   disease.
XX
PS   Claim 1; Fig 1; 145pp; English.
XX
CC   The present sequence encodes a human citron rho/rac-interacting kinase-
CC   short kinase polypeptide. The polynucleotide and polypeptide of the
CC   invention are useful in preventing, ameliorating, or treating diseases
CC   associated with the polypeptide dysfunction. The expression vector or the
CC   reagent is useful in the preparation of a medicament for modulating the
CC   activity of a human citron rho/rac-interacting kinase-short kinase in a
CC   disease, such as obesity or chronic obstructive pulmonary disease. These
CC   may also be used for treating obesity/ overweight-associated
CC   comorbidities, such as hypertension, diabetes, coronary artery disease,
CC   hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep
CC   apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced
CC   fertility, and depression
XX
SQ   Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;

Query Match   97.8%; Score 1481.8; DB 10; Length 1485;
Best Local Similarity   99.9%;
Matches 1483; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy      7 ATGTTGAAGTTCAAATATGAGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGAAGTTCAAATATGAGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy     67 GCCAACGGGGCCTCCAGGCTGAATCTGTTCTTCCGAGAAGGGATATTAGATGCCCTCTTT 126
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCAGCGGGGCCTCCAGGCTGAATCTGTTCTTCCGAGAAGGGATATTAGATGCCCTCTTT 120

Qy    127 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

Qy    187 GAATGCAGTCAGCCTGCTCGCTGCTGATGAAGATTAAGCACGTGAGCAACTTGTCGCCGGAAGTAT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAATGCAGTCAGCCTGCTCGCTGCTGATGAAGATTAAGCACGTGAGCAACTTGTCGCCGGAAGTAT 240

Qy    247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 300

Qy    307 AGTCTTGTAGGTTGTGTGTGTCACTTTGCTGTCAAGTGCAGGTGCAGGTGGTAAGGACACCGGG 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGTCTTGTAGGTTGTGTGTGTCACTTTGCTGTCAAGTGCAGGTGCAGGTGGTAAGGACACCGGG 360

Qy    367 GACATCTATGCTATGAAAGTGATGAAGAAGAAGAAGCTTTATTGGCCCAGGAGCAGGTTTCA 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACATCTATGCTATGAAAGTGATGAAGAAGAAGAAGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy    427 TTTTTTGAGGAAGAGCGGAACATATTATCTGAAGCCCGTGGATCCCCAATTA 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTTTTTGAGGAAGAGCGGAACATATTATCTGAAGCCCGTGGATCCCCAATTA 480

Qy    487 CAGTATGCCTTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGTATGCCTTTCAGGACACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540

Qy    547 GACTTGCTGCTGCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACTTGCTGCTGCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTT 600

Qy    607 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy    667 GACATCAAGCCTGAGAACATTCTCGTTCGTTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GACATCAAGCCTGAGAACATTCTCGTTCGTTCGTTGACCGCCACAGGACACATCAAGCTGGTGGATTTT 720

Qy    727 GGATCTGCCGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGCCGCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy    787 CCAGATTACATGGCTCCTGAGTGCTGACTGGTGCTGATGAACGGGGATGGAAAAGGCACCTAC 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCAGATTACATGGCTCCTGAGTGCTGACTGGTGCTGATGAACGGGGATGGAAAAGGCACCTAC 840

Qy    847 GGCCTGACTGTGACTGGTCAGTGGGCGTGAATGCCTATGAGATGATTATGGGGAGA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGCCTGACTGTGACTGGTCAGTGGGCGTGAATGCCTATGAGATGATTATGGGGAGA 900

Qy    907 TCCCCCTTCGGACGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TCCCCCTTCGGACGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960

Qy    967 TTTTGAAATTCCGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTTGAAATTCCGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020

Qy   1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGCTCTTTGCTGCCATCCTTCTTC 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGCTCTTTGCTGCCATCCTTCTTTCTTC 1080

Qy   1087 TCTAAAATTGACTGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCCTCAAG 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TCTAAAATTGACTGGACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCCTCAAG 1140

Qy   1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTTGGGTTTCATCCTCT 1206
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTTGGGTTTCATCCTCT 1200

Qy   1207 CCGTGCCAGCTGAGCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCGTGCCAGCTGAGCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1260

Qy   1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTTGTGTCGGGTCTGGACTCC 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTTGTGTCGGGTCTGGACTCC 1320

Qy   1327 CCTGCCAAGACTCAGCTCCATGGAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAGAGAC 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CCTGCCAAGACTCAGCTCCATGGAAAGAAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1380

Qy   1387 TCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCGCCTCCTTCCTTGCTCCAGG 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TCTCAGGACAAGTGTCACAAGGTATTATTTCCGCAGCCGCCGCCTCCTTCCTTGCTCCAGG 1440

Qy   1447 ATCCTCCCGTCCGTATATGCCAAGGATCCCCAAGGGACCGGGCCGCTGC 1491
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATCCTCCCGTCCGTATATGCCAAGGATCCCCAAGGGACCGGGCCGCTGC 1485
```

RESULT 7
AAD38864
ID   AAD38864 standard; cDNA; 6298 BP.
XX
AC   AAD38864;
XX
DT   23-SEP-2002 (first entry)
XX
DE   Human kinase (PKIN)-21 cDNA.
XX

```
KW   Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
KW   acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW   asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW   development; hepatitis; cardiovascular; hypertension; drug screening;
KW   myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW   fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW   hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-HIV;
KW   neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;
KW   hyperlipidaemia; enzyme; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            55..6219
FT                  /tag= a
FT                  /product= "Human kinase (PKIN)-21"
XX
PN   WO20023099-A2.
XX
PD   25-APR-2002.
XX
PF   20-OCT-2001; 2001WO-US047728.
XX
PR   20-OCT-2000; 2000US-0242410P.
PR   20-OCT-2000; 2000US-0244068P.
PR   27-OCT-2000; 2000US-0245708P.
PR   03-NOV-2000; 2000US-0247572P.
PR   09-NOV-2000; 2000US-0247572P.
PR   16-NOV-2000; 2000US-0249565P.
PR-  22-NOV-2000; 2000US-0252730P.
PR   01-DEC-2000; 2000US-0250807P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;
PI   Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
PI   Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
PI   Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
PI   Thangavelu K, Khan FA, Ison CH;
XX
DR   WPI; 2002-454603/48.
DR   P-PSDB; AAE24150.
XX
PT   New human kinase polypeptide, for diagnosing, preventing and treating
PT   cancer, immune system disorders, growth and development disorders,
PT   cardiovascular disorders and lipid disorders.
XX
PS   Claim 5; Page 207-209; 210pp; English.
XX
CC   The invention relates human kinases (PKIN) and their corresponding
CC   nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC   treating and preventing cancer, an immune system disorder (e.g., acquired
CC   immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
CC   atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC   growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC   cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC   Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC   Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC   hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC   compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC   condition or a disease associated with the expression of PKIN in a
CC   biological sample. A composition comprising PKIN or an agonist or
CC   antagonist of PKIN is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional PKIN.
CC   PKIN is useful in a number of drug screening techniques and to analyse
CC   the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC   knockin humanised animals or transgenic animals to model human diseases,
CC   and in somatic or germline gene therapy. The present sequence is human
CC   PKIN cDNA
XX
SQ   Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;

Query Match             92.7%;  Score 1404.2;  DB 6;  Length 6298;
Best Local Similarity   99.8%;  Pred. No. 0;

Matches 1406;  Conservative 0;  Mismatches 0;  Indels 3;  Gaps 0;

Qy     1 GGGGAGATGTTGAAGTTCAAATATGGAGCGGGAATCCTTTGGATGCTGGTGGTCTGCTGAA  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    49 GGGGAGATGTTGAAGTTCAAATATGGAGCGGGAATCCTTTGGATGCTGGTGGTCTGCTGAA 108

Qy    61 CCCATTGCCAACGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCACCCTTTATG 120
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 CCCATTGCCAGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAACCACCCTTTATG 168

Qy   121 ACTCAACAGCAGATGTCTCCTTTCCGAGAAGGGATATTAGATGCGCCTCTTTGTTCTC 180
         ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db   169 ACTCAACAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCGCCTCTTTGTTCTC 228

Qy   181 TTTGAAGAATGCAGTCAGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229 TTTGAAGAATGCAGTCAGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG 288

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGACGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 AAGTATTCCGACACCATAGCTGAGTTACAGACGCTCCAGCCTTCGGCAAAGGACTTCGAA 348

Qy   301 GTCAGAAGTCTTGTAGGTTGTGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAGCA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 GTCAGAAGTCTTGTAGGTTGTGTCACTTTGCTGAGTGCAGGTGGTAAGAGAGAAGCA 408

Qy   361 ACCGGGGACAATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 ACCGGGGACAATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAG 468

Qy   421 GTTTCATTTTTGAGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 GTTTCATTTTTGAGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 528

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 588

Qy   541 GGAGGGGACTTGCTGTCGTCACTTTGATAATAGATGATTAGATGAAAACCTGATA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 GGAGGGGACTTGCTGTCGTCACTTTGATAATAGATGATTAGATGAAAACCTGATA 648

Qy   601 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 CAGTTTTACCTAGCTGAGCTGATTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 708

Qy   661 CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGACGAGCACATCAAGCTGGTG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   709 CATCGAGACATCAAGCTGAGAACATTCTCGTTGACCGACGAGCACATCAAGCTGGTG 768

Qy   721 GATTTTGGATCGCCGCGAAAATGAATTCAAACACAGTGAATGCCAAACTCCCGATT 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 GGGAGATCCCGCGGGAATGCAAACGGGATGAACTGTGACTGTGACTCCCAATT 828

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGC 888

Qy   841 ACCTACGGCCTGGACTGTGACTGGTGCAGTGGGCGGCCTATGAGATGATTTAT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 ACCTACGGCCTGGACTGTGACTGGTGCAGTGGGCGGCCTATGAGATGATTTAT 948

Qy   901 GGGAGATCCCCCCTTTCGCAGAGGGAACCTCCGAGAACCTTCAATAACATTATGAATTTC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 GGGAGATCCCCCCTTTCGCAGAGGGAACCTCCGAGAACCTTCAATAACATTATGAATTTC 1008

Qy   961 CAGCCGGTTTGTGTGCGGCCAGAAAGACCCCAAAGTGAGCAGTGACTTTCTTGTCATCTGATT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1009 CAGCCGGTTTGTGTGCGGCCAGAAAGACCCCAAAGTGAGCAGTGACTTTCTTGTCATCTGATT 1068

Qy  1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTTGAAGGTTTGAAGGTCTTTGCCCATCCT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1069 CAAAGCTTGTGTGTGCGGCCAGAAAGAGAGACTTGAAGGTTTGAAGGTCTTTGCTGCCATCCT 1128
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Qy   1081  TCCTTCTCTAAAATTGACTGGAACAACACATTCGTAACTCTCCCCCCCTTCGTTCCCACC 1140
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129  TTCTTCTCTAAAATTGACTGGAACAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1188

Qy   1141  CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAATTCGTGGGTTTCA 1200
           ||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1189  CTCAAGTCTGACGATGACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA 1248

Qy   1201  TCCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1260
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1249  TCCTCCGTGCCAGCTGAGCCGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1308

Qy   1261  TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309  TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGTCGGGTCTG 1368

Qy   1321  GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCATCAAAAGCAAAGAGCTA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369  GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCATCAAAAGCAAAGAGCTA 1428

Qy   1381  CAAGACTCTCAGGACAAGTGTCACAAGGT 1409
           ||||||||||||||||||||||||||
Db   1429  CAAGACTCTCAGGACAAGTGTCACAAGAT 1457
```

RESULT 8
ADA05643
ID   ADA05643 standard; cDNA; 1870 BP.
XX
AC   ADA05643;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Human NOV1b encoding cDNA SEQ ID NO:3.
XX
KW   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW   immunomodulator; cytostatic; nootropic; neuroprotective;
KW   antiparkinsonian; antilipaemic; gene therapy; human disease;
KW   metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Location/Qualifiers
FT   CDS   2..1870
FT   /*tag= a
FT   /product= "NOV1b"
XX
PN   WO2003029424-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031373.
XX
PR   02-OCT-2002; 2001US-0326483P.
PR   05-OCT-2001; 2001US-0327435P.
PR   05-OCT-2001; 2001US-0327449P.
PR   09-OCT-2001; 2001US-0327917P.
PR   09-OCT-2001; 2001US-0328029P.
PR   09-OCT-2001; 2001US-0328044P.
PR   09-OCT-2001; 2001US-0328056P.
PR   12-OCT-2001; 2001US-0328849P.
PR   15-OCT-2001; 2001US-0329414P.
PR   17-OCT-2001; 2001US-0330142P.
PR   18-OCT-2001; 2001US-0330309P.
PR   22-OCT-2001; 2001US-0341058P.
PR   24-OCT-2001; 2001US-0339266P.
PR   24-OCT-2001; 2001US-0343629P.
PR   29-OCT-2001; 2001US-0349575P.
PR   01-NOV-2001; 2001US-0346357P.
PR   17-APR-2002; 2002US-0373260P.

PR   19-APR-2002; 2002US-0373815P.
PR   19-APR-2002; 2002US-0373817P.
PR   19-APR-2002; 2002US-0373826P.
PR   19-APR-2002; 2002US-0373884P.
PR   22-APR-2002; 2002US-0374977P.
PR   16-MAY-2002; 2002US-0381037P.
PR   16-MAY-2002; 2002US-0381038P.
PR   16-MAY-2002; 2002US-0381042P.
PR   17-MAY-2002; 2002US-0381642P.
PR   28-MAY-2002; 2002US-0383656P.
PR   29-MAY-2002; 2002US-0383831P.
PR   25-JUN-2002; 2002US-0391335P.
PR   01-OCT-2002; 2002US-0262511.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI   Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI   Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI   Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI   Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR   WPI; 2003-381626/36.
DR   P-PSDB; ADA05644.
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT   preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT   cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 20; Page 100; 586pp; English.
XX
CC   The present invention describes NOVX proteins, where X can be 1 to 55
CC   (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC   described above and a carrier; (2) a kit comprising, in one or more
CC   containers, the composition described above; (3) an isolated nucleic acid
CC   molecule which encodes a NOVX protein of the invention; (4) a vector
CC   comprising the nucleic acid molecule described above; (5) a cell
CC   comprising the vector; (6) an antibody that immunospecifically
CC   binds to the polypeptide described above; (7) methods for determining the
CC   presence or amount of the above polypeptide or nucleic acid molecule in a
CC   sample; (8) methods for determining the presence of or predisposition to
CC   a disease associated with altered levels of expression of the above
CC   polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC   method of identifying an agent that binds to the polypeptide described
CC   above; (10) a method for identifying a potential therapeutic agent for
CC   use in treating a pathology that is related to an aberrant expression or
CC   aberrant physiological interactions of the polypeptide; (11) a method of
CC   screening for a modulator of activity or of latency or predisposition to
CC   a pathology associated with the polypeptide; (12) a method for modulating
CC   the activity of the polypeptide described above; (13) methods of treating
CC   or preventing a pathology associated with the above polypeptide in a
CC   mammal; and (14) a method for producing the above polypeptide. NOVX
CC   sequences have antidiabetic, anorectic, antibacterial, virucide,
CC   immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC   and antilipaemic activities, and can be used in gene therapy. The
CC   polypeptide is useful in manufacturing a medicament for treating a
CC   syndrome associated with a human disease. The polypeptide or the nucleic
CC   acid molecule may be used to diagnose, treat or prevent metabolic
CC   disorders such as diabetes or obesity, infections, cachexia, cancer,
CC   neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC   disease, immune disorders, haematopoietic disorders and various
CC   dyslipidaemias. The nucleic acids can also be used as hybridisation
CC   probes, in chromosome mapping, tissue typing, preventive medicine and
CC   pharmacogenomics. The present sequence encodes a human NOVX protein from
CC   the present invention.
XX
SQ   Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

Query Match   92.3%; Score 1398.2; DB 8; Length 1870;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1400;   Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1146
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1153

Qy    1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAAGAAGAATTCGTGGGTTCATCCTCT 1206
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1154 TCTGACGATGACACCTCCAATTTGATGAACCAGAAGAAGAATTCGTGGGTTCATCCTCT 1213

Qy    1207 CCGTGCCAGCTGAGCCCCTCCAGCTTCTCGGGTGAAGAACTGCCGGTTGTGGGGTTTTCG 1266
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1214 CCGTGCCAGCTGAGCCCCTCCAGCTTCTCGGGTGAAGAACTGCCGGTTGTGGGGTTTTCG 1273

Qy    1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTCGTCGGGTCGGACTCC 1326
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1274 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTCGTCGGGTCGGACTCC 1333

Qy    1327 CCTGCCAAGACTAGTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1386
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1334 CCTGCCAAGACTAGTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1393

Qy    1387 TCTCAGGACAAGTGTCACAAGGT 1409
           ||||||||||||||||||||||
Db    1394 TCTCAGGACAAGTGTCACAAGAT 1416
```

RESULT 9
ABQ78871
ID   ABQ78871 standard; cDNA; 5877 BP.
XX
AC   ABQ78871;
XX
DT   10-OCT-2002 (first entry)
XX
DE   Human kinase cDNA #2.
XX
KW   Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
KW   Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..5877
FT   /*tag= a
FT   /product= "Kinase"
XX
PN   WO200259325-A2.
XX
PD   01-AUG-2002.
XX
PF   20-DEC-2001; 2001WO-US050497.
XX
PR   27-DEC-2000; 2000US-0258335P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Yu X,   Miranda M,   Friddle CJ;
XX
DR   WPI; 2002-599796/64.
DR   P-PSDB; ABB81928.
XX
PT   Novel polynucleotide encoding human proteins that are structurally
PT   similar to animal kinases, useful for drug screening, diagnosis, in gene
PT   therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT   applications.
XX
PS   Disclosure; Page 44-45; 50pp; English.
XX
CC   The invention relates to a novel human protein that shares structural
CC   similarity with animal kinases, including serine-threonine kinases,
CC   particularly Citron rho-interacting kinases. The proteins of the
CC   invention have nootropic and cytostatic activity. The polynucleotides may
CC   have a use in gene therapy. The encoded novel polypeptides are useful for

```
Qy     7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    14 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 73

Qy    67 GCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 GCCAGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 133

Qy   127 CAGCAGATGTCTCCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAA 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAGCAGATGTCTCCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTGTTCTCTTTGAA 193

Qy   187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 253

Qy   247 TCCGACACCATAGCTGAGTTACAGAGCTTCCAGCCTTCGGCAAGGACTTCGAAGTCAGA 306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 TCCGACACCATAGCTGAGTTACAGAGCTTCCAGCCTTCGGCAAGGACTTCGAAGTCAGA 313

Qy   307 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGCGTAAGAGAGAAAGCAACCGGG 366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGCGTAAGAGAGAAAGCAACCGGG 373

Qy   367 GACATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 GACATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCA 433

Qy   427 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 486
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 493

Qy   487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 553

Qy   547 GACTTGCTCGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   554 GACTTGCTCGTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 613

Qy   607 TACCTTAGCTGAGCTGATTTTGGCGTGTTCACAGCGGTTCATCTGATGGGATACGTGCATCGA 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 TACCTTAGCTGAGCTGATTTTGGCGTGTTCACAGCGGTTCATCTGATGGGATACGTGCATCGA 673

Qy   667 GACATCAAGCCTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGGATTTT 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 GACATCAAGCCTGAGAACATTCTCGTTGACCGGCACAGGACACATCAAGCTGGTGGATTTT 733

Qy   727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   734 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 793

Qy   787 CCAGATTACAATGGCCTCCTGAAGTGCTGACTGCTGATGAACGGGATGGAAAAGGCCACCTAC 846
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   794 CCAGATTACAATGGCCTCCTGAAGTGCTGACTGCTGATGAACGGGATGGAAAAGGCCACCTAC 853

Qy   847 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA 906
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   854 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA 913

Qy   907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGCG 966
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   914 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGCG 973

Qy   967 TTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC 1026
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   974 TTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC 1033

Qy  1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGCTGTCCATCCTTTCTTC 1086
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1034 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGGTTGAAGGTCTTTGCTGTCCATCCTTTCTTC 1093
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CC    generating antibodies, as reagents in diagnostic assays, for identifying
CC    other cellular gene products related to NHP and as reagents in assays for
CC    screening for compounds that are useful in the treatment of mental,
CC    biological or medical disorders and diseases including cancer. The
CC    sequence encodes a novel human kinase of the invention
XX
SQ    Sequence 5877 BP; 1680 A; 1433 C; 1583 G; 1181 T; 0 U; 0 Other;

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 5877;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        7 ATGTTGAAGTTCAAATAATATGGAGCGCGAATCCTTTGATGCTGGTGCTGCTGAACCCATT 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGTTGAAGTTCAAATAATATGGAGCGCGAATCCTTTGATGCTGGTGCTGCTGAACCCATT 60

Qy       67 GCCAACCGGGCCTCCAGGCTGAATCTGTCTTCCCAGGGGAAACCACCCTTTATGACTCAA 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCCAGCCGGGCCTCCAGGCTGAATCTGTCTTCCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy      127 CAGCAGATGTCTCCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGCAGATGTCTCCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

Qy      187 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 240

Qy      247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 300

Qy      307 AGTCTTGTAGGTTGTGTGCACTTGCTCGTGAAGTGCAGTCAGTGAAGAGAAAGCAACCGGG 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AGTCTTGTAGGTTGTGTGCACTTGCTCGTGAAGTGCAGTCAGTGAAGAGAAAGCAACCGGG 360

Qy      367 GACATCTATGCTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCCAGGAGGCAGGTTCA 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GACATCTATGCTATGAAAGTGATGAAGAGAGAGGCTTTATTGGCCCAGGAGGCAGGTTCA 420

Qy      427 TTTTTGAGAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TTTTTGAGAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 480

Qy      487 CAGTATGCCTTTCAGGACACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CAGTATGCCTTTCAGGACACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG 540

Qy      547 GACTTGCTGTGTCACTTTTGAATAGATATGAGGACCAGTTGAGATGAAAACCTGATACAGTT 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GACTTGCTGTGTCACTTTTGAATAGATATGAGGACCAGTTGAGATGAAAACCTGATACAGTT 600

Qy      607 TACCTAGCTGAGCTGATTTTGGCTGTGTCACAGCCGTTCATCTGATGGGATACGTGCATCGA 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TACCTAGCTGAGCTGATTTTGGCTGTGTCACAGCCGTTCATCTGATGGGATACGTGCATCGA 660

Qy      667 GACATCAAGCCTGAGAACATTCTCGTTGACCGACCACAGGACAACATCAAGCTGGTGGATTT 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GACATCAAGCCTGAGAACATTCTCGTTGACCGACCACAGGACAACATCAAGCTGGTGGATTT 720

Qy      727 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy      787 CCAGATTACATGGCTCCGAAGTGCTGACTGGACGGGATGGAAAAGGCACCTAC 846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCAGATTACATGGCTCCGAAGTGCTGACTGGACGGGATGGAAAAGGCACCTAC 840

Qy      847 GGCCTGGACTGCTGGTGGTCAGTGGCGGCCTGATGGGGCCTGATTGCCTGTATGATGATTATGGGAGA 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GGCCTGGACTGCTGGTGGTCAGTGGCGGCCTGATGGGGCCTGATTGCCTGTATGATGATTATGGGAGA 900

Qy      907 TCCCCCTTCGCAGAGGGAACCTTCGCCAGAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
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Db      901 TCCCCCTTCGCAGAGGGAACCTTCGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      967 TTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020

Qy     1027 TTGTTGTGCGGCCAGAAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCGCCATCCTTTCTTC 1086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTGTTGTGCGGCCAGAAAAGAGAGACTGAAGTTGAAGGTCTTGCTGCCATCCTTTCTTC 1080

Qy     1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCACCCTTCAAG 1146
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCACCCTTCAAG 1140

Qy     1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCT 1206
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy     1207 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGGAACTGCGCGTTGTGGGGTTTCG 1266
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGGAACTGCGCGTTGTGGGGTTTCG 1260

Qy     1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGGAATCTGAGTCTCTGTGTCGCGGGCTCGTGGACTCC 1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGGAATCTGAGTCTCTGTGTCGCGGGCTCGTGGACTCC 1320

Qy     1327 CCTGCCAAGACTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1386
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 CCTGCCAAGACTAGCTCCATGAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1380

Qy     1387 TCTCAGGACAAGTGTCACAAGT 1409
            ||||||||||||||||||||||
Db     1381 TCTCAGGACAAGTGTCACAAGAT 1403
```

```
RESULT 10
AAL55217
ID   AAL55217 standard; DNA; 6156 BP.
XX
AC   AAL55217;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Human CRIK related DNA sequence, SEQ ID No 8.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   diabetes; pain; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003004523-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0338651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
XX
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PT   New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 217-222; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human
CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho/rac-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This polynucleotide sequence represents a DNA sequence
CC   relating to the human CRIK protein of the invention
XX
SQ   Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

Query Match             92.3%;  Score 1398.2;  DB 9;  Length 6156;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy        7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy       67 GCCAACCGGGCCTCCAGGCTGAAATCGTCTTCTTCCAGGGGGAAATCCCCTTTATGACTCAA 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCCAGCCGGGCCTCCAGGCTGAAATCGTCTTCTTCCAGGGGGAAATCCCCTTTATGACTCAA 120

Qy      127 CAGCAGATGTCTCCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGCAGATGTCTCCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

Qy      187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 240

Qy      247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCGAAAGGACTTCGAAGTCAGA 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCGAAAGGACTTCGAAGTCAGA 300

Qy      307 AGTCTTGTAGGTTGTGGTCACTTTGGTGGTCAAGTGCAGGTGGTAAGAGAAAGCAACCGGG 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AGTCTTGTAGGTTGTGGTCACTTTGGTGGTCAAGTGCAGGTGGTAAGAGAAAGCAACCGGG 360

Qy      367 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy      427 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 486
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 480

Qy      487 CAGTATGCCTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 546
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CAGTATGCCTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 540
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Qy      547 GACTTGCTGTCACTTTTGAATAGATATGAGACCAGTTAGATGAAAACCTGATACAGTTT 606
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GACTTGCTGTCACTTTTGAATAGATATGAGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy      607 TACCTAGCTGAGCTGATTTGGCTGTTCACGCGTTCATCTGATGGGATACGTGCATCGA 666
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TACCTAGCTGAGCTGATTTGGCTGTTCACGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy      667 GACATCAAGCCTGAGACATTCTCGTGACCGACACATCAAGCTGGTGGATTTT 726
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GACATCAAGCCTGAGACATTCTCGTGACCGACACATCAAGCTGGTGGATTTT 720

Qy      727 GGATCTGCCGCGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy      787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGCACCTAC 846
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGCACCTAC 840

Qy      847 GGCCTGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA 906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GGCCTGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA 900

Qy      907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGG 966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGG 960

Qy      967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATTCAAGC 1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGAGCAGTGACTTTCTTGATTCAAGC 1020

Qy     1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAGGTCTTTGCTGCCATCCTTTCTTC 1086
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAGGTCTTTGCTGCCATCCTTTCTTC 1080

Qy     1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCTCCTCGTTCCACCCTCAAG 1146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCTCCTCGTTCCACCCTCAAG 1140

Qy     1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy     1207 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAGGAAATCGTGCCGTTTGTGGGGTTTCG 1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAGGAAACTGCCGTTTGTGGGGTTTCG 1260

Qy     1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGCGGGTCTGAGACTCC 1326
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTGCGGGTCTGAGACTCC 1320

Qy     1327 CCTGCCAAGACTAGCTCCATGCAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 CCTGCCAAGACTAGCTCCATGCAAAAGAAACTTCTCATCAAAAGCAAAGAGTACAAGAC 1380

Qy     1387 TCTCAGGACAAGTGTCACAAGGT 1409
            |||||||||||||||||||||
Db     1381 TCTCAGGACAAGTGTCACAAGAT 1403
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RESULT 11
ABQ78870
ID   ABQ78870 standard; cDNA; 6165 BP.
XX
AC   ABQ78870;
XX
DT   10-OCT-2002 (first entry)
XX
DE   Human kinase cDNA #1.
XX
KW   Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
KW   Citron rho-interacting kinase; gene therapy; mental disorder; cancer;

```
KW   gene; ss.
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..6165
FT                    /*tag= a
FT                    /product= "Kinase"
FT   variation        replace(5218,G)
FT                    /*tag= b
FT                    /standard_name= "Single nucleotide polymorphism"
FT   variation        replace(6065,G)
FT                    /*tag= b
FT                    /standard_name= "Single nucleotide polymorphism".
XX
PN   WO20259325-A2.
XX
PD   01-AUG-2002.
XX
PF   20-DEC-2001; 2001WO-US050497.
XX
PR   27-DEC-2000; 2000US-0258335P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Yu X, Miranda M, Friddle CJ;
XX
DR   WPI; 2002-599796/64.
DR   P-PSDB; ABB81927.
XX
PT   Novel polynucleotide encoding human proteins that are structurally
PT   similar to animal kinases, useful for drug screening, diagnosis, in gene
PT   therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT   applications.
XX
PS   Claim 1; Page 37-39; 50pp; English.
XX
CC   The invention relates to a novel human protein that shares structural
CC   similarity with animal kinases, including serine-threonine kinases,
CC   particularly Citron rho-interacting kinases. The proteins of the
CC   invention have nootropic and cytostatic activity. The polynucleotides may
CC   have a use in gene therapy. The encoded novel polypeptides are useful for
CC   generating antibodies, as reagents in diagnostic assays, for identifying
CC   other cellular gene products related to NHP and as reagents in assays for
CC   screening for compounds that are useful in the treatment of mental,
CC   biological or medical disorders and diseases including cancer. The
CC   sequence encodes a novel human kinase of the invention
XX
SQ   Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 6165;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy     7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTCGTGCTGAACCCATT 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTCGTGCTGAACCCATT 60

Qy    67 GCCAACCGGCGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCCAGCCGGCGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy   127 CAGCAGATGTCCTCCTTCCCTCCTTTCCCGAGAGAGGGATATTAGATGCCCTTCTTGTTCTCTTGAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CAGCAGATGTCCTCCTTCCCTCCTTTCCCGAGAGAGGGATATTAGATGCCCTTCTTGTTCTCTTGAA 180

Qy   187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGCAACTTTGTCCGGAAGTAT 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGCAACTTTGTCCGGAAGTAT 240

Qy   247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 300
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Qy   307 AGTCTTGTAGGTTGTGTCACTTTGCTGAACGTGCAGTGGTGTAAGAGAAGCAACCGGG 366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTCTTGTAGGTTGTGTCACTTTGCTGAACGTGCAGTGGTGTAAGAGAAGCAACCGGG 360

Qy   367 GACATCTATGCTATGAAAGTGATGAGAAGAGGCTTTATTGGCCAGGCAGAGTTTCA 426
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACATCTATGCTATGAAAGTGATGAGAAGAGGCTTTATTGGCCAGGCAGAGTTTCA 420

Qy   427 TTTTTTGAGGAGAGCGGAACATATTATTCTGAAGCACAAGCCGTGCATCCCCAATTA 486
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   421 TTTTTTGAGGAGAGCGGAACATATTATTCTGAAGCACAAGCCGTGGATCCCCAATTA 480

Qy   487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540

Qy   547 GACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy   607 TACCTAGCTGAGCTGATTTTGCGTGTTCATCTGATGGGATACGTGCATCGA 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCTAGCTGAGCTGATTTTGCGTGTTCATCTGATGGGATACGTGCATCGA 660

Qy   667 GACATCAAGCCTGAGAACATTCTCGTTGACCGGACACATCAAGCTGGTGGATTTT 726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GACATCAAGCCTGAGAACATTCTCGTTGACCGGACACATCAAGCTGGTGGATTTT 720

Qy   727 GGATCTGCCGCGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGATCTGCCGCGCAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy   787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGGAAAAGCCACCTAC 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGGAAAAGCCACCTAC 840

Qy   847 GGCCTGGACTGTGGACTGGTGGTCAGTGGCCTATGCCATGAGATGATTTATGGGAGA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGCCTGGACTGTGGACTGGTGGTCAGTGGCCTATGCCATGAGATGATTTATGGGAGA 900

Qy   907 TCCCCCTTCGGCGAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTCCAGCGG 966
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TCCCCCTTCGGCGAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTCCAGCGG 960

Qy   967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGATTCAAAGC 1020

Qy  1027 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTGCTGCTGCCATCCTTTCTC 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTGCTGCTGCCATCCTTTCTC 1080

Qy  1087 TCTAAAATTGACTGGACAACATTCGTAACTCGTACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TCTAAAATTGACTGGACAACATTCGTAACTCGTACTCTCCTCCCCCTTCGTTCCACCCTCAAG 1140

Qy  1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCT 1206
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy  1207 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTCCGGGTTTTCG 1266
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  1201 CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTCGGGGTTTTCG 1260

Qy  1267 TACAGCAAGGACTGGGGATTCTGGTAGATCTGAGTCTGTAGTCGTGTTGTGTCGGGACTCC 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TACAGCAAGGACTGGGGATTCTGGTAGATCTGAGTCTGTAGTCGTGTTGTGTCGGGACTCC 1320

Qy  1327 CCTGCCAAGACTAGCTCGAGTTACAGGAGCTCCATGGAAAAAGCAAAAGACTTCGAAGTCAGA 1386
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CCTGCCAAGACTAGCTCGAGTTACAGGAGCTCCATGGAAAAAGCAAAAGACTTCGAAGTCAGA 1380
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Qy   1387 TCTCAGGACAAGTGTCACAAGGT 1409
          ||||||||||||||||||||||
Db   1381 TCTCAGGACAAGTGTCACAAGAT 1403
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RESULT 12
AAL55214
ID   AAL55214 standard; DNA; 6165 BP.
XX
AC   AAL55214;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Human CRIK encoding DNA sequence, SEQ ID No 1.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   diabetes; pain; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..6165
FT                   /tag= a
FT                   /product= "Human CRIK protein"
XX
PN   WO2003004523-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0338651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
DR   P-PSDB; AA026959.
XX
PT   New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Example 1; Fig 1; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human
CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho/rac-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction, such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
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CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This polynucleotide sequence represents a DNA sequence
XX   encoding a human CRIK protein of the invention
SQ   Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

     Query Match      92.3%;  Score 1398.2;  DB 9;  Length 6165;
     Best Local Similarity  99.8%;  Pred. No. 0;
     Matches 1400;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy     7 ATGTTGAAGTTCAAATATGGAGCGCCGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTTGAAGTTCAAATATGGAGCGCCGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy    67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTATGACTCAA 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTATGACTCAA 120

Qy   127 CAGCAGATGTCTCCTCTTCCCGAGAGGAGGGATATTAGATGATGCCCTCTTGTTCTCTTTGAA 186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CAGCAGATGTCTCCTCTTCCCGAGAGGAGGGATATTAGATGATGCCCTCTTGTTCTCTTTGAA 180

Qy   187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT 240

Qy   247 TCCGACACCATAGTCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGTCAGA 306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCGACACCATAGTCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGACTTCGAAGTCAGA 300

Qy   307 AGTCTTGTAGGTGTCGGTCACTTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGG 366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTCTTGTAGGTGTCGGTCACTTTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGG 360

Qy   367 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy   427 TTTTTTGAGGAAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTTGAGGAAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCAATTA 480

Qy   487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540

Qy   547 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy   607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 660

Qy   667 GACATCAAGCCTGAGAACATTCTGTTGACCGCCACAGGACACATCAAGCTGCTGGTGATTT 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GACATCAAGCCTGAGAACATTCTGTTGACCGCCACAGGACACATCAAGCTGCTGGTGATTT 720

Qy   727 GGATCTGCGCGGAAAATGAATTCAAACAAGATGGTGAAGTGCCAAACTCCCGATTGGGACC 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGATCTGCGCGGAAAATGAATTCAAACAAGATGGTGAAGTGCCAAACTCCCGATTGGGACC 780

Qy   787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTAC 846
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCACCTAC 840

Qy   847 GGCCTTGGACTGGACTGGACTGGCTGTCAGTGGGCGTCAGTGGGCGTCCTATGAGATGATTATGGGAGA 906
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGCCTTGGACTGTGACTGGCTGTCAGTGGGCGTCCTATGAGATGATTATGGGAGA 900

Qy   907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCAGCGGG 966
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PT   New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT   polynucleotide, useful in preventing, ameliorating or treating diseases
PT   associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT   Alzheimer's disease.
XX
PS   Disclosure; Fig 4; 237pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a human
CC   citron rho/rac-interacting kinase polypeptide. The isolated
CC   polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC   specification. The human citron rho-interacting kinase (CRIK)
CC   polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC   treating diseases associated with human CRIK dysfunction such as obesity
CC   and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC   disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC   cancer including endometrial, breast, prostate and colon cancer),
CC   anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC   disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC   disease), chronic obstructive pulmonary disease, or diabetes. These can
CC   also be used to treat pain associated with the disorders. The human CRIK
CC   polypeptide is also useful in diagnostic assays or in genetic testing.
CC   The expression vector or the reagent is useful in preparing a medicament
CC   for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC   central nervous system disorder, or chronic obstructive pulmonary
CC   disease. The fusion protein is useful for generating antibodies against a
CC   CRIK polypeptide and for use in various assay systems. The methods are
CC   useful in producing and detecting the polynucleotide and polypeptide and
CC   in screening for agents that modulate the activity of the human CRIK
CC   polypeptide. This polynucleotide sequence represents a DNA sequence
CC   relating to the human CRIK protein of the invention
XX
SQ   Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other;

Query Match             92.3%;  Score 1398.2;  DB 9;  Length 8603;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy      67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATGACTCAA 126
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy     127 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTCTTGTTCTCTTTGAA 186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTCTTGTTCTCTTTGAA 180

Qy     187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy     247 TCCGACACCATAGCTGAGTTACAGGAGCTTCAGCCTTCGGCAAGGACTTCGAAGTCAGA 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCCGACACCATAGCTGAGTTACAGGAGCTTCAGCCTTCGGCAAGGACTTCGAAGTCAGA 300

Qy     307 AGTCTTGTAGGTTGTGTCACTTGCTGAAGTGAAGAAAGCAACGGG 366
           |||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGTCTTGTAGGTTGTGTCACTTGCTGAAGTGAAGAAAGCAACGGG 360

Qy     367 GACATCTATGCTATGAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACATCTATGCTATGAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy     427 TTTTTGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTTTGGAAGAGCGGAACACATATTATCTCGAAGCACAAGCCGTGGATCCCCAATTA 480

Qy     487 CAGTATGCCTTTCAGGACAAAAATCACCTTATCTCGGTCATGAATATCAGCCTGGAGGG 546
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGGTCATGAATATCAGCCTGGAGGG 540

Db     901 TCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGCGG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020

Qy    1027 TTGTTGTCGGCCGAGAAAGAGAGACTGAAGTTGAAGGGTCTTTGCTGCCATCCTTTCTTC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTGTTGTCGGCCGAGAAAGAGAGACTGAAGTTGAAGGGTCTTTGCTGCCATCCTTTCTTC 1080

Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCCGTTCCCACCCTCAAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCCGTTCCCACCCTCAAG 1140

Qy    1147 TCCGACGATGACACCTCCAATTTGATGACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TCTGACGATGACACCTCCAATTTGATGACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy    1207 CCGTGCCAGTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCG 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CCGTGCCAGTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGGGGTTTTCG 1260

Qy    1267 TACAGCCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTGCGGTCTCGGACTCC 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TACAGCCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTGCGGTCTCGGACTCC 1320

Qy    1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGAGAGACTACAAGAC 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAGAGAGACTACAAGAC 1380

Qy    1387 TCTCAGGACAAGTGTCACAAGGT 1409
           ||||||||||||||||||||||
Db    1381 TCTCAGGACAAGTGTCACAAGAT 1403
```

```
RESULT 13
AAL55215
ID   AAL55215 standard; DNA; 8603 BP.
XX
AC   AAL55215;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Human CRIK related DNA sequence, SEQ ID No 4.
XX
KW   Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective;
KW   antigout; osteopathic; antiarthritic; cytostatic; antidepressant;
KW   immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
KW   neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW   human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating;
KW   obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KW   central nervous system disorder; chronic obstructive pulmonary disease;
KW   diabetes; pain; ds.
XX
OS   Homo sapiens.
XX
PN   WO200304523-A1.
XX
PD   16-JAN-2003.
XX
PF   28-JUN-2002; 2002WO-EP007156.
XX
PR   02-JUL-2001; 2001US-0301841P.
PR   11-DEC-2001; 2001US-0338651P.
PR   25-APR-2002; 2002US-0375014P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-221576/21.
XX
```

```
KW   skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;
KW   immune disorder; neoplastic disorder; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..18
FT                   /*tag= a
FT   CDS             19..6180
FT                   /*tag= b
FT                   /product= "Human MDPK protein"
FT   misc_feature    19..6177
FT                   /*tag= c
FT                   /note= "This region is specifically referred in claim 1
FT                   as SEQ ID NO:3"
FT   3'UTR           6181..6574
FT                   /*tag= d
XX
PN   WO20023489 6-A2.
XX
PD   02-MAY-2002.
XX
PF   23-OCT-2001; 2001WO-US050636.
XX
PR   23-OCT-2000; 2000US-0242429P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R;
XX
DR   WPI; 2002-479720/51.
DR   P-PSDB; AAB24079.
XX
PT   Human myotonic dystrophy type protein kinase polypeptide and
PT   polynucleotide useful for prognosticating, diagnosing, preventing or
PT   inhibiting tumourigenesis, tumor growth, tumor metastasis and viral
PT   infection.
XX
PS   Claim 1; Fig 1; 148pp; English.
XX
CC   The invention relates to human myotonic dystrophy type protein kinase
CC   (MDPK) polypeptides designated as 13245 and nucleic acid molecules
CC   encoding such polypeptides. 13245 molecules are used to develop
CC   diagnostic and therapeutic agents for prognosticating, diagnosing,
CC   preventing, inhibiting, alleviating or curing MDPK-related disorders.
CC   Polypeptides of the invention are used to develop diagnostic and
CC   therapeutic agents for 13245-mediated or related disorders such as
CC   tumourigenesis, tumour growth, tumour metastasis, viral infection of a
CC   cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),
CC   immune disorders and neoplastic disorders. The invention is also used in
CC   gene therapy. The present sequence is human MDPK cDNA
XX
SQ   Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;
```

Query Match   92.3%;   Score 1397.8;   DB 6;   Length 6574;
Best Local Similarity   99.5%;
Matches 1402;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy        1 GGGGAGGATGTTGAAGTTCAAATATGGAGCGCGCGAATCCTTTGGATGCTGGTGCTGCTGAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13 GGGGAGGATGTTGAAGTTCAAATATGGAGCGCGCGAATCCTTTGGATGCTGGTGCTGCTGAA   72

Qy       61 CCCATTGCCAACCGGGCCTGAAGCCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       73 CCCATTGCCAGCCGGGCCTGAAGCCTGAATCGTTCTTCCAGGGGAAACCACCCTTTATG   132

Qy      121 ACTCAACAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTCTC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      133 ACTCAACAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC   192

Qy      181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAGATTAAGCACGTGAGCAACTTTGTCCGG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      193 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAGATTAAGCACGTGAGCAACTTTGTCCGG   252
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Qy      547 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT   606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT   600

Qy      607 TACCTAGCTGAGCTGATTTTTGGCTGTCGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA   666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TACCTAGCTGAGCTGATTTTTGGCTGTCGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA   660

Qy      667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGTGGATTTT   726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGTGGATTTT   720

Qy      727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   780

Qy      787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGATGGAAAAGGCACCTAC   846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGATGAACGGGATGGAAAAGGCACCTAC   840

Qy      847 GGCCTGGACTGACTGGTGTGGTGCTGCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGAGA   906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GGCCTGGACTGACTGGTGTGGTGCTGCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGAGA   900

Qy      907 TCCCCCTTCGCAGAGGGAACCTCTGCCCAGAACCTTCAATAACATTATGAATTTCCAGCGCGG   966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TCCCCCTTCGCAGAGGGAACCTCTGCCCAGAACCTTCAATAACATTATGAATTTCCAGCGCGG   960

Qy      967 TTTTGAAATTCCAGATGACCCCAAAGTGACTTCTGATCTGATTCAAAGC   1026
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTTTGAAATTCCAGATGACCCCAAAGTGACTTCTGATCTGATTCAAAGC   1020

Qy     1027 TTGTTGTGCGGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTC   1086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTGTTGTGCGGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCTTTCTTC   1080

Qy     1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCCACCCTCAAG   1146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCCTTCGTTCCCACCCTCAAG   1140

Qy     1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT   1206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT   1200

Qy     1207 CCGTCGCAGCTGAGCCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTTGTGTGGGGTTTCG   1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CCGTCGCAGCTGAGCCCCTCAGGCTTCTCGGTGAAGAACTGCCGTTTGTGTGGGGTTTCG   1260

Qy     1267 TACAGCAAGGCACTCGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC   1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCC   1320

Qy     1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC   1386
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAAACTTCTCATCAAAAGCAAAGAGAGCTACAAGAC   1380

Qy     1387 TCTCAGGACAAGTGTCACAGGT   1409
            | ||||||||||||||||||
Db     1381 TCTCAGGACAAGTGTCACAGAGAT   1403
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RESULT 14
AAD39191
ID   AAD39191 standard; cDNA; 6574 BP.
XX
AC   AAD39191;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Human MDPK cDNA.
XX
KW   Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;
KW   tumourigenesis; tumour growth; tumour metastasis; viral infection;
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Qy    241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAAGGACTTCGAA 312

Qy    301 GTCAGAAGTCTTGTTAGGTTGGTCACTTTGCTGAAGTGGTAAGAGAGAAAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 GTCAGAAGTCTTGTTAGGTTGGTCACTTTGCTGAAGTGCAGTGTAAGAGAGAAAGCA 372

Qy    361 ACCGGGGACACTCATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCAGGAGCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 432

Qy    421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGGATCCCC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 GTTTCATTTTTGAGGAAGAGAGCGGAACATATTATCTCGAAGCACACAAGCCCGTGGATCCCC 492

Qy    481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    493 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGATGGAGGAATATCAGCCT 552

Qy    541 GGAGGGGACTTGCTGTGCACTTTGAATAGATATGAGGACAGTTAGTAGAAAACCTGATA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 GGAGGGGACTTGCTGTGCACTTTGAATAGATATGAGGACCAGTTAGTAGAAAACCTGATA 612

Qy    601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 672

Qy    661 CATCGAGACACATCAAGCCTGAGAACATTCTCGTTGACCGCACACAGGACACATCAAGCTGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673 CATCGAGACACATCAAGCCTGAGAACATTCTCGTTGACCGCACACAGGACACATCAAGCTGGTG 732

Qy    721 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGACAGTGGTGAATGCCAAACTCCCGATT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733 GATTTTGGATCTGCCGCGGAAAATGAATTCAAACAAGACAGTGGTGAATGCCAAACTCCCGATT 792

Qy    781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    793 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC 852

Qy    841 ACCTACGGCCTGGACTGTGGTGACTGGGTCAGTGGTGGGCGTGATTGCCTATGGATGATTTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    853 ACCTACGGCCTGGACTGTGGTGACTGGGTCAGTGGTGGGCGTGATTGCCTATGGATGATTTAT 912

Qy    901 GGGAGATCCCCCTTCGCGAGAGGGAACCTCGCCAGAACCTTCAATAACATTATGAATTTC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    913 GGGAGATCCCCCCTTCGCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 972

Qy    961 CAGCGGTTTTGAAATTTCAGATGACCCCAAAGTGAGCAGTGACTTCTTCTGATCTGATT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    973 CAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTCTGATCTGATT 1032

Qy   1021 CAAAGCTTGTGTGCGGCCAGAAAGAAGAGAGACTGAAGTTTGAAGGTCTTGCTGCCATCCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1033 CAAAGCTTGTGTGCGGCCAGAAAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1092

Qy   1081 TTCTTCCTAAATTGACTGAACAACATTGTAACTCTCCCCCCTTGTTCCCACC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1093 TTCTTCCTAAATTGACTGGAACAACATTGTAACTCTCCCCCCCTTCGTTCCCACC 1152

Qy   1141 CTCAAGTCCGACGATGACACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGGTTTCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1153 CTCAAGTCTGACGATGACACACCTCCAATTTGATGAACCAGAAGAATTCGTGGGGTTTCA 1212

Qy   1201 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1213 TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1272

Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGTAGATCTGAGTCTGTGTGTCGGGGTCTG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1273 TTTTCGTACAGCAAGGCACTGGGGATTCTTGTAGATCTGGAGTCTGTGTGTCGGGGTCTG 1332
```

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Qy   1321 GACTCCCCTGCCAAGACTAGCTCCATGGAAAGAGAAACTTCTCATCAAAAAGCAAAGAGCTA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1333 GACTCCCCTGCCAAGACTAGCTCCATGGAAAGAGAAACTTCTCATCAAAAAGCAAAGAGCTA 1392

Qy   1381 CAAGACTCTCAGGACAAGTGTCACAAGGT 1409
          ||||||||||||||||||||||||||||
Db   1393 CAAGACTCTCAGGACACAAGTGTCACAAGAT 1421
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Query Match             92.3%;  Score 1397.8;  DB 10;  Length 6574;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1402;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGTGGTGCTGA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    13 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGTGGTGCTGA 72

Qy    61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    73 CCCATTGCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 132

Qy   121 ACTCAACAGCAGATGTCTCCCTCCCTCTTCCCGAGAAGGGATATTAGAATCGTTGTTCTC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTG 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1273 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTGTCGGGTCTG 1332

Qy  1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1380
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1333 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAAGAAACTTCTCATCAAAAGCAAAGAGCTA 1392

Qy  1381 CAAGACTCTCAGGACAAGTGTCACAAGGT 1409
         |||||||||||||||||||||||||||||
Db  1393 CAAGACTCTCAGGACAAGTGTCACAAGAT 1421
```

Search completed: March 19, 2005, 08:21:29
Job time : 774.108 secs

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Db   133 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 192

Qy   181 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   193 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGAATTAAGCACGTGAGCAACTTTGTCCGG 252

Qy   241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 312

Qy   301 GTCAGAAGTCTTGTAGGTGTGGTCACTTTGCTCGTGAAGTGCAGTGGTAAGAGAGAAAGCA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 GTCAGAAGTCTTGTAGGTGTGGTCACTTTGCTCGTGAAGTGCAGTGGTAAGAGAGAAAGCA 372

Qy   361 ACCGGGGACATCTATGCTATGAAGAGTGATGAAGAAGAAGGCTTTATTGGCCCAGAGCAG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 ACCGGGGACATCTATGCTATGAAGAGTGATGAAGAAGAAGGCTTTATTGGCCCAGAGCAG 432

Qy   421 GTTTCATTTTTGAGGAAGAGCCGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 GTTTCATTTTTGAGGAAGAGCCGAACACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 492

Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540
         |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   493 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTGGAGAATATCAGCCT 552

Qy   541 GGAGGGGACTTGCTGTCACTTTGAATAGATATGGAGGACCAGTTAGATGAAAACCTGATA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GGAGGGGACTTGCTGTCACTTTGAATAGATATGGAGGACCAGTTAGATGAAAACCTGATA 612

Qy   601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCTGTTCACCAGCGGTTCATCTGATGGATACGTG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTCTGTTCACCAGCGGTTCATCTGATGGATACGTG 672

Qy   661 CATCGAGAACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720
         |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 CATCGAGACACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 732

Qy   721 GATTTTGGATCTGCGCGCGGAAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   733 GATTTTGGATCTGCGCGCGGAAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATT 792

Qy   781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   841 ACCTACGGCCTGGACTGTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 900
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Db   853 ACCTACGGCCTGGACTGTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT 912

Qy   901 GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGATGAATTTC 960
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Qy   961 CAGCGGTTTTTGAAATTTGCGCGGCCAGAAATTCCAGATGACCCCAAAGTGAGCAGTGACTT 1020
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Qy  1021 CAAAGCTGTGTGTGCGCGGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080
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Qy  1141 CTCAAGTCCGACGATGACACACCTCCAATTTTGATGAACCAGAGAAGTTCGTGGGTTTCA 1200
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Qy  1201 TCCTCTCCCGTGCCAGCTGAGCCCCTGCAGCTTCTCGGGTGAAGAAGACTGCCGTTTGTGGGGG 1260
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                  GenCore version 5.1.6
           Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      March 19, 2005, 06:53:57 ; Search time 6455.94 Seconds
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Match Length	DB	ID	Description			
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2	1515	100.0	1515	6	AR453415	AR453415	Sequence		
3	1510.0	99.7	2066	6	AX642956	AX642956	Sequence		
4	1505.8	99.4	1765	6	AX671044	AX671044	Sequence		
5	1481.8	97.8	1485	6	AX671037	AX671037	Sequence		
6	1404.2	92.7	6298	6	AX504254	AX504254	Sequence		
7	1404.2	92.7	8576	9	AY257469	AY257469	Homo sapi		
8	1399.4	92.4	1799	9	AY209000	AY209000	Homo sapi		
9	1398.2	92.3	5877	6	AR534559	AR534559	Sequence		
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12	1398.2	92.3	6165	6	AR534558	AR534558	Sequence		
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15	1398.2	92.3	8603	6	AX671108	AX671108	Sequence		
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18	1382	91.2	6159	6	AX166510	AX166510	Sequence		
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ALIGNMENTS

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LOCUS       AR253937                   1515 bp    DNA        linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6479269.
ACCESSION   AR253937
VERSION     AR253937.1  GI:27302420
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1515)
  AUTHORS   Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6479269-A 1 12-NOV-2002;
FEATURES             Location/Qualifiers
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ORIGIN
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       Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AR453415
LOCUS        AR453415                1515 bp    DNA       linear   PAT 20-FEB-2004
DEFINITION   Sequence 1 from patent US 6680188.
ACCESSION    AR453415
VERSION      AR453415.1  GI:42686143
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 1515)
  AUTHORS    Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
  TITLE      Isolated human kinase proteins, nucleic acid molecules encoding
             human kinase proteins, and uses thereof
  JOURNAL    Patent: US 6680188-A 1 20-JAN-2004;
FEATURES             Location/Qualifiers
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Db   301 GTCAGAAGTCTTGTAGGTTGTGTCACTTGCTGAAGTGCTGGGAAACCACCCTTTATG 360

Qy   361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 420
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Qy   421 GTTTCATTTTTTGAGGAAGAGCGGGAACATATTATCTGAAGCACAAGCCGTGATCCCC 480
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Qy   481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTGTCATGGAATATCAGCCT 540
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AX642956
LOCUS   AX642956   2066 bp   DNA   linear   PAT 24-FEB-2003
DEFINITION   Sequence 33 from Patent WO01096547.
ACCESSION   AX642956
VERSION   AX642956.1 GI:28550096
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
                Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
                Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
                Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
                Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
                Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,
                Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
  TITLE   Humain kinases
  JOURNAL   Patent: WO 01096547-A 33 20-DEC-2001;
                Incyte Genomics, Inc. (US)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="Incyte ID No: 3951059CB1"
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Matches 1512; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy   181 TTTGAAGAATGCAGTCAGCCTGCTGATGAAGTGATGAAGAAGAAGATGAAGCACGTGAGCAACTTGTCTGCGG 240
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Qy   241 AAGTATTCCGACACCATAGCTGAGTTGTGTCACTTTGCTGAGTGTGTGTCGGGGTCTG 300
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Db   248 AAGTATTCCGACACCATAGCTGAGTTGTGTCACTTTGCTGAGTGTGTGTCGGGGTCTG 307

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Db   1501 GCCGCCTGATCCGTA 1515

RESULT 3

ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Zhu,Z.
TITLE   Regulation of human citron rho/rac-interacting kinase-short kinase
JOURNAL   Patent: WO 03004629-A 8 16-JAN-2003;
          Bayer Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
source   1..1765
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          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
ORIGIN

Query Match   99.4%; Score 1505.8; DB 6; Length 1765;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1507; Conservative   0; Mismatches   0; Indels   2; Gaps   0;

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Qy       7 ATGTTGAAGTTCAAATATGGAGCGCCGGAATCCTTGGATGCTGGTGCTGAACCCATT   66
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Db       1 ATGTTGAAGTTCAAATATGGAGCGCCGGAATCCTTGGATGCTGGTGCTGAACCCATT   60

Qy      67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGGAAACCACCCTTTATGACTCAA  126
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Db      61 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGGAAACCACCCTTTATGACTCAA  120

Qy     127 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGACACGTGCCCTCTTGTCTCTTTGAA  186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGACACGTGCCCTCTTGTCTCTTTGAA  180

Qy     187 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT  246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT  240

Qy     247 TCCGACACCATAGCTGAGTTACAGAGGGTACAGAGGCTCCAGCCTTCGCAAAGGACTTCAAGTCAGA  306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCCGACACCATAGCTGAGTTACAGAGGGTACAGAGGCTCCAGCCTTCGCAAAGGACTTCAAGTCAGA  300

Qy     307 AGTCTTGTAGGTGTGTCACTTGCTGTCGCAGTGCAGGTGGTAAGAGAAAAGCAACCGGG  366
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGTCTTGTAGGTGTGTCACTTGCTGTCGCAGTGCAGGTGGTAAGAGAAAAGCAACCGGG  360

Qy     367 GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCGTGTCGGGGTCTG  426
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCGTGTCGGGGTCTG  420

Qy     427 TTTTTTGAGGAAGAGCGGAACATATATCTGAAGCACAAGCCCGTGGATCCCCAATTA  486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTTTTGAGGAAGAGCGGAACATATATCTGAAGCACAAGCCCGTGGATCCCCAATTA  480

Qy     487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGGAGGG  546
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Db     481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCTGGAGGG  540

Qy     547 GACTTGCTGTCACTTTTGAATGATATGAGGACCAGTTGATAATGAAACCTGATACAGTTT  606
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Db     541 GACTTGCTGTCACTTTTGAATGATATGAGGACCAGTTGATAATGAAACCTGATACAGTTT  600

Qy     607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGATACGTGCATCGA  666
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGATACGTGCATCGA  660

Qy     667 GACATCAAGCCTGAGAACATTCTCGTTCGTTCGTGACCGACCAGGACACATCAAGCTGGTGGATTT  726
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GACATCAAGCCTGAGAACATTCTCGTTCGTTCGTGACCGACCAGGACACATCAAGCTGGTGGATTT  720

Qy     727 GGATCTGCCGCGGCAAAATGAATTCAAACAAGATGGTCAAACTCCCAATTCCGGACC  786
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGATCTGCCGCGGCAAAATGAATTCAAACAAGATGGTCAAACTCCCAATTCCGGACC  780

Qy     787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGGACTGTGATGAACGGGATGGAAAAGCCACCTAC  846
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Qy     601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTG  660
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Db     608 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTG  667

Qy     661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTCGTTGACCGACCGCACAGGACACATCAAGCTGGTG  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 CATCGAGACATCAAGCCTGAGAACATTCTCGTTCGTTGACCGACCGCACAGGACACATCAAGCTGGTG  727

Qy     721 GATTTGGATCTGCCGCGGCAAAATGAATTCAAACAACAAGATGTGAATGCCAAACTCCCGATT  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     728 GATTTGGATCTGCCGCGGCAAAATGAATTCAAACAACAAGATGTGAATGCCAAACTCCCGATT  787

Qy     781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC  847

Qy     841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     848 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTAT  907

Qy     901 GGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTC  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     908 GGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACACATTATGAATTC  967

Qy     961 CAGCGGTTTTTGAAATTCCAGATGACACCCAAAGTGAGCAGTGACTTTCTTGATCTGATT  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     968 CAGCGGTTTTTGAAATTCCAGATGACACCCAAAGTGAGCAGTGACTTTCTTGATCTGATT  1027

Qy    1021 CAAAGCTTGTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTTGCTCGCCATCCT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1028 CAAAGCTTGTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTTGCTCGCCATCCT  1087

Qy    1081 TTCTTCTCTAAAATTGACTGGAACAACACTTCGTAACTCTCCTCCCCCCTTCGTTCCCACC  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1088 TTCTTCTCTAAAATTGACTGGAACAACACTTCGTAACTCTCCTCCCCCCCTTCGTTCCCACC  1147

Qy    1141 CTCAAGTCCGACGATGACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1148 CTCAAGTCCGACGATGACACTTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA  1207

Qy    1201 TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTGGGTGAAGAACTGCCGTTTGTGTGGGG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1208 TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTGGGTGAAGAACTGCCGTTTGTGTGGGG  1267

Qy    1261 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCTGAGTCTGTCGTGTGTGTCGGGTCTG  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1268 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCTGAGTCTGTCGTGTGTGTCGGGTCTG  1327

Qy    1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA  1380
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Db    1328 GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTA  1387

Qy    1381 CAAGACTCTCAGGACACAAGTGTCACAAGGTATTTATTTCCCGCAGCCGGCCTCCTTGC  1440
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Db    1388 CAAGACTCTCAGGACACAAGTGTCACAAGGTATTTATTTCCCGCAGCCGGCCTCCTTGC  1447

Qy    1441 TCCAGGATCCTCCCGTCCCGTATATGCCAAGGGATCCGCCGCCGGGGGCCGGCTGGCTCTGA  1500
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Db    1448 TCCAGGATCCTCCCGTATATGCCAAGGGATCCGCCGCCGGGGGCCGGCTGGCTCTGA  1507

Qy    1501 GCCGCCTGATCCGTA  1515
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Db    1508 GCCGCCTGATCCGTA  1522
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RESULT 4
AX671044
LOCUS   AX671044   1765 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION Sequence 8 from Patent WO03004629.
ACCESSION   AX671044
VERSION   AX671044.1   GI:29329510
KEYWORDS
SOURCE   Homo sapiens (human)

Query Match   97.8%;   Score 1481.8;   DB 6;   Length 1485;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1483;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

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Qy       7 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGAACCCATT 66
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Db       1 ATGTTGAAGTTCAAATATGGAGGCGCGGAATCCTTTGGATGCTGGTGCTGAACCCATT 60

Qy      67 GCCAACCGGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATGACTCAA 126
           |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCAGCCGCGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTTATGACTCAA 120

Qy     127 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGACGGGGATGATGAAAAGGCACCTAC 186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCAGATGTCTCCTCTTCCCGAGAAGGGATATTAGACGGGGATGATGAAAAGGCACCTGAA 180

Qy     187 GAATGCAGCCTGCTCTGTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAATGCAGCCTGCTCTGTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 240

Qy     247 TCCGACACCATAGCTGAGTTACAGGAGCTCGAAGTGCAGTGCAGGTGGTAAGAGAAGCAACCGGG 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCCGACACCATAGCTGAGTTACAGGAGCTCGAAGTGCAGTGCAGGTGGTAAGAGAAAGCAACCGGG 300

Qy     307 AGTCTTGTTAGTTGTGTCACTTTGCTGAAGTGCAGTGCAGTGCAGTGCAGGTTTTCG 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGTCTTGTTAGTTGTGTCACTTTGCTGAAGTGCAGTGCAGTGCAGTGCAGGTTTTCG 360

Qy     367 GACATCTATGCTATGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACATCTATGCTATGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420

Qy     427 TTTTTGAGGAGAGCGGAACATATTATCTCGTTGACGACAAGCCCGTGGATCCCCCAATTA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTTTGAGGAGAGCGGAACATATTATCTCGTTGACGACAAGCCCGTGGATCCCCCAATTA 480

Qy     487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 540

Qy     547 GACTTGCTGTCGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 606
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Db     541 GACTTGCTGTCGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy     607 TACCTAGCTGAGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TACCTAGCTGAGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660

Qy     667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGTGTGGATTTT 726
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Db     661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGTGTGGATTTT 720

Qy     727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGGCCAAACTCCCGATTGGGACC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGGCCAAACTCCCGATTGGGACC 780

Qy     787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTAC 846
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Db     781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTAC 840

Qy     847 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 906
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Db     841 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 900

Qy     907 TCCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960

Qy     967 TTTTTGAAATTTCCAGATGAGCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
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Db     961 TTTTTGAAATTTCCAGATGAGCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020
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Db     781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAAGGCACCTAC 840

Qy     847 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA 900

Qy     907 TCCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCCCTTGCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960

Qy     967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTTGAAGGTCTTTGCTGCCATCCTTCTTC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTTGAAGGTCTTTGCTGCCATCCTTCTTC 1020

Qy    1027 TTGTGTGCGGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTGTGTGCGGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTCTTC 1080

Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTGTCCCACCCTCAAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTGTCCCACCCTCAAG 1140

Qy    1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1206
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Db    1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1200

Qy    1207 CCGTGCCAGCTGAGCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1266
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Db    1201 CCGTGCCAGCTGAGCCCTCCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1260

Qy    1267 TACAGCAAGGCACTCGGGATTCTTGGTAGATCGAGTCTGTTGTGTCGGGTCTGGACTCC 1326
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Qy    1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTACAAGAC 1386
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Db    1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGACTACAAGAC 1380

Qy    1387 TCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGCCTCCTTCCGGTCTGCGCCGC 1446
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Db    1381 TCTCAGGACAAGTGTCACAAGGTATTTATTTCCGCAGCCGCCTCCTTCCGGTCTGCGCCGC 1440

Qy    1447 ATCCTCCCGTCCGTATATGCCAAGGGGATCCGCCCCGGGGCCGCCGCGGGGCCGCCGC 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATCCTCCCCGTCCGTATATGCCAAGGGGATCCGCCCCGGGGCCGCCGCGGGGCCGCCGC 1500

Qy    1507 TGATCCGTA 1515
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Db    1501 TGATCCGTA 1509
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RESULT 5
AX671037
LOCUS   AX671037   1485 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION   Sequence 1 from Patent WO03004629.
ACCESSION   AX671037
VERSION   AX671037.1   GI:29329507
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE   Regulation of human citron rho/rac-interacting kinase-short kinase
  JOURNAL   Patent: WO 03004629-A 1 16-JAN-2003;
             Bayer Aktiengesellschaft (DE)
FEATURES   Location/Qualifiers
     source   1..1485
                     /organism="Homo sapiens"
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Qy    121  ACTCAACAGCAGATGTCTCCTCTTTCCCGAAGAGGAGGGATATTAGATGCCCTCTTGTTCTC  180
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Db    169  ACTCAACAGCAGATGTCTCCTCTTTCCCGAAGAGGAGGGATATTAGATGCCCTCTTGTTCTC  228

Qy    181  TTTGAAGAATGCAGTCAGTCGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229  TTTGAAGAATGCAGTCAGTCGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG  288

Qy    241  AAGTATTCCGACACCATAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAA  300
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Db    289  AAGTATTCCGACACCATAGCTGAGTTACAGAGACTCCAGCCTTCGGCAAAGGACTTCGAA  348

Qy    301  GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTCGAAGTGCAGGTGCGTAAGAGAGAAAGCA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349  GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTCGAAGTGCAGGTGCGTAAGAGAGAAAGCA  408

Qy    361  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTATTGGCCCAGGAGCAG  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTATTGGCCCAGGAGCAG  468

Qy    421  GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGACCCGTGGATCCCC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469  GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGACCCGTGGATCCCC  528

Qy    481  CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT  540
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Db    529  CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT  588

Qy    541  GGAGGGGACTTGCTGTCTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589  GGAGGGGACTTGCTGTCTCACTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA  648

Qy    601  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTCGTGTTCACAGCGTTCATCTGATGGGATACTG  660
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Db    649  CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTCGTGTTCACAGCGTTCATCTGATGGGATACTG  708

Qy    661  CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCCTCCGATT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709  CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCCTCCGATT  768

Qy    721  GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAACAAGATGTGAATGCCAAACTCCCGATT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769  GATTTTGGATCTGCCCGCGAAAATGAATTCAAACAACAAGATGTGAATGCCAAACTCCCGATT  828

Qy    781  GGGACCCCAGATTACATGGCTCCTGAGTGCTGTGATGAACGGGATGGAAAGGC  840
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Db    829  GGGACCCCAGATTACATGGCTCCTGAGTGCTGTGATGAACGGGATGGAAAGGC  888

Qy    841  ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATGGCCTATGAGATGATTTAT  900
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Db    889  ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATGGCCTATGAGATGATTTAT  948

Qy    901  GGGAGATCCCCCTTCGCAGAGGGAACCTCGCCAGAACTTCAATAACATTATGAATTTC  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949  GGGAGATCCCCCTTCGCAGAGGGAACCTCGCCAGAACTTCAATAACATTATGAATTTC  1008

Qy    961  CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTCTTGATCTGATT  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1009 CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTCTTGATCTGATT  1068

Qy    1021 CAAAGCTTGTTGTGCGCGCCAGAAAGAGAGACTGAAGGTTTGAAGGTTTGCTGCCATCCT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1069 CAAAGCTTGTTGTGCGCGCCAGAAAGAGAGACTGAAGGTTTGAAGGTTTGCTGCCATCCT  1128

Qy    1081 TTCTTCTTCTAAAATTGACTGGAACAACATTCCTTTGGATGCGTGCTCGCTGCTGAA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1129 TTCTTCTTCTAAAATTGACTGGAACAACATTCCTTTGGATGCGTGCTCGCTGCTGAA  1188

Qy    1141 CTCAAGTCCGACGGGCCTTCCAGGCTGAATCGTGTTCTTCAGGGGAAACCACCCTTTATG  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1189 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAATTCGTCGGGTTTCA  1248

Qy    1201 TCCTCTCCGTGCCCAGCTCGAGCCCCTGAGCCCCTCTCGGGTTCTCGGGATCTTGTGGGG  1260
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Qy    1027 TTGTTGTGCGCGCCAGAAAGAGAGACTGAAGGTTTGAAGGTCTTTGCTGCCATCCTTCTTC  1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTGTTGTGCGCGCCAGAAAGAGAGACTGAAGGTTTGAAGGTCTTTGCTGCCATCCTTCTTC  1080

Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCTCCCCCTTCGTTCCACCCTCAAG  1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCTCCCCCTTCGTTCCACCCTCAAG  1140

Qy    1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCT  1206
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCT  1200

Qy    1207 CCGTGCCAGTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG  1266
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CCGTGCCAGTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG  1260

Qy    1267 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCC  1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGACTCC  1320

Qy    1327 CCTGCCAAGACTAGCTCCATGGGAAAAGAAACTTCATCAAAGCAAAAGAGCTACAAGAC  1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CCTGCCAAGACTAGCTCCATGGGAAAAGAAACTTCATCAAAGCAAAAGAGCTACAAGAC  1380

Qy    1387 TCTCAGGACAAGTGTCACAAGGTATTATTTCCGAGCCGCCTCCTTCCTTCCTTGCTCCAGG  1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TCTCAGGACAAGTGTCACAAGGTATTATTTCCGAGCCGCCTCCTTCCTTCCTTGCTCCAGG  1440

Qy    1447 ATCCTCCCGTCCGTATATGCCAAGGGATCCGCGCCGGGGGCCGCTGC  1491
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Db    1441 ATCCTCCCGTCCGTATATGCCAAGGGATCCGCGCCGCCCCGGGCCGCTGC  1485
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RESULT 6
AX504254
LOCUS         AX504254                 6298 bp    DNA        linear      PAT 27-SEP-2002
DEFINITION    Sequence 43 from Patent WO0233099.
ACCESSION     AX504254
VERSION       AX504254.1  GI:23386094
KEYWORDS      .
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
  AUTHORS     Gururajan,R., Baughn,M.R., Walia,N.K., Elliott,V.S., Xu,Y.,
              Arvizu,C., Yao,M.G., Ramkumar,J., Ding,L., Tang,Y.T., Hafalia,A.J.,
              Nguyen,D.B., Gandhi,A.R., Lu,Y., Yue,H., Burford,N., Bandman,O.,
              Tribouley,C.M., Lal,P.G., Lu,D.A., Recipon,S.A., Borowsky,M.L.,
              Thornton,M., Swarnaker,A., Thangavelu,K., Khan,F.A. and Ison,C.H.
  TITLE       Human kinases
  JOURNAL     Patent: WO 0233099-A 43 25-APR-2002;
              Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..6298
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID NO: 7484498CB1"
ORIGIN

Query Match             92.7%;  Score 1404.2;  DB 6;  Length 6298;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1406;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy       1  GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCGTGCTCGCTGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49  GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCGTGCTCGCTGAA  108

Qy      61  CCCATTGCCAACCGGGCCTTCCAGGCTGAATCGTGTTCTTCAGGGGAAACCACCCTTTATG  120
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Db     109  CCCATTGCCAACCGGGCCGGCCTTCCAGGCTGAATCGTGTTCTTCAGGGGAAACCACCCTTTATG  168
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Db   1249 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TCCTCTCCGTGCCAGTCAGCCACTGGAGCCCCTCAGGCTTCTCGGGTAGATCTGAGTCCGTTTGTCGGGTCTG 1308

Qy   1261 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCTGGTAGATCTGAGTCTGTTGTCGGGTCTG 1320
          |||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1309 TTTTCGTACAGCAAGGCACTGGGATTCTTGGTAGATCTGGTAGATCTGAGTCTGTTGTCGGGTCTG 1368

Qy   1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAGCAAAGAGCTA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 GACTCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAGCAAAGAGCTA 1428

Qy   1381 CAAGACTCTCAGGACAAGTGTCACAGGT 1409
          |||||||||||||||||||||
Db   1429 CAAGACTCTCAGGACAAGTGTCACAAGAT 1457
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RESULT 7
AY257469

LOCUS   AY257469   8576 bp   mRNA   linear   PRI 23-APR-2003
DEFINITION Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete
            cds.
ACCESSION   AY257469
VERSION   AY257469.1 GI:30088959
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 8576)
  AUTHORS   Huang,C.Q., Wu,S.L., Shan,Y.X., Liu,S. and Xiao,P.J.
  TITLE   Direct Submission
  JOURNAL   Submitted (18-MAR-2003) Department of Biochemistry and Molecular
            Biology, Basic Medicine, Suzhou University, Renming Road 48,
            Suzhou, Jiangsu 215007, China
FEATURES   Location/Qualifiers
     source   1..8576
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="12"
                     /map="12q24.23"
     gene   1..8576
                     /gene="CIT"
                     /note="synonym: CRIK"
     CDS   54..6137
                     /gene="CIT"
                     /note="serine/threonine protein kinases"
                     /codon_start=1
                     /product="rho/rac-interacting citron kinase"
                     /protein_id="AAP13528.1"
                     /db_xref="GI:30088970"
                     /translation="MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMS
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                     VGCGHPAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEERNILSRSTSPWIPQL
                     QYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYV
                     HRDIKPENILVDRTGHIKLVDFGSAAKNSNKMVNAKLPIGTPDYMAPEVLTVMNGDG
                     KGTYGLDCDWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDF
                     LDLIQSLLCGQKERLKFGGLCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPE
                     KNSWVSSSPCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKK
                     LLIKSKELQDSODKHMEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLEQDLA
                     TYITECSSIKRSLEQARMEVSQEDDKALQLLHDIREQSRKLQEIKEQEYQAQVEEMRL
                     MNNQLEEDLVSARRSDLYESELRESRLAAEEFFKRKATECOHKLLAKDQGKPEVGEY
                     AKLEKINAEQQLKIQELQELKIQHYEEKIKVLDNQIKDLADKE
                     SEGIRKKLVEAEBELEKHREAQVSAQHLEVHLKQKEOHYEEKIKVLDNQIKDLADKE
                     TLENMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT
                     QRNMKAQEMISELRQQKFYLETOAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELET
                     RLREVSLEHEEQKELKRQLTELQLSLQERESQLTALQAARALESQLRQAKTELEET
                     TAEABEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSK
                     QLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCMLEEQVMDLE
                     ALNDELLEKEROWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRITESRQV
                     VBLAVKEHKAEILALQQALKEQKLKAESLSDKLNDLEKKHAMLEMNARSLQKLETER
                     ELKQRLLEBQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERSDLEYQLENIQVL
                     YSHEKVRMEGTISQQTKLIDFLQAKMDQPAKKKKGLFSRRKEDPALPTQVPLQYNELK 840
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ORIGIN

Query Match   92.7%; Score 1404.2; DB 9; Length 8576;
Best Local Similarity 99.8%; Pred. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

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Qy    1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAA 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   48 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAA 107

Qy   61 CCCATTGCCAACGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  108 CCCATTGCCAACGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 167

Qy  121 ACTCAACAGCAGATGTCTCCTCTTTCCGAGAAGGGATATTAGATGCCTCTTTGTTCTC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 ACTCAACAGCAGATGTCTCCTCTTTCCGAGAAGGGATATTAGATGCCTCTTTGTTCTC 227

Qy  181 TTTGAAGAATGCAGTCAGTCAGCCGCTGCTCTGATGAAGTTACAGACGCCTCCAGCAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  228 TTTGAAGAATGCAGTCAGTCAGCCGCTGCTCTGATGAAGTTACAGACGCCTCCAGCAC 287

Qy  241 AAGTATTCCGACACCATAGCTGAGTTACAGACGCCTCCAGCCTTCGGCAAAGGACTTCGAA 300
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Db  288 AAGTATTCCGACACCATAGCTGAGTTACAGACGCCTCCAGCCTTCGGCAAAGGACTTCGAA 347

Qy  301 GTCAGAAGTCTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAAAGCA 360
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Db  348 GTCAGAAGTCTTGTGGTCACTTTGCTGAGTGCAGGTGCAGGTGTAAGAGAGAAAGCA 407

Qy  361 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  408 ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAG 467

Qy  421 GTTTCATTTTTGAGGAGAGCGGAACATATTCCGTTGACCAAGCACAAGCCGTGGATCCCC 480
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Db  468 GTTTCATTTTTGAGGAGAGCGGAACATATTCCGTTGACCAAGCACAAGCCGTGGATCCCC 527

Qy  481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCT 540
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Db  528 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTCGTCATGGAATATCAGCCT 587

Qy  541 GGAGGGGACTTGCTGTCACTTTTGGCTGTCATCTGAGCGTTCATCTGATGGGATACGTG 600
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Db  588 GGAGGGGACTTGCTGTCACTTTTGGCTGTCATCTGAGCGTTCATCTGATGGGATACGTG 647

Qy  601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  648 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 707

Qy  661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGGACAGGACACATCAAGCTGGTG 720
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Db  708 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGGACAGGACACATCAAGCTGGTG 767

Qy  721 GATTTTGGATCGGCCGCGAAAATGATTCAAACAAGATGGTCAAACAAGATGGTCAAAACCTCCCGATT 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  768 GATTTTGGATCGGCCGCGAAAATGATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 827

Qy  781 GGGACCCCAGATTACATGGCCTCCTGAAGTGCTGACTGTGATGAACGGAGATGAAAAGGC 840
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Db    828 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAGGC 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    841 ACCTACGGCCTGGACTGTGGTGGTCAGTGGGCGTGGTGCCTATGAGATGATTTAT 900
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Db    888 ACCTACGGCCTGGACTGTGGTGGTCAGTGGGCGTGGTGCCTATGAGATGATTTAT 947

Qy    901 GGGGGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC 960
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Db    948 GGGGAGATCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC 1007

Qy    961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTGATCTGATT 1020
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Db   1008 CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTCTTGATCTGATT 1067

Qy   1021 CAAAGCTTGTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCTT 1080
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Db   1068 CAAAGCTTGTTGTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1127

Qy   1081 TTCTTCTCTAAAATGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1140
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Db   1128 TTCTTCTCTAAAATGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1187

Qy   1141 CTCAAGTCCGACGATGACACCTGGGATTCTTGATGAACCAGCAGGAATTCGTGGGTTTCA 1200
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Db   1188 CTCAAGTCTGACGATGACACCTGGGATTCTTGATGAACCAGCAGGAATTCGTGGGTTTCA 1247

Qy   1201 TCCTCTCCGTGCCAGCTGAGCCCTCCAGGCTTCGGGGTGAAGAACTGCCGTTTGTGGGGG 1260
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Db   1248 TCCTCTCCGTGCCAGCTGAGCCCTCCAGGCTTCGGGGTGAAGAACTGCCGTTTGTGGGGG 1307

Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGTCGTGGTCTGTGTGTCGGGTCTG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1308 TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGTCGTGGTCTGTGTGTCGGGTCTG 1367

Qy   1321 GACTCCCCTGCCAAGAGCTAGCTGGGAAACTTCTCATGAAAAGAAACTTCTCATCAAAAGAGCTA 1380
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Db   1368 GACTCCCCTGCCAAGAGCTAGCTGGGAAACTTCTCATGAAAAGAAACTTCTCATCAAAAGAGCTA 1427

Qy   1381 CAAGACTCTCAGGACAAGTGTCACAAGGT 1409
          ||||||||||||||||||||||||||||
Db   1428 CAAGACTCTCAGGACAAGTGTCACAAGAT 1456
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RESULT 8
AY209000

LOCUS   AY209000   1799 bp   mRNA   linear   PRI 01-FEB-2004
DEFINITION   Homo sapiens citron Rho-interacting kinase short form mRNA,
             complete cds.
ACCESSION   AY209000
VERSION   AY209000.1 GI:37784566
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1799)
  AUTHORS   Mao,Y., Xie,Y. and Wu,Q.
  TITLE   Cloning and characterizing a novel human CRIK-SK gene
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1799)
  AUTHORS   Mao,Y., Xie,Y. and Wu,Q.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
             220 Handan Road, Shanghai 200433, P.R. China
FEATURES   Location/Qualifiers
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/protein_id="AAP43922.1"
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HRDIKPENLIVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDG
KGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDF
LDLIQSLLCGQKERLKFEGLCCHPFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPE
KNSWVSSPCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKK
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ORIGIN

        Query Match   92.4%;   Score 1399.4;   DB 9;   Length 1799;
        Best Local Similarity   99.6%;   Pred. No. 0;
        Matches 1403;   Conservative 0;   Mismatches 6;   Indels 6;   Gaps 0;

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Qy      1 GGGGGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTGGATGCTGGTGCTGCTGAA 60
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Db     48 GGGGGAGTGTTGAAGTTCAAATATGAGCGCGGAATCCTTCGGATGCTGGTGCTGCTGAA 107

Qy     61 CCCATTGCCACCGGGCCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    108 CCCATTGCCAGCCGGGCCTCCAGGCTGAATCGTGTTCTTCCAGGGGAAACCACCCTTTATG 167

Qy    121 ACTCAACAGCAGATGTCTCCTTTCCCGAGAAGGGATATTAGAGTGCCCTCTTTGTCTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    168 ACTCAACAGCAGATGTCTCCTTCTTCCCGAGAAGGGATATTAGAGTGCCCTCTTAGTTCTC 227

Qy    181 TTTGAAGAATGCAGTCAGCTCTCTGATGAAGTGAAGTCACGTGAGCAACTTGTCGCGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    228 TTTGAAGAATGCAGTCAGCCTGCTCTCTGATGAAGTGAAGTCACGTGAGCAACTTGTCGCGG 287

Qy    241 AAGTATTCCGACACCATAGCTGAGTTACAGAGGCTCAGCCTTCGGCAAAGGACTTCGAA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 AAGTATTCCGACACCATAGCTGAGTTACAGAGGCTCCAGCCTTCGGCAAAGGACTTCGAA 347

Qy    301 GTCAGAAGTCTTGTAGGTGTCGTCATGTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGCAG 360
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Db    348 GTCAGAAGTCTTGTAGGTGTCGTCATGTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGCAG 407

Qy    361 ACCGGGGACATCTATGCTATGAAAGTGATGAAAGTGATGAAGAAGGCTTATTGGCCCAGGAGCAG 420
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Db    408 ACCGGGGACATCTATGCTATGAAAGTGATGAAAGTGATGAAGAAGGCTTATTGGCCCAGGAGCAG 467

Qy    421 GTTTCATTTTTTGAGGAGAGCGGAACATATATCTGAAGCACAAGCCCGTGGATCCCC 480
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Db    468 GTTTCATTTTTTGAGGAGAGCGGAACATATATCTGAAGCACAAGCCCGTGGATCCCC 527

Qy    481 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 540
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Db    528 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCT 587

Qy    541 GGAGGGGACTTGCGTCGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 GGAGGGGACTTGCGTCGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 647

Qy    601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAATATCAGCTG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGAATATCAGCTG 707

Qy    661 CATCGAGACATCAAGCCTGAGAACATTCGTTGACCGGCACAGGACACATCAAGCTGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    708 CATCGAGACATCAAGCCTGAGAACATTCGTTGACCGGCACAGGACACATCAAGCTGGTG 767

Qy    721 GATTTTGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTCAAACTCCCGATT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    768 GATTTTGATCTGCCCGCGAAAATGAATTCAAACAAGATGGTCAAACTCCCGATT 827

Qy    781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGATGGAAAGGC 840
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Db    828 GGGACCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGC 887

Db     61 GCCAGCGCCGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCTTATGACTCAA 120
Qy    127 CAGCAGATGTCTCCTCTTTCCCGAGAGGGATATTAGATGCCCTGTTCTCTTGAA 186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGATGTCTCCTCTTTCCCGAGAGGGATATTAGATGCCCTGTTCTCTTTGAA 180
Qy    841 ACCTACGGCCTGGACTGTGCTGGTGCTGGTGGGGCGTGACTGGGGCGTGCCTATGAGATGATTTAT 900
Qy    187 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCACTTGTCCGGAAGTAT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAATGCAGTCAGCCTGCTCGATGAAGATTAAGCACGTGAGCACTTGTCCGGAAGTAT 240
Db    888 ACCTACGGCCTGGACTGTGCTGGTGCTGGTGGGGCGTGACTGGGGCGTGCCTATGAGATGATTTAT 947
Qy    247 TCCGACACCATAGTCAGTTACAGGAGCAGTGACTTTCTTGATCTGATT 306
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCCGACACCATAGTCAGTTACAGGAGCAGTGACTTTCTTGATCTGATT 300
Qy    901 GGGGATCCCCCTTCGCAGAGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTC 960
Qy    307 AGTCTTGTAGGTTGTGTCACTTGCTGAAGGTGAAGGTCTTTGCTGCCATCCT 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGTCTTGTAGGTTGTGTCACTTGCTGAAGGTGAAGGTCTTTGCTGCCATCCT 360
Db    948 GGGGATCCCCCTTCGCAGAGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTC 1007
Qy    367 GACATCTATGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACATCTATGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 420
Qy    961 CAGGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020
Qy    427 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCCAATTA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCGTGATCCCCAATTA 480
Db   1008 CAGGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1067
Qy    487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG 540
Qy   1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGGACGTGAAGGTTGAGGTCTTTGCTGCCATCCT 1080
Qy    547 GACTTGCTGTCACTTTTGAATAGATAGAGATGAGATGAGGATGAGGACCAGTTAGACACAGTT 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACTTGCTGTCACTTTTGAATAGATAGAGATGAGATGAGGATGAGGACCAGTTAGACACAGTT 600
Db   1068 CAAAGCTTGTGTGCGGCCAGAAAGAGAGGACGTGAAGGTTGAGGTCTTTGCCATCCT 1127
Qy    607 TACCTAGCTGAGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACCTAGCTGAGCTGATTTTGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 660
Qy   1081 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1140
Qy    667 GACATCAAGCTCTGAGAACATTCGTTGCTGACCCGACCAGGACACATCAAGCTGGTGGATTTT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GACATCAAGCTCTGAGAACATTCGTTGCTGACCCGACCAGGACACATCAAGCTGGTGGATTTT 720
Db   1128 TTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACC 1187
Qy    727 GGATCTGCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCGATTGGGACC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGATCTGCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCGATTGGGACC 780
Qy   1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTTGGGTTTCA 1200
Qy    787 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCCACCTAC 846
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Db    781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGAAAAGGCCACCTAC 840
Db   1188 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAGAATTCGTTGGGTTTCA 1247
Qy    847 GGCCTGGACTGTGCTGGTGCTGGTGGGGCGTGATGCCTATGAGATGATTATGGGGAGA 905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGCCTGGACTGTGCTGGTGCTGGTGGGGCGTGATGCCTATGAGATGATTATGGGGAGA 900
Qy   1201 TCCTCCGTGCCAGCTGAGCCCTTCAGGCCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1260
Qy    907 TCCCCCTGCCAAGACTAGCTCCATGGAAAAAGAAACTTCCATCAAAGCAAAGAGCTA 966
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Db    901 TCCCCCTGCCAAGACTAGCTCCATGGAAAAAGAAACTTCCATCAAAGCAAAGAGCTA 960
Db   1248 TCCTCCGTGCCAGCTGAGCCCTTCAGGCCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1307
Qy    967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020
Qy   1261 TTTTCGTACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTCTGTGTCGGGTCTG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1308 TTTTCGTACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTCTGTGTCGGGTCTG 1367
Qy   1027 TTGTTGTGCGGCCAGAAAGAGAGGACTGAAGTTTGAAGGTTGAGGTCTTTGCTGCCATCCTTTCTC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTGTTGTGCGGCCAGAAAGAGAGGACTGAAGTTTGAAGGTTGAGGTCTTTGCTGCCATCCTTTCTC 1080
Qy   1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAAAGAAACTTCCATCAAAAGCAAAGAGCTA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1368 GACTCCCTGCCAAGACTAGCTCCATGGAAAAAGAAACTTCCATCAAAAGCAAAGAGCTA 1427
Qy   1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCCATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCCATT 1140
Qy   1381 CAAGACTCTCAGGACGACAAGGT 1409
           |||||||||||||||||||
Db   1428 CAAGACTCTCAGGACGACAAGGTGTCACAAGAT 1456
Qy      7 ATGTTGAAGTTCAAATATGGAGCCGCGGGAATCCTTTGGATGCTGGTGCTGCTGACCCATT 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGAAGTTCAAATATGGAGCCGCGGGAATCCTTTGGATGCTGGTGCTGCTGACCCATT 60
Qy     67 GCCAACCGGCCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCACCCCTTATGACTCAA 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCTGACGATGACACCTTCCCAATTTGATGAACCAGAGAATTCGTTGGGTTTCATCCCCT 1200
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RESULT 9
AR534559

LOCUS	AR534559 5877 bp DNA linear PAT 08-OCT-2004
DEFINITION	Sequence 3 from patent US 6734009.
ACCESSION	AR534559
VERSION	AR534559.1 GI:5924886
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 5877)
AUTHORS	Yu,X.S., Miranda,M. and Friddle,C.J.
TITLE	Human kinases and polynucleotides encoding the same
JOURNAL	Patent: US 6734009-A 3 11-MAY-2004;
FEATURES	Location/Qualifiers
source	1..5877
	/organism="unknown"
	/mol_type="genomic DNA"
ORIGIN	

Query Match   92.3%;   Score 1398.2;   DB 6;   Length 5877;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1400;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

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Qy   1207  CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTTCG  1266
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTGTGTGGGTTTTCG  1260

Qy   1267  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTTGTCGGGTCTGGACTCC   1326
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTTGTCGGGTCTGGACTCC   1320

Qy   1327  CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCCATCAAAAGCAAAGAGCTACAAGAC  1386
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCCATCAAAAGCAAAGAGCTACAAGAC  1380

Qy   1387  TCTCAGGACAAGTGTCACAAGGT  1409
                 |||||||||||||||||||||| |
Db   1381  TCTCAGGACAAGTGTCACAAGAT  1403
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RESULT 10
AX574427
LOCUS   AX574427   5877 bp   DNA   linear   PAT 07-JAN-2003
DEFINITION Sequence 3 from Patent WO02059325.
ACCESSION   AX574427
VERSION   AX574427.1 GI:27551752
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Yu,X., Miranda,M. and Friddle,C.J.
TITLE   Human kinases and polynucleotides encoding the same
JOURNAL   Patent: WO 02059325-A 3 01-AUG-2002;
            Lexicon Genetics Incorporated (US)
FEATURES   Location/Qualifiers
     source   1..5877
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   92.3%; Score 1398.2; DB 6; Length 5877;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1400; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy     7  ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATT    66
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGATGCTGGTGCTGCTGAACCCATT    60

Qy    67  GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA   126
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA   120

Qy   127  CAGCAGATGTCTCCTTTCCCTCCTTTCCCGAGAAGGAGGATATTAGATGCCCTTGTTCTTTGAA   186
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CAGCAGATGTCTCCTTTCCCTCCTTTCCCGAGAAGGAGGATATTAGATGCCCTTCTTTGTTCTTTGAA   180

Qy   187  GAATGCAGTCAGCCACTTTGTCCGGAAGTAT   246
                ||||||||||||||||||||||||||||||
Db   181  GAATGCAGTCAGCCACGTTGTCCGGAAGTAT   240

Qy   247  TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA   306
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA   300

Qy   307  AGTCTTGTAGGTTGTGGTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTTCA   366
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGTCTTGTAGGTTGTGGTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTTCA   360

Qy   367  GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTTCA   426
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTATTGGCCCAGGAGCAGGTTTCA   420
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Qy   427  TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA   486
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TTTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAATTA   480

Qy   487  CAGTATGCCTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG   546
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CAGTATGCCTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG   540

Qy   547  GACTTGCTGTCACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT   606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GACTTGCTGTCACTTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT   600

Qy   607  TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA   666
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA   660

Qy   667  GACATCAAGCCTGAGAACATTCTCGTTGACCGGACACATCAAGCTCGTGTGGATTTT   726
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  GACATCAAGCCTGAGAACATTCTCGTTGACCGGACACATCAAGCTCGTGTGGATTTT   720

Qy   727  GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   780

Qy   787  CCAGATTACAATGGCTCCTGAAGTGCTGACTGTGAAGCGGGATGAACGGGGATGAAAAGGCACCTAC   846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  CCAGATTACAATGGCTCCTGAAGTGCTGACTGTGAAGCGGGATGAACGGGGATGAAAAGGCACCTAC   840

Qy   847  GGCCTGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGGAGA   906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGCCTGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGGAGA   900

Qy   907  TCCCCCTTCGGAGGGGAACCCTCTGCCAGAGAACCTTCAATAACATTATGAATTTCCAGCGCG   966
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TCCCCCTTCGGAGGGGAACCCTCTGCCAGAGAACCTTCAATAACATTATGAATTTCCAGCGCG   960

Qy   967  TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGGATTCAAAGC  1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCGGATTCAAAGC  1020

Qy  1027  TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTGCTGCGCCATCCTTTCTC  1086
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTGCTGCGCCATCCTTTCTTC  1080

Qy  1087  TCTAAAATTGACTGGAACAACATTCGTAACTCGTGGTTCTCCCCCCTTCGTTCGTCCCACCCTCAAG  1146
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TCTAAAATTGACTGGAACAACATTCGTAACTCGTGGTTCTCCCCCCTTCGTTCGTCCCAAG  1140

Qy  1147  TCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCT  1206
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Db  1141  TCTGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTCATCCTCT  1200

Qy  1207  CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTCGGGTTTTCG  1266
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTCGGGTTTTCG  1260

Qy  1267  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTTGTCGGGTCTGGACTCC   1326
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Db  1261  TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCGTGTTGTCGGGTCTGGACTCC   1320

Qy  1327  CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCCATCAAAAGCAAAGAGCTACAAGAC  1386
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Db  1321  CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCCATCAAAAGCAAAGAGCTACAAGAC  1380

Qy  1387  TCTCAGGACAAGTGTCACAAGGT  1409
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Db  1381  TCTCAGGACAAGTGTCACAAGAT  1403
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RESULT 11
AX671112
LOCUS   AX671112   6156 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION Sequence 8 from Patent WO03004523.

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ACCESSION   AX671112
VERSION     AX671112.1  GI:29329572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE     Regulation of human citron rho/rac-interacting kinase
  JOURNAL   Patent: WO 03004523-A 8 16-JAN-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..6156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 6156;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative   0;  Mismatches   3;  Indels    0;  Gaps    0;
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Qy          7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGACGTGGTGCTGCTGAACCCATT  66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGACGTGGTGCTGCTGAACCCATT  60

Qy         67 GCCAACCGGCGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA  126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCAGCCGGCGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA  120

Qy        127 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCGCCTCTTTGTTCTCTTTGAA  186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCGCCTCTTTGTTCTCTTTGAA  180

Qy        187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTAAGCACGTGAGCAACTTGTCCGGAAGTAT  246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT  240

Qy        247 TCCGACACCATAGCTGAGTTACAGGAGCTTCAGCCTTCGGCAAAGGACTTCGAAGTCAGA  306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCGACACCATAGCTGAGTTACAGGAGCTTCAGCCTTCGGCAAAGGACTTCGAAGTCAGA  300

Qy        307 AGTCTTGTAGGTTGTGTGGTCACTTGCTGAGTGCAGGTGTGTAAGAGAAAGCAACCGGG  366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTCTTGTAGGTTGTGTGGTCACTTGCTGAGTGCAGGTGTGTAAGAGAAAGCAACCGGG  360

Qy        367 GACATCTATGCTATGAAAGTGATGAAGAAGAGAGGCGTTTATTGGCCCAGAGAGCAGGTTTCA  426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACATCTATGCTATGAAAGTGATGAAGAAGAGAGGCGTTTATTGGCCCAGAGAGCAGGTTTCA  420

Qy        427 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTTGATCCCCAATTA  486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTTGATCCCCAATTA  480

Qy        487 CAGTATGCCTTTCAGGACACAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGG  546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTATGCCTTTCAGGACACAAAATCACCCTTTATCTGTCATGGAATATCAGCCTGGAGGG  540

Qy        547 GACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT  606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTTGCTGTCACTTTGAATAGATGAGGACCAGTTAGATGAAAACCTGATACAGTTT  600

Qy        607 TACCTAGCTGAGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA  666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAGCTGAGCTGATTTTGGCTGTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA  660

Qy        667 GACATCAAGCCTGAGAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC  726
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Db        661 GACATCAAGCCTGAGAGACATTCTCGTTGACCGGACCACAGGACACATCAAGCCTGGTGGTGATTTT  720

Qy        727 GGATCTGCCGCGAAATGAATTGAATTCAAACAGATGTGATGCTGCAATGCCAAACTCCCGATTGGGACC  786
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Db        721 GGATCTGCCGCGAAATGAATTGAATTCAAACAGATGTGATGCTGCAATGCCAAACTCCCGATTGGGACC  780

Qy        787 CCAGATTACATGGCTCCTGAAGTGCTGACGTCGTGTGGTGATGAACGGGATGGAAAAGGCACCTAC  846
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Db        781 CCAGATTACATGGCTCCTGAAGTGCTGACGTCGTGTGGTGATGAACGGGATGGAAAAGGCACCTAC  840

Qy        847 GGCCTGGACTGTGACTGGTGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGA  906
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Db        841 GGCCTGGACTGTGACTGGTGGTGTCAGTGGGCGGTGATTGCCTATGAGATGATTATGGGAGA  900

Qy        907 TCCCCCTTCGGCAGGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG  966
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Db        901 TCCCCCTTCGGCAGGGGAACCCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG  960

Qy        967 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGC  1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTGATCTGATTCAAAGC  1020

Qy       1027 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTC  1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTC  1080

Qy       1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAG  1146
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Db       1081 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAG  1140

Qy       1147 TCCGACGATGACACCTCCAATTTGATGAACCAGAGGAATTCGTGGGTTTCATCCTCT  1206
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Db       1141 TCTGACGATGACACCTCCAATTTGATGAACCAGAGGAATTCGTGGGTTTCATCCTCT  1200

Qy       1207 CCGTGCCAGCTGAGCCCCTCAGGCTTCGGGGTGAAGAACTGCCGTTGTGTCGGGTTTTCG  1266
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Db       1201 CCGTGCCAGCTGAGCCCCTCAGGCTTCGGGGTGAAGAACTGCCGTTGTGTCGGGTTTTCG  1260

Qy       1267 TACAGCAAGGACTGGGATTCTTGGTAGATCGGAGTCTGAGTCGTGTCGTGTGTGTCGGGTCGGACTCC  1326
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Db       1261 TACAGCAAGGACTGGGATTCTTGGTAGATCGGAGTCTGAGTCGTGTCGTGTGTGTCGGGTCGGACTCC  1320

Qy       1327 CCTGCCAAGACTAGCTCCATGGAAAGAAAACTTCTCATCAAAAGCAAAAGAGCTACAAGAC  1386
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Db       1321 CCTGCCAAGACTAGCTCCATGGAAAGAAAAGAAAACTTCTCATCAAAAGCAAAAGAGCTACAAGAC  1380

Qy       1387 TCTCAGGACAAGTGTCACAAGGT  1409
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Db       1381 TCTCAGGACAAGTGTCACAAGAT  1403
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RESULT 12
AR534558
LOCUS       AR534558               6165 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6734009.
ACCESSION   AR534558
VERSION     AR534558.1  GI:53924885
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6165)
  AUTHORS   Yu,X.S.; Miranda,M. and Friddle,C.J.
  TITLE     Human kinases and polynucleotides encoding the same
  JOURNAL   Patent: US 6734009-A 1 11-MAY-2004;
FEATURES             Location/Qualifiers
     source          1..6165
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 6165;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative   0;  Mismatches   3;  Indels    0;  Gaps    0;
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Qy          7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGACGTGGTGCTGCTGAACCCATT  66
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Db   1   ATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAACCCCATT   60
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```
Qy   67  GCCAACCGGCCTCCAGGCTGAAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA   126
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCCAGCCGGCCGGGCCTCCAGGCTGAAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA   120
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Qy   127 CAGCAGATGTCTCCCTTCCCGAGAAGGGTATTAGATGCCCTTCTTGTCTCTTTGAA   186
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Db   121 CAGCAGATGTCTCCCTTCCCGAGAAGGGTATTAGATGCCCTTCTTGTCTCTTTGAA   180
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Qy   187 GAATGCAGTCAGCCGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT   246
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAATGCAGTCAGCCGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGGAAGTAT   240
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Qy   247 TCCGACACCATAGCTGAGTGTGTGTCACAGGACGTCCGGCAAAGGACTTCGAAGTCAGA   306
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Db   241 TCCGACACCATAGCTGAGTGTGTGTCACAGGACGTCCGGCAAAGGACTTCGAAGTCAGA   300
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Qy   307 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGG   366
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGG   360
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Qy   367 GACATCTATGCTATGAAAGTCATGAAGAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA   426
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA   420
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Qy   427 TTTTTGAGAAGAGAGGGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA   486
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTGAGAAGAGAGGGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA   480
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Qy   487 CAGTAGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG   546
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Db   481 CAGTAGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGAGGG   540
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Qy   547 GACTTGCTGTCACTTTGAATAGATATGAGGACCCAGTTAGAAAACCTGATACAGTTT   606
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Db   541 GACTTGCTGTCACTTTGAATAGATATGAGGACCCAGTTAGAAAACCTGATACAGTTT   600
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Qy   607 TACCTAGCTGAGCTGATTTGGCTTCACAGCCGTTCATCTGAATGGGATACGTGCATCGA   666
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCTAGCTGAGCTGATTTGGCTGTTCACAGCCGTTCATCTGAATGGGATACGTGCATCGA   660
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Qy   667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATTTT   726
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTCGGTGGATTTT   720
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Qy   727 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   786
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Db   721 GGATCTGCCGCGGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC   780
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Qy   787 CCAGATTACATGGCTCCTGAGTGCTGACTGGTGATGAACGGGATGGAAAAGGCACCTAC   846
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCAGATTACATGGCTCCTGAGTGCTGACTGGTGATGAACGGGATGGAAAAGGCACCTAC   840
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Qy   847 GGCCTGACTGTGACTGGTGTCAGTGGGCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA   906
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Db   841 GGCCTGGACTGTGACTGGTGTCAGTGGGCGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA   900
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Qy   907 TCCCCCTTCGCAGAGAGGGAACCTCTGCCCGACAACCTTCAATAACATTATGAATTTCCAGCGG   966
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Db   901 TCCCCCTTCGCAGAGAGGGAACCTCTGCCCGACAACCTTCAATAACATTATGAATTTCCAGCGG   960
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Qy   967 TTTTTGAAATTTCCAGATTTCTTCGGCAGTGAGCGAGTGACTTTCTTGATCTGATTCAAAGC   1026
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Db   961 TTTTTGAAATTTCCAGATTTCTTCGGCAGTGAGCGAGTGACTTTCTTGATCTGATTCAAAGC   1020
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Qy   1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCGCCATCCTTTCTTC   1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGCGCCATCCTTTCTTC   1080
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Qy   1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCGTTCCCACCCTCAAG   1146
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Qy   1147 TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT   1206
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Db   1141 TCTGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT   1200
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Qy   1207 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCCCGTTGTGGGGTTTCG   1266
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Db   1201 CCGTGCCAGCTGAGCCCCTCCAGGCTTCTCGGGTGAGAACTGCCCGTTGTGGGGTTTCG   1260
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Qy   1267 TACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTGTGTCGCGGCTCTGACTCC   1326
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Db   1261 TACAGCAAGGCACTGGGGATTCTTCGGTAGATCTGAGTCTGTGTCGCGGCTCTGACTCC   1320
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Qy   1327 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGAC   1386
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Db   1321 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAGAC   1380
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Qy   1387 TCTCAGGACAAGTGTCACAAGGT   1409
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Db   1381 TCTCAGGACAAGTGTCACAAGAT   1403
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RESULT 13
AX574425
LOCUS        AX574425                6165 bp    DNA      linear    PAT 07-JAN-2003
DEFINITION   Sequence 1 from Patent WO02059325.
ACCESSION    AX574425
VERSION      AX574425.1   GI:27551751
KEYWORDS
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Yu,X., Miranda,M. and Friddle,C.J.
  TITLE      Human kinases and polynucleotides encoding the same
  JOURNAL    Patent: WO 02059325-A 1 01-AUG-2002;
             Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1..6165
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 6165;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative  0;  Mismatches   3;  Indels   0;  Gaps   0;
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Qy   7   ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTCGTGCTGCTGAACCCCATT   66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTCGTGCTGCTGAACCCCATT   60
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Qy   67  GCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA   126
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCCAACCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA   120
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Qy   127 CAGCAGATGTCTCCGGCCTCGGATCGTGATTGCCTATGAGTTACAGGACTTTATGACTCAA   186
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Db   121 CAGCAGATGTCTCCGGCCTCGGATCGTGATTGCCTATGAGTTACAGGACTTTATGACTCAA   180
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Qy   187 CAGCAGATGTCTCCTCCTCTTTCCCGAGAGGGATATTAGATGCCCTTTGTGTTCTCTTTGAA   186
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Qy   187 CAGCAGATGTCTCCTCCTCTTTCCCGAGAGGGATATTAGATGCCCTTTGTGTTCTCTTTGAA   246
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Db   181 CAGCAGATGTCTCCTCCTCTTTCCCGAGAGGGATATTAGATGCCCTTTGTGTTCTCTTTGAA   240
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Qy   247 TCCGACACCATAGCTGAGTTACAGGACTCGAGTTACAGGACTTCGAAGTCAGA   306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCCGACACCATAGCTGAGTTACAGGACTCGAGTTACAGGACTTCGAAGTCAGA   300
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Qy   307 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGCTCAGGTGCTGAAGTCGAACCGGG   366
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LOCUS           AX671105                6165 bp    DNA        linear   PAT 27-MAR-2003
DEFINITION      Sequence 1 from Patent WO03004523.
ACCESSION       AX671105
VERSION         AX671105.1  GI:29329569
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
  AUTHORS       Zhu,Z.
  TITLE         Regulation of human citron rho/rac-interacting kinase
  JOURNAL       Patent: WO 03004523-A 1 16-JAN-2003;
                Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..6165
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             92.3%;  Score 1398.2;  DB 6;  Length 6165;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 1400;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    0;
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Qy          7 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT 60

Qy         67 GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCTTTATGACTCAA 126
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Db         61 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCTTTATGACTCAA 120

Qy        127 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
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Db        121 CAGCAGATGTCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180

Qy        187 GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT 246
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Qy        247 TCCGACACCATAGCTGAGTTACAGGAGCTCAGGAGGGTACGGACTTCGGCAAAGGACTTCGAAGTCAGA 306
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Db        241 TCCGACACCATAGCTGAGTTACAGGAGCTCAGGAGGGTACGGACTTCGGCAAAGGACTTCGAAGTCAGA 300

Qy        307 AGTCTTGTAGGTGTGTCACTTTGCTGAAGTGCAGGTGGTAAGAGGAAAGCAACCGGG 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTCTTGTAGGTGTGTCACTTTGCTGAAGTGCAGGTGGTAAGAGGAAAGCAACCGGG 360

Qy        367 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGGTTTCA 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGGTTTCA 420

Qy        427 TTTTTTGAGGAAGAGCGGAACACATATATCTCGAAGCACAAGCCGTGAATATCAGCCTGGAGGG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTTTTGAGGAAGAGCGGAACACATATATCTCGAAGCACAAGCCGTGAATATCAGCCTGGAGGG 480

Qy        487 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 546
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Db        481 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540

Qy        547 GACTTGCTGTCACTTTTGAATAGATATGAGGACACCAGTTAGATGAAAACCTGATACAGTTT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTTGCTGTCACTTTTGAATAGATATGAGGACACCAGTTAGATGAAAACCTGATACAGTTT 600

Qy        607 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAGCTGAGCTGATTTTGGCTGTTCATCTGATGGGATACGTGCATCGA 660

Qy        667 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACACATCAAGCTCGTGGATTTT 726
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Qy        367 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGGCAGGTTTCA 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTATTGGCCAGGAGGCAGGTTTCA 420

Qy        427 TTTTTTGAGGAAGAGCGGAACATATTCTGAAGCACAAGCCCTTATTGGCCCCAATTA 486
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Db        421 TTTTTTGAGGAAGAGCGGAACATATTCTGAAGCACAAGCCCTTATTGGCCCCAATTA 480

Qy        487 CAGTATGCCTTTCAGGACAAAAATCACCTTTAGTAGAGAACCTGATACAGTTT 546
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Db        481 CAGTATGCCTTTCAGGACAAAAATCACCTTTAGTAGAGAACCTGATACAGTTT 540

Qy        547 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 606
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Db        541 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 600

Qy        607 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 660

Qy        667 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 726
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Db        661 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 720

Qy        727 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780

Qy        787 CCAGATTACATGGCTCCTGAAGTGCTCTGACTGTGACTGTGACTGATGAAAAGGCACCTAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAGATTACATGGCTCCTGAAGTGCTCTGACTGTGACTGTGACTGATGAAAAGGCACCTAC 840

Qy        847 GGCCTGGACTGGACTGTGACTGGGCGCGTGAGTTGAAGGTCTTGAAGGTCTTGAAGGATTATGGGAGA 906
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Db        841 GGCCTGGACTGGACTGTGACTGGGCGCGTGAGTTGAAGGTCTTGAAGGATTATGGGAGA 900

Qy        907 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960

Qy        967 TTTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTCAGTGAATTCTTGATTCAAAGC 1026
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Db        961 TTTTTTGAAATTCCAGATGACCCCAAAGTGAGCAGTCAGTGAATTCTTGATTCAAAGC 1020

Qy       1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1086
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Db       1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1080

Qy       1087 TCTAAAATTGACTGGAACAACATTCGTAACCTCTCCCCCCTTCGTTCCCACCCTCAAG 1146
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Query Match   92.3%;   Score 1398.2;   DB 6;   Length 8603;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1400; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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VERSION   AX671108.1   GI:29329570
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REFERENCE   1
  AUTHORS   Zhu,Z.
  TITLE   Regulation of human citron rho/rac-interacting kinase
  JOURNAL   Patent: WO 03004523-A 4 16-JAN-2003;
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ORIGIN

Mon Mar 21 11:57:50 2005

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Qy    1087 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAG 1146
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